LEIBNIZ-INSTITUT FÜR PFLANZENGENETIK UND
KULTURPFLANZENFORSCHUNG (IPK)

Forschungsbericht
Scientific Report 2010/2011

Leibniz Gemeinschaft

IPK GATERSLEBEN

Leibniz Institute of Plant Genetics and Crop Plant Research (IPK)

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[1)] Management

LEIBNIZ-INSTITUT FÜR PFLANZENGENETIK UND KULTURPFLANZENFORSCHUNG (IPK)

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Vorwort

Im vor uns liegenden Jahr jährte sich die Neugründung des Instituts am 1. Januar 1992 zum 20. Mal. Dieses Jubiläum gibt Anlass zur Rückschau auf eine Zeit, in der das Institut sich, zweifelsohne mit großem Erfolg, in der neu gestalteten gesamtdeutschen Wissenschaftslandschaft etablieren konnte. Basierend auf dem Einsatz aller Mitarbeiter und der Unterstützung durch Land und Bund nimmt das IPK heute eine weithin sichtbare Rolle in der internationalen Pflanzenforschung ein. Die Forschungsarbeiten reichen von der Bearbeitung grundlegender Fragestellungen der Samenentwicklung und der Fortpflanzungsbiologie, der Erforschung spezieller Chromosomenstrukturen oder dem Studium von Artbildungs- und Anpassungsmechanismen bis hin zu angewandten Fragestellungen mit Bezügen zur Pflanzenzüchtung und Pflanzenernährung sowie zur Biotechnologie.

Seit dem Jahr der Neugründung des IPK stieg die Erdbevölkerung um weitere 1,5 Milliarden auf aktuell 7 Milliarden Menschen an. Die tägliche Bevölkerungszunahme beträgt damit rund 200.000 Menschen, deren Lebensgrundlagen es zu sichern gilt. Angesichts der weltweit begrenzten Verfügbarkeit landwirtschaftlicher Nutzflächen erfordert die Deckung des Bedarfs an Nahrungsmitteln, erneuerbaren Energien und nachwachsenden Rohstoffen eine leistungsfähige Pflanzenproduktion. Die am Institut erarbeiteten Erkenntnisse liefern Beiträge für die züchterische Verbesserung von Kulturpflanzen, insbesondere im Hinblick auf die Steigerung des Ertrags, die Verbesserung der Nährstoffeffizienz und die Erhöhung der Resistenz bzw. Toleranz gegenüber biotischen und abiotischen Stressfaktoren. Letzteren kommt angesichts der Veränderung des Klimas - 2010 war das wärmste Jahr seit Beginn der Wetteraufzeichnungen - eine besonders große Bedeutung zu.

Die am Institut durchgeführten Forschungsarbeiten zur Aufklärung der Struktur und Funktion der Genome wichtiger Kulturpflanzen werden langfristig die Grundlage für die Nutzung der in der Genbank erhaltenen pflanzengenetischen Ressourcen darstellen. Hierbei gilt es auch die Potenziale der Grünen Gentechnik auszuschöpfen. Dies betrifft zum einen den Einsatz gentechnischer Verfahren als Hilfsmittel bei der Bearbeitung verschiedenster wissenschaftlicher Fragestellungen und zum anderen die Nutzung und Weiterentwicklung der Grünen Gentechnik zur Verbesserung pflanzlicher Merkmale und Eigenschaften, der Entwicklung verbesserter Züchtungsverfahren sowie die Verwendung von Pflanzen als Bioreaktor für die Erzeugung neuartiger

Introduction

In 2012 IPK will celebrate the twentieth anniversary of its refoundation, a milestone which prompts us to take a retrospective look back over the period during which the Institute has succeeded so well in cementing a firm place in the much altered German scientific landscape. Building on the enthusiasm, knowledge and skills of our employees, and based on continuing financial support from both the State of Saxony-Anhalt and the Federal Government, IPK has achieved a high degree of visibility in the international plant science community. Its activities span the range of plant science research, from fundamental topics such as seed development and reproductive biology, chromosome structure and function, adaptation and speciation, to more applied ones such as crop improvement, plant nutrition and biotechnology.

Since 1992, the size of the world's population has risen by 1.5 billion to reach its current level of seven billion, equivalent to a daily increase of some 200,000 people, all of whose livelihoods need to be secured. Given that the area of arable land is necessarily capped, the growing demand for food, renewable energy and renewable materials requires a steep change in crop productivity. The IPK research programme makes a unique contribution in the area of genetic-based crop improvement, with a special emphasis on increasing yield, nutrient use efficiency and the level of resistance and/or tolerance to both biotic and abiotic stress. The latter is particularly important in the context of global climate change, a process which was hard to ignore during 2010, globally the warmest year on record.

Research targeted at elucidating the structure and understanding the functioning of key crop genomes is likely to drive the utilization of the genetic resources maintained in the IPK Genebank. Gene technology can be expected to play an important role, both by allowing the means to study a number of the most fundamental aspects of plant biology, and by helping to improve the expression of crop traits (such as, for example, abiotic stress tolerance) which have proven so difficult to manipulate using conventional breeding technology. A further potential area for the application of transgenesis in plants lies in developing bioreactors able to synthesize novel chemical compounds, antigens or antibodies in an inexpensive and environmentally benign manner. The controversial (at least in Europe) nature of genetically modified (GM) plants and the dwindling political support for this technology notwithstand-

Stoffe, wie z. B. Antikörpern. Trotz der kontroversen Diskussion zur Grünen Gentechnik in Europa und ungeachtet der schwindenden politischen Unterstützung der Grünen Gentechnik sieht sich das Institut weiterhin in der wissenschaftlichen Verantwortung, die Potenziale dieser Technologie zu erforschen.

Ebenfalls im Jahr 2012 jährt sich die Verabschiedung der Konvention über die Biologische Vielfalt zum 20. Mal. Mit dem Abkommen sollen der Erhalt der biologischen und genetischen Vielfalt, ihre Nutzung und Nutzbarmachung sowie der Zugang und der Vorteilsausgleich langfristig gesichert werden. Die Bundeszentrale *Ex-situ*-Genbank am IPK stellt einen zentralen Pfeiler zum Erreichen der genannten Ziele im Zuge des „Nationalen Fachprogramms zur Erhaltung und nachhaltigen Nutzung pflanzengenetischer Ressourcen landwirtschaftlicher und gartenbaulicher Kulturpflanzen" dar. Die große Nachfrage nach Material aus der Genbank stellt einen Beleg für die Bedeutsamkeit der IPK-Sammlungen für Forschung, Züchtung sowie weitere Anwendungen dar.

Ohne Zweifel ist die Sicherung der Lebensgrundlagen der Menschen an die weitere Verbesserung der Leistungsfähigkeit unserer Kulturpflanzen gebunden. Leistungsfähige, ausschließlich an wissenschaftlicher Exzellenz orientierte Grundlagenforschung ist der Nährboden für die Erarbeitung von Lösungen, die in den kommenden Jahrzehnten verfügbar sein müssen. Auf diesem Weg gilt es auch, den Erkenntnisgewinn aus der Grundlagenforschung so rasch wie möglich in Anwendungen zu überführen. Dies erfordert die Aufklärung der genetischen, biochemischen und zellbiologischen Prozesse, die an der Ausprägung der Leistungsmerkmale von Pflanzen beteiligt sind und ihre Anpassung an unterschiedliche Umweltbedingungen bewirken. Dem enormen technischen Fortschritt auf dem Gebiet der DNA-Sequenzierung und der Analyse von primären und sekundären Metaboliten des pflanzlichen Stoffwechsels standen bisher nur begrenzte Möglichkeiten zur Erfassung phänotypischer Merkmale gegenüber. Aus diesem Grund hat das Institut in den vergangenen Jahren neben dem kontinuierlichen Ausbau der experimentellen Laborinfrastruktur umfangreiche Investitionen im Gewächshausbereich vorgenommen. Mit Hilfe modernster Methoden der Bilderfassung wird es möglich sein, weitestgehend unabhängig von störenden Umwelteinflüssen, zeitliche Wachstumsverläufe systematisch zu erfassen. Die angestrebten Verbesserungen in der phänotypischen Analyse werden vor allem die Aufklärung quantitativ vererbter Merkmalskomplexe ermöglichen.

Vor diesem Hintergrund wurden in den vergangenen beiden Jahren wieder eine Reihe interessanter und wichtiger Forschungsergebnisse erzielt, welche wichtige Beiträge sowohl zur Aufklärung grundlegender als auch angewandter Fragestellungen lieferten. Einzelheiten hierzu finden Sie in dem vorliegenden Forschungsbericht.

Andreas Graner
Geschäftsführender Direktor

ing, the Institute recognizes its major scientific responsibility to continue leading the public-funded research effort aimed at assessing the true potential of GM technology.

The year 2012 also marks the twentieth anniversary of the signing of the Convention on Biodiversity (CBD) by 193 parties, a treaty which attempted to ensure the long-term conservation, utilization and valorization of biodiversity, as well as providing a framework to regulate access to germplasm and introduce mechanisms for benefit sharing. The IPK Genebank, which curates a range of agricultural and horticultural crop species, is a central component of the German "National Programme for the Conservation and Utilization of Plant Genetic Resources". The continuing high demand of the international plant science community for samples of Genebank accessions is a measure of the importance of the collection for research, crop breeding and other uses.

There can be no doubt that securing human livelihood requires the continuing improvement of our crop plants. High profile fundamental research, which is predicated first and foremost on scientific excellence, lays the groundwork for developing solutions to many of the most pressing societal challenges. At the same time, there is a need to convert the knowledge emerging from basic research into practical applications. This paradigm requires that the genetic, biochemical and cell biological processes which underlie agronomic performance and environmental adaptation be elucidated as a priority. The enormous technical advances achieved in the ability to both sequence DNA and to identify primary and secondary metabolites currently greatly outstrips our capacity to analyse variation in phenotype and specific plant traits. This gap is being addressed by the Institute through a series of substantial investments in the technical infrastructure required to systematize the assessment of phenotype. The establishment of highly automated image analysis systems should allow, for example, an accurate description of temporal growth patterns. The hoped-for improvements in phenotypic analysis will have a major beneficial impact on the measurement of those quantitative traits which lie at the heart of crop productivity.

Against this backdrop, the IPK research programme over the past two years has yielded a series of exciting and important results, addressing both fundamental and applied research questions. Further details are given in the research report which follows this brief overview.

Andreas Graner
Managing Director

Das Leibniz-Institut für Pflanzengenetik und Kulturpflanzenforschung (IPK)

Aufgabenstellung und Finanzierung

Das IPK wurde auf der Grundlage von Vorgängereinrichtungen 1992 als eine Stiftung des öffentlichen Rechts gegründet und ist Mitglied der Leibniz-Gemeinschaft. Sein Zuwendungsbedarf wird gemäß Artikel 91 b des Grundgesetzes nach dem Finanzierungsmodell der „Blauen Liste" zu gleichen Teilen von Bund und Sitzland (plus Länderanteile) erbracht. Zuwendungsgeber ist das Land Sachsen-Anhalt, vertreten durch die Ministerin für Wissenschaft und Wirtschaft.

„Zweck der Stiftung ist die Förderung von Wissenschaft und Forschung. Ihre Aufgabe ist, grundlagen- und anwendungsorientierte Forschung auf den Gebieten der Pflanzengenetik und Kulturpflanzenforschung zu betreiben. Ihre wissenschaftlichen Schwerpunkte liegen insbesondere auf der Erarbeitung neuer Erkenntnisse über Struktur, Funktion und Evolution des Erbmaterials, auf der Erhaltung, Erforschung und Erschließung der erblichen Vielfalt von Kulturpflanzen, ihrer Vorfahren und Verwandten sowie auf Beiträgen zur Züchtungsgenetik im Vorfeld der praktischen Pflanzenzüchtung. Ein wesentliches Anliegen der Stiftung ist die interdisziplinäre Zusammenarbeit der verschiedenen in ihr vertretenen biologischen Fachrichtungen." (zitiert aus der IPK-Satzung)

Durch die Kombination von Grundlagen- und angewandter Forschung mit Fokus auf Kulturpflanzen sieht sich das Institut gleichermaßen prädestiniert und verpflichtet, Beiträge zur Lösung zukünftiger Herausforderungen auf den Gebieten der Nahrungssicherung, der Erzeugung nachwachsender Rohstoffe und erneuerbarer Energien, der Nachhaltigkeit sowie der Anpassung von Kulturpflanzen an den Klimawandel zu erarbeiten. Entsprechende Forschungsarbeiten schließen sowohl die Nutzbarmachung biologischer Vielfalt als auch die Entwicklung und Anwendung biotechnischer Verfahren ein.

Stiftungsorgane, Funktionsträger und Organisationsstruktur des IPK

Organe der Stiftung sind der **Stiftungsrat**, das **Direktorium** und der **Wissenschaftliche Beirat.** Für die speziellen Belange der Bundeszentralen *Ex-situ*-Genbank steht dem Wissenschaftlichen Beirat der **Genbank-Beirat** zur Seite. Die personelle Zusammensetzung der Beiräte im Berichtsjahr ist in einer Übersicht auf S. 283 dargestellt. Die Übersicht führt zudem die IPK-Mitarbeiterinnen und Mitarbeiter auf, die mit speziellen Funktionen innerhalb des IPK betraut waren und sind.

The Leibniz Institute of Plant Genetics and Crop Plant Research (IPK)

Objectives and Funding

The IPK was formally re-established in 1992 as a Foundation under Public Law, continuing an unbroken tradition reaching back to the Kaiser-Wilhelm-Institute of Crop Plant Research, which was founded in 1943 near Vienna (Austria) and moved to Gatersleben in 1945. It is administered under the legal and administrative supervision of the State of Saxony-Anhalt. According to article 91b of the Federal Constitution its funding is provided by Ministry of Science and Economy of the State of Saxony-Anhalt (along with contributions from other German States), and by the Federal Ministry of Education and Research.

The Institute's statutes state: '*The mission of the Foundation is the advancement of science and research. Its goals are to carry out basic and application-oriented research in the fields of plant genetics and crop plant research. Special emphasis is given to the generation of new knowledge on the structure, function and evolution of genetic material, on the preservation, research and use of the biodiversity of crop plants and their wild relatives, as well as contributions to applied genetics with regard to crop breeding. A major concern of the Foundation is to encourage interdisciplinary cooperation of the various biological disciplines in the Institute.*' (translated from the German original)

By the combination of basic and applied research with emphasis on cultivated crop species the Institute considers itself both predestinated and obliged to develop contributions to solve future challenges regarding food security, the generation of renewable resources and renewable energies, sustainability and the adaptation of crop plants to a changing climate. Corresponding research activities include both, the utilisation and valorisation of plant genetic resources as well as the development and deployment of biotechnological approaches.

Boards, Staff with Functional Responsibilities and Organisational Structure of the IPK

The organisational bodies of the Foundation are the **Governing Council**, the **Board of Directors** and the **Scientific Advisory Board** which is supported by the **Genebank Advisory Board**. Members of these bodies are listed on p. 283. In addition, the list includes all IPK staff members with specific responsibilities.

Das IPK ist in vier wissenschaftliche **Abteilungen** (Genbank, Cytogenetik und Genomanalyse, Molekulare Genetik, Physiologie und Zellbiologie) und die Abteilung Verwaltung und Zentrale Dienste gegliedert. Die einzelnen Abteilungen untergliedern sich wiederum in Forschungsbereiche und Arbeitsgruppen (s. Organigramm, innere Umschlagseite). Als abteilungsübergreifende Struktureinheit mit spezieller Aufgabenstellung fungiert das **Pflanzengenom-Ressourcen-Centrum (PGRC)** (s. S. 151). Darüber hinaus werden die Forschungs- und Entwicklungsarbeiten im Bereich **Bioinformatik** abteilungsübergreifend koordiniert (s. S. 153). Die Einwerbung von Drittmitteln resultiert in einer wesentlichen Aufstockung der Personal- und Forschungsmittelausstattung (s. Drittmittelübersicht S. 249 ff).

Forschungskonzept

Die strategische und inhaltliche Ausrichtung der Forschungsarbeiten am Institut wird in einer jährlich aktualisierten Programmplanung festgelegt, die folgende Programme umfasst:

1. **Management, Analyse und Evolution pflanzengenetischer Ressourcen** (Abteilung Genbank)
2. **Cyto-molekulare Genomanalyse** (Abteilung Cytogenetik und Genomanalyse)
3. **Molekulare Entwicklungsphysiologie** (Abteilung Molekulare Genetik)
4. **Angewandte Physiologie und Zellbiologie** (Abteilung Physiologie und Zellbiologie).

Die Programmthemen spiegeln in wesentlichen Zügen die sich komplementierenden zentralen Arbeitsfelder der Abteilungen wider und werden in den einführenden Abteilungskapiteln näher spezifiziert.

Im Rahmen der genannten, weitgehend disziplinär ausgerichteten Forschungsprogramme werden Beiträge zu drei großen Schwerpunkten erarbeitet:

(a) Forschung zur **Erschließung, Erhaltung und Nutzung genetischer Diversität**, welche in erster Linie die aus der Genomanalyse gewonnenen Erkenntnisse nutzt, um die genetischen Grundlagen der enormen Vielfalt pflanzlicher Formen und Leistungen zu verstehen und taxonomisch zu ordnen um daraus Handlungsanweisungen für eine bessere Erhaltung und Nutzung pflanzengenetischer Ressourcen zu gewinnen;

(b) Forschung zur **Dynamik pflanzlicher Genome**, die das Bild von der Starrheit der Genome zunehmend ändert und insbesondere die Rolle epigenetischer (bedingt vererbbarer, nicht auf DNA-Sequenzebene wirkender) Prozesse erhellt, deren Kenntnis mehr und mehr praktische Bedeutung gewinnt und

The Institute is structured into four scientific departments (Genebank, Cytogenetics and Genome Analysis, Molecular Genetics, Physiology and Cell Biology), and the Department of Administration and Central Services. The departments are further divided into Programmes ('Bereiche') and research groups (see organisation chart inside back cover). The **Plant Genome Resources Centre (PGRC, p. 151)** performs tasks relevant to all departments. Regarding Bioinformatics, research and service activities in the different departments are coordinated via the **IPK Bioinformatics Platform (p. 153)**. Extramural funding contributes substantially to the implementation of the research programme (cf. survey on p. 249)

Research Mission

The strategic development of the research programme is outlined in a budgeted programme that is annually updated. It presently comprises the following fields:

1. **Management, Analysis and Evolution of Plant Genetic Resources** (Genebank)
2. **Cyto-molecular Genome Analysis** (Cytogenetics and Genome Analysis)
3. **Molecular Physiology of Development** (Molecular Genetics)
4. **Applied Physiology and Cell Biology** (Physiology and Cell Biology).

The topics mirror the complementing research fields of the individual departments. Details are described in the relevant departmental reports.

The research fields contribute to three priority themes of contemporary plant research, which are outlined in the strategic research agenda of the IPK as follows:

(a) **Conservation and Utilisation of Crop Plant Diversity**, which applies the knowledge gained from the analysis of genomes to understand the genetic basis of plant diversity and to create a taxonomic order. The corresponding insights will leverage the use of plant genetic resources.

(b) **Dynamics of Plant Genomes**, which is increasingly challenging the conventional static picture of the genome and is leading to a realisation of the importance of epigenetic processes. This knowledge is becoming of increasing practical significance.

(c) **Integrative Biology of Plant Performance**, which strives to generate a holistic understanding of plants based on multidisciplinary investigation, incorporating a strong component of bioinformatics aiming at modelling of metabolic processes, i. e. pursuing a Systems Biology approach.

(c) systembiologisch orientierte Forschung zur **integrativen Biologie pflanzlicher Leistungen**, die aus der Fülle der mit neuen Methoden gewonnenen Daten versucht, systematische Zusammenhänge zu entwickeln, diese zu modellieren und daraus ein neues Verständnis des komplexen Systems Pflanze zu gewinnen.

Vor dem Hintergrund der in der Genbank erhaltenen Kulturpflanzenvielfalt konzentrieren sich die Forschungsarbeiten in erster Linie auf landwirtschaftlich bedeutsame Pflanzenarten. Die Arbeiten an Gerste als Modellsystem für die Genomanalyse für Getreide wurden in den vergangenen Jahren auf Weizen, Mais und Raps ausgeweitet. Nach der erfolgreichen Etablierung einer leistungsfähigen technischen und bioinformatischen Infrastruktur für die Genomforschung werden methodenorientierte Forschungs- und Entwicklungsansätze zunehmend durch die Bearbeitung biologischer Fragestellungen ergänzt. Spezielle Fragen zur Samenentwicklung werden seit vielen Jahren an Leguminosen untersucht. Die Bearbeitung einer Reihe grundlegender Fragestellungen erfolgt in Modellpflanzen wie *Arabidopsis,* Tabak und *Hypericum*. Ergänzend hierzu werden ausgewählte Forschungsthemen zur angewandten Biotechnologie an Hefe bearbeitet.

Integrative Strukturen und Netzwerke

Das IPK verfügt über abteilungsübergreifende Strukturen, welche zum einen als Plattformen für interne Dienstleistungen und wissenschaftliche Querschnittsaktivitäten dienen. Daneben ist das Institut in über die Projektförderung hinaus gehende nationale und internationale Forschungskooperationen eingebunden. Diese dienen der Entwicklung und Förderung langfristiger Kooperationsprojekte, der Einwerbung von Projektmitteln und der Gewinnung von wissenschaftlichem Nachwuchs.

Das 1997 gegründete **Pflanzengenom-Ressourcen-Centrum (PGRC)** bildet eine Dienstleistungsplattform für die DNA-Sequenzierung und die DNA-Markeranalyse. Weitere Informationen zum PGRC finden sich auf Seite 151.

Die **IPK-Bioinformatik-Plattform** ist eine koordinative Struktur, in der alle in den verschiedenen Abteilungen angesiedelten Bioinformatik-Gruppen vernetzt sind. Im Berichtszeitraum wurde der Bereich Bioinformatik durch Etablierung einer Arbeitsgruppe zur Bildanalyse verstärkt. Weitere Einzelheiten sind auf Seite 153 zu finden.

Das 2003 gegründete **Europäische Genomforschungs-Netzwerk Gerste (BarleyGenomeNet – BGN)** ist ein Zusammenschluss von Forschungseinrichtungen, welche sich schwerpunktmäßig mit der Genomforschung bei Gerste befassen. Neun Einrichtungen aus fünf europäischen Ländern kooperieren gegenwärtig im Rahmen verschiedener EU-Verbundprojekte. Weitere Einzelheiten sind unter www.barleynet.org zu finden.

Against the backdrop of the large number of species maintained by the Genebank research activities of the Institute mainly focus on agriculturally important crop plants. Barley (*Hordeum vulgare*) has been developed as a model system for the *Triticeae* cereals owing to its agronomic importance and its elaborate genetics. After having established the technical and bioinformatic infrastructure to perform systematic genome research in this species the research portfolio of the Institute has been stepwise expanded to include other priority crops like wheat, maize and rapeseed. In addition, specific questions of seed development are being investigated in legumes. While the above mentioned crop species are mostly the target for applied research, model organisms such as *Arabidopsis*, *Nicotiana* and *Hypericum* are employed to study fundamental questions in plant biology. In addition, yeast (*Arxula adeninivorans*) is being used as a system for research and development in the field of applied biotechnology.

Integrative Structures and Networks

The Institute has established platforms for internal services and scientific cross section activities. Beyond the level of individual projects IPK is embedded in national and international research cooperations, aiming at promoting long-term collaborations, the acquisition of research grants and to attract young scientists.

The **Plant Genome Resources Centre (PGRC)**, established in 1997, represents a service platform for DNA sequencing and DNA marker analysis (see p. 151).

Research into Bioinformatics is being performed in close collaboration with the experimental groups. In order to warrant a tight interaction of the individual bioinformatics groups both within the Institute and with the University, the coordinator of the **IPK Bioinformatics Platform** is jointly appointed with the University of Halle. In the reporting period the research group "Image Analysis" has been established and now forms an integral constituent of the Platform (see p. 153).

The **European Barley Genomic Research Network** (Barley GenomeNet, BGN) was founded in 2003, and represents a consortium of presently nine institutions from five European countries focussing on genome research in barley. BGN partners presently collaborate within several EU projects. Further information can be retrieved from the BGN website (www.barleynet.org).

In 2006 the **International Barley Sequencing Consortium** (IBSC, http://barleygenome.org) was founded. The consortium presently comprises nine members from seven countries and aims at generating a full genome sequence of barley based on a continuously updated research agenda.

Das **"International Barley Sequencing Consortium"** (IBSC, http://barleygenome.org) wurde im Dezember 2006 gegründet. Das Ziel ist die Totalsequenzierung des Gerstengenoms. Die Arbeiten basieren auf einer unter den neun Mitgliedsinstitutionen aus sieben Ländern fortwährend abgestimmten Forschungsagenda.

Ergänzend zu den genannten Plattformen und Verbünden gibt es ein umfangreiches Netzwerk von nationalen und internationalen Verbundprojekten, sowie arbeitsgruppen- und abteilungsübergreifenden IPK-internen Projekt-Kooperationen. Ergänzend zu den bestehenden Kooperationen mit der Martin-Luther-Universität Halle, der Universität Kiel und dem National Institute for Agrobiological Sciences (NIAS) in Tsukuba, Japan, wurde im Dezember 2010 die Zusammenarbeit mit dem Julius Kühn-Institut (Quedlinburg) durch eine Kooperationsvereinbarung formalisiert und abgesichert.

In addition to the platforms and networks mentioned above, there is an extensive network of collaborations within the Institute across research groups and departments. Numerous national and international cooperations are being maintained. To further extend ongoing cooperation with the University of Halle, the University of Kiel and the National Institute for Agrobiological Sciences (NIAS) in Tsukuba, Japan a collaboration agreement was signed with the Julius Kühn-Institute (JKI), Quedlinburg in December 2010.

Das Institut in den Jahren 2010 und 2011

Die vergangenen zwei Jahre waren durch eine Fülle interessanter Forschungsergebnisse, die Weiterentwicklung der wissenschaftlich-technischen Infrastruktur, umfangreiche Drittmitteleinwerbung und fortgesetzte nationale und internationale Kooperationen gekennzeichnet. Neben der Erhaltung der pflanzengenetischen Ressourcen in der Bundeszentralen *Ex-situ*-Genbank und den damit verbundenen Dienstleistungsaufgaben erstreckten sich die Forschungsaktivitäten von der Aufklärung grundlegender biologischer Prozesse bis hin zu Bearbeitung angewandter Fragestellungen im Vorfeld der Pflanzenzüchtung und der Biotechnologie. Damit engagiert sich das Institut auf mehreren, der in der nationalen Forschungsstrategie der Bundesregierung „BioÖkonomie 2030" aufgeführten Handlungsfeldern und leistet vielfältige Beiträge zur Realisierung der darin dargelegten Ziele. Nachfolgende Abschnitte sollen dem Leser einen raschen Überblick zu den wichtigsten Entwicklungen am IPK vermitteln. Weitere Informationen zu den Forschungsarbeiten sind den Berichten der Abteilungen und der einzelnen Arbeitsgruppen zu entnehmen.

Organisatorische Veränderungen

Zum 1. Januar 2010 übernahm Sybille-Andrea Lorenz als Nachfolgerin von Bernd Eise die administrative Leitung des IPK.

Am 1. Mai 2010 nahm die Arbeitsgruppe (Ag) Bildanalyse unter der Leitung von Dr. Christian Klukas ihre Arbeit auf. Die Arbeitsgruppe erarbeitet u. a. neue Auswertealgorithmen für die Analyse von Bilddaten, die im Zusammenhang mit der automatisierten Phänotypisierung anfallen.

Seit dem 1. November 2010 wird die durch das Interdisziplinäre Zentrum für Nutzpflanzenforschung finanzierte Nachwuchsgruppe Stress-Genomik von Dr. Nese Sreenivasulu geleitet. Hauptgegenstand der Forschungsarbeiten ist die Aufklärung von Genregulationsnetzwerken sowie der Rolle des Pflanzenhormons Abscisinsäure (ABA) bei der Anpassung von Getreide an Trockenstress.

Ende 2010 ging die Leiterin der Ag *In-vitro*-Differenzierung, Prof. Dr. Anna Wobus, in den Ruhestand. Ein Teil der Forschungsarbeiten zu embryonalen Stammzellen wird an der Martin-Luther-Universität in Halle weitergeführt.

Im August 2011 wurde die Ag Expressionsanalyse (Leiter Dr. Lothar Altschmied) in die Ag Heterosis (Leiter: Prof. Dr. Thomas Altmann) integriert.

Zum 1. Januar 2012 wurde die Ag Taxonomie Pflanzengenetischer Ressourcen in die Ag Experimentelle Taxonomie (Leiter Dr. Frank Blattner) überführt.

The Institute in 2010 and 2011

The past two years have seen a number of notable research outcomes, the ongoing development of the research infrastructure involving new build, capital equipment and plant growth facilities, the winning of substantial external funding, and the cementing of current national and international collaborations. In addition to the conservation of plant genetic resources in the IPK Genebank and associated services, the Institute's research activities have included topics ranging from the analysis of fundamental biological processes to applied questions related to crop breeding and biotechnology. In this way, the Institute has involved itself in several of the fields of actions outlined in "BioEconomy 2030" (a national strategy of the German Federal Government). An overview of the most important developments during the reporting period is given below. More detailed information regarding the research programmes can be found in the reports produced by the individual departments and research groups.

Organizational changes

Following the retirement of Bernd Eise at the end of 2009, Sybille-Andrea Lorenz became the Institute's head of administration.

The "Image Analysis" research group, led by Dr. Christian Klukas, was established on 1 May 2010. The group's mandate centres mainly on the development and implementation of novel algorithms required for the analysis of the imaging data generated by automated phenotyping platforms.

The "Stress Genomics" research group was initiated 1 November 2010, led by Dr. Nese Sreenivasulu and funded by the Interdisciplinary Centre of Crop Plant Research at the Martin Luther University, Halle. Its focus lies in the analysis of regulatory gene networks and the role of the phytohormone abscisic acid in the adaptation of plants to drought stress.

Prof. Anna Wobus, head of the "*In vitro* Differentiation" research group retired at the end of 2010, and the group was discontinued. Part of its research programme has been transferred to the Martin Luther University, Halle.

In August 2011 the "Expression Analysis" research group led by Dr. Lothar Altschmied was incorporated into the "Heterosis" research group, headed by Prof. Thomas Altmann.

On 1 January 2012 the "Taxonomy of Plant Genetic Resources" research group was merged with the "Experimental Taxonomy" research group headed by Dr. Frank Blattner.

Entwicklungen von zentraler Bedeutung

(1) Die Einwerbung von Drittmitteln stellt eine wichtige Grundlage für die Umsetzung des Forschungsprogramms dar. Im Berichtszeitraum hat sich das Institut in verschiedenen Förderprogrammen, allen voran in der vom BMBF aufgelegten Förderlinie „Pflanzenbiotechnologie der Zukunft", erfolgreich um die Einwerbung von Drittmitteln bemüht. Daneben konnten im Jahr 2011 Fördermittel aus dem *WGL* Pakt für Forschung und Innovation für den Aufbau einer Graduiertenschule zum Thema „Yield formation in cereals – overcoming yield-limiting factors" eingeworben werden. Erfreulich ist auch der Anstieg von eingeworbenen Fördermitteln der DFG. Diese stellen ein wichtiges Exzellenzkriterium dar. Der guten Drittmittelsituation entsprechend waren im Berichtszeitraum durchgängig über 500 Personen am Institut beschäftigt.

(2) Forschungsergebnisse wurden in den vergangenen beiden Jahren in 306 Artikeln in referierten Fachzeitschriften veröffentlicht. Hinzu kommen 46 Publikationen, die als Buchbeiträge erschienen sind.
Im Zuge der Ausbildung von wissenschaftlichem Nachwuchs wurden im Berichtszeitraum 20 Bachelor-, 14 Diplom- und 7 Masterarbeiten sowie 31 Dissertationen und eine Habilitation abgeschlossen. Eine detaillierte Aufstellung bzw. Zuordnung ist in den Berichten der einzelnen Arbeitsgruppen zu finden.

(3) Der Ausbau der Gewächshausanlagen stellt eine wichtige Voraussetzung für die Erfassung pflanzlicher Merkmale mit Hilfe moderner bildgebender Verfahren dar. Daher wurde das vorhandene Gewächshaus zur automatischen Phänotypisierung von Getreide mit der Inbetriebnahme einer weiteren Anlage, die auf maximal 1600 Töpfe ausgelegt ist und in der Pflanzen bis zu einer Wuchshöhe von 2,50 m angezogen werden können, ergänzt. Parallel hierzu erfolgte die Inbetriebnahme einer ebenfalls mit einer automatischen Phänotypisierungseinheit ausgestatteten Klimakammer.

(4) Im Rahmen von zwei externen Audits in den Jahren 2010 und 2011 wurde der Zertifizierungsstatus des Qualitätsmanagements nach DIN EN ISO 9001:2008 der Genbank und der Abteilung Verwaltung und Zentrale Dienste bis 2013 bestätigt.

(5) Im Dezember 2010 wurde ein Kooperationsabkommen mit dem Julius Kühn-Institut (JKI) in Quedlinburg zur Formalisierung und Intensivierung der wissenschaftlichen Zusammenarbeit der beiden Einrichtungen unterzeichnet.
Die Zusammenarbeit mit der Martin-Luther-Universität Halle wurde weiter ausgebaut. Gemeinsam mit dem Leibniz-Institut für Pflanzenbiochemie (IPB) und dem Leibniz-Institut für Agrarentwicklung in Mittel- und Osteuropa (IAMO) erfolgte im Frühjahr 2011 die Gründung des Leibniz-Wissenschaftscampus für „Pflanzenbasierte Bioökonomie". Die Anschubfinanzierung erfolgt aus Mitteln des Landes und der Leibniz-Gemeinschaft.

Developments of particular importance

(1) The winning of external funding has long been seen as essential for the implementation of the Institute's research programme. The Institute has been successful in acquiring such support from a range of agencies, in particular the BMBF "Plant Biotechnology of the Future" programme. Another notable donor is the Leibniz Association, which has helped establish a graduate school under the theme "Yield formation in cereals – overcoming yield-limiting factors", due to be launched in 2012. Financial support from the German Research Council (DFG) has increased substantially, in recognition of the national significance of the fundamental research programme carried out at IPK. Thanks to the maintenance of a high level of external funding, the number of employees at IPK has remained above 500 throughout the reporting period.

(2) IPK's research outcomes over the past two years have resulted in the publication of 306 peer-reviewed papers and 46 book chapters. On the education side, as part of the Institute's formal arrangements with the Martin Luther University, Halle, the period has seen the completion of ten BSc, 14 Diploma, seven MSc and 31 PhD theses, along with one habilitation. Details of the respective thesis topics are given in the reports of the individual research groups.

(3) A continuing programme of extension and modernization to the stock of greenhouses at the site has been carried out to support the focus on phenotypic analysis via automated imaging. The pre-existing system designed to phenotype cereal plants has been strengthened by the addition of a second system able to handle up to 1,600 pots containing plants as tall as 2.50 m. The growth chamber area was extended by 80 m^2, incorporating an automated phenotyping unit targeting *Arabidopsis thaliana* plants.

(4) The Genebank and the Administration and Central Services Departments successfully underwent an external audit in 2010 and 2011, leading to their being awarded DIN EN ISO 9001:2008 quality management certification.

(5) In December 2010, IPK signed a bilateral agreement with the Julius Kühn Institute, Quedlinburg, to formalize and further extend current collaborations between the two institutions. In spring 2011, the relationship with the Martin Luther University, Halle was strengthened by the establishment of the "Leibniz Science Campus", which has brought together two of the University's faculties, IPK and two other Leibniz Institutes (the Leibniz Institute of Plant Biochemistry and the Leibniz Institute of Agricultural Development in Central and Eastern Europe). The mandate of this consortium is to develop a research programme along the theme "the plant-based bioeconomy".

Abb. 1
Die Gewinner der Forschungspreise des Landes Sachsen-Anhalt 2011: Prof. Dr. Niels Olaf Angermüller (l.; Hochschule Harz, Wernigerode), Dr. Daniela C. Dieterich (Mitte; Leibniz-Institut für Neurobiologie, Magdeburg) und Prof. Dr. Gotthard Kunze. (r., IPK Gatersleben; Foto: H. Ernst/IPK Gatersleben)
Fig. 1
The award winners of the Research Awards of Saxony-Anhalt 2011: Prof. Niels Olaf Angermüller (University of Applied Sciences Harz, Wernigerode), Dr. Daniela C. Dieterich (Leibniz Institute for Neurobiology, Magdeburg) and Prof. Gotthard Kunze (IPK, Gatersleben), (l. to r.; Photo: H. Ernst/IPK Gatersleben).

(6) Auch im Berichtszeitraum wurde eine Reihe von Forschern des Instituts mit Preisen ausgezeichnet. Stellvertretend sei an dieser Stelle Dr. Nils Stein aufgeführt, der im März 2010 den Günter und Anna Wricke Preis für seine Arbeiten zur Genomforschung und anwendungsorientierten Genetik bei Getreide (Triticeae) erhielt. Im Dezember 2011 wurde Prof. Dr. Gotthard Kunze für seine Arbeiten auf dem Gebiet der Hefebiotechnologie mit dem Forschungspreis des Landes Sachsen-Anhalt für angewandte Forschung ausgezeichnet (Abb. 1).
Mit Prof. Dr. Anna und Prof. Dr. Ulrich Wobus wurden im September 2011 zwei herausragende, ehemalige Mitarbeiter des Instituts, deren Namen untrennbar mit der Entwicklung des IPK Gatersleben verbunden sind, von der Deutschen Akademie für Naturforscher Leopoldina für ihr wissenschaftliches Lebenswerk mit der Cothenius-Medaille gewürdigt.

Die Arbeit der Gremien

Wie in den vergangenen Jahren trafen sich der Wissenschaftliche Beirat und der Genbank-Beirat anlässlich des Institutstags zur ihrer Begutachtung. Im Jahr 2010 (4. bis 6. Oktober) befasste sich der Wissenschaftliche Beirat mit den Abteilungen

(6) During the current reporting period, a number of IPK researchers received recognition in the form of awards. The most prominent were the "Günter und Anna Wricke" prize given to Dr. Nils Stein in March 2010 for his research on genome analysis and applied genetics in cereals, and the "Applied Research Award of Saxony-Anhalt" awarded to Prof. Gotthard Kunze in December 2011 in recognition of his contribution to the field of yeast biotechnology (Fig. 1). In September 2011, Prof. Anna and Prof. Ulrich Wobus, two recently retired IPK staff who guided the development of the Institute over many years, received the prestigious Cothenius Medal of the German Academy of Sciences Leopoldina in honour of their outstanding scientific achievements.

Activities of the Advisory Boards

As in previous years, the **Scientific Advisory Board** and the **Genebank Advisory Board** convened after the Institute Day. In 2010 (4-6 October), the Scientific Advisory Board reviewed the Genebank and the Cytogenetics and Genome Analysis Departments, whereas in 2011 (4-6 October), the research groups housed within the Molecular Genetics Department and the Physiology and Cell Biology Department were evaluated. In parallel, the Genebank Advisory Board visited the Genebank in both

Abb. 2
Die Teilnehmer der 10. Gatersleben Research Conference „Sequence-informed Crop Research" Ende November 2010. (Foto: R. Schnee/ IPK Gatersleben)
Fig. 2
Participants of the 10th Gatersleben Research Conference "Sequence-informed Crop Research" late November 2010. (Photo: R. Schnee/ IPK Gatersleben)

Genbank sowie Cytogenetik und Genomanalyse, im Jahr 2011 (4. bis 6. Oktober) wurden die Forschungsarbeiten in den Abteilungen Molekulare Genetik sowie Physiologie und Zellbiologie begutachtet. Parallel hierzu besuchte der Genbank-Beirat in beiden Jahren die Genbank.

Der Stiftungsrat tagte in beiden Jahren jeweils am 7. Oktober unter der Leitung des Vorsitzenden, MinDirig Dr. Joachim Welz. Im Mittelpunkt der Besprechungen standen die Fortführung des Programmbudgets, Planungen zum weiteren Ausbau der Gewächshaus- und Klimakammerkapazitäten, die Beschaffung von Großgeräten, sowie der im Jahr 2012 anstehenden Nachbesetzung der Stelle des Leiters der Abteilung Cytogenetik und Genomanalyse.

Tagungen und Workshops

Im Berichtszeitraum waren Forscher des IPK an der Ausrichtung zahlreicher nationaler und internationaler Tagungen, Symposien und Workshops beteiligt. 2010 veranstaltete das IPK vom 22. bis 24. November die 10. Gatersleben Research Conference zum Thema „Sequence-informed Crop Research" (Abb. 2). Über 160 Wissenschaftler diskutierten am IPK rezente Entwicklungen und Ergebnisse aus dem Bereich der pflanzlichen Genomforschung. Vom 20. bis 24. September des gleichen Jahres wurde eine von der European Science Foundation (ESF) geförderte Summer School „Plant Epigenetics 2010" ausgerichtet, an der 32 Nachwuchswissenschaftler/-innen aus ganz Europa teilnahmen. Das Programm der Summer School beinhaltete sowohl theoretische Wissensvermittlung in Form von eingeladenen Vorträgen international anerkannter Epigenetiker oder von Wissenschaftlern aus angrenzenden Feldern als auch Labor-Kurse.

years.

The **Governing Board** convened in both 2010 and 2011 on 7 October under the chairmanship of Dr. Joachim Welz from the Ministry of Science and Economics of Saxony-Anhalt. The topics for consultation included programme budgeting, infrastructure on the campus, the acquisition of capital equipment, and the succession for head of the Cytogenetics and Genome Analysis Department.

Conferences and Workshops

In 2010 and 2011, IPK scientists were engaged in the organization of a number of both national and international conferences and workshops. The 10th Gatersleben Research Conference with the theme Sequence-informed Crop Research took place on 22-24 November 2010, attracting over 160 delegates interested in the current state of plant genome research (Fig. 2). From 20-24 September 2010, 32 junior researchers from all over Europe gathered to participate in the European Science Foundation (ESF)-funded "Plant Epigenetics 2010" Summer School. The scientific programme comprised invited lectures from internationally renowned (plant) epigeneticists and fields complementary to epigenetics, and a series of laboratory exercises was also included.

IPK also continued its ongoing discourse with other scientific disciplines and the public. From 12-14 May 2011, about 90 participants of the 12. Gaterslebener Begegnung (12th Gatersleben Meeting) discussed the topic "Reifung und Wachstum in Natur und Gesellschaft" (Maturation and growth in nature and society) which had particular resonance in the light of the ongoing turmoil affecting the financial markets. The conference was jointly organised with the German Academy of Sciences Leopoldina (see Fig. 3, p. 14). From 31 October to 3 November 2011 IPK hosted a workshop funded jointly by DFG and the

Abb. 3
Prof. Dr. Ulrich Wobus und Prof. Dr. Anna M. Wobus engagieren sich seit Jahren in der Organisation und Durchführung der Gaterslebener Begegnungen. (Foto: H. Ernst/ IPK Gatersleben)
Fig. 3
The 'inventors' of the 'Gaterslebener Begegnungen' (Gatersleben Meetings): Profs. Ulrich and Anna M. Wobus. (Photo: H. Ernst/ IPK Gatersleben)

Vom 12. bis 14. Mai 2011 begrüßte das IPK die etwa 90 Teilnehmer/-innen der 12. Gaterslebener Begegnung zum Thema „Reifung und Wachstum in Natur und Gesellschaft", die wiederum gemeinsam mit der Leopoldina ausgerichtet wurde (Abb. 3). Mit Vorträgen von Publizisten und Wissenschaftlern wurde die Thematik im Lichte der aktuellen Entwicklungen an den Finanzmärkten insbesondere im Hinblick sozial- und wirtschaftspolitischer Gesichtspunkte erörtert.
Vom 31. Oktober bis zum 3. November 2011 war das IPK Gastgeber für einen von der DFG und der Japanischen Society for the Promotion of Sciences (JSPS) finanzierten Workshops zu „Frontiers of Plant Chromosome Research: Centromeres and Artificial Chromosomes". An der Veranstaltung nahmen vorrangig Wissenschaftler aus Deutschland und Japan teil, um die Kommunikation in der Chromosomenbiologie zu intensivieren und die jeweils letzten Forschungsergebnisse zu präsentieren.

Das IPK Student Board veranstaltete vom 15. bis 18. Juni 2010 die 6. Plant Science Student Conference am IPK, die im Wechsel mit der Doktorandenorganisation des IPB in Halle seit 2005 jährlich stattfindet.

Eine Übersicht zu allen am IPK veranstalteten Symposien und der Beteiligung an der Ausrichtung externer Tagungen und Symposien in 2010 und 2011 findet sich auf S. 208 ff.

Japanese Society for the Promotion of Sciences on the topic 'Frontiers of Plant Chromosome Research: Centromeres and Artificial Chromosomes'. The focus of this meeting was to encourage German and Japanese scientists to exchange recent achievements in chromosome biology and to intensify bilateral contacts. The members of the Student Board organized the 6th Plant Science Students' Conference from 15-18 June 2010 at IPK. An overview of all the conferences and symposia held at IPK, as well as a list of the external conferences whose organizers included IPK scientists is given on page 208.

Cooperation with Universities and Research Institutes
Interactions at the institutional level are an important component of the development of IPK's research agenda, since these take advantage of complementarities in scientific know-how and technical infrastructure. Close interactions between the Institute and neighbouring universities are expected to increase the attractiveness of IPK as a destination for young academics. In December 2010, an agreement was signed with the Julius Kühn Institute to formalize and promote the scientific collaborations enjoyed by staff of the two institutes. The "Leibniz Science Campus" was founded in 2011 as a means of deepening the already well established relationship between the Martin Luther University, Halle and its neighbouring Leibniz Institutes. The hoped-for outcome is that the campus will evolve into an interdisciplinary research platform addressing the plant-based bioeconomy, involving participants from both the life and the social sciences. Start-up funding was provided by the State of Saxony-Anhalt and the Leibniz Association (Fig. 4, p. 15).

Abb. 4
Unterzeichnung der Kooperationsvereinbarung am 4. März 2011: Die Kultusministerin, Frau Prof. Birgitta Wolff, und der Präsident der Leibniz-Gemeinschaft, Prof. Karl Ulrich Mayer, unterzeichnen die Vereinbarung zum WissenschaftsCampus. (Foto: R. Honeit/ IAMO Halle)
Fig. 4
Signing the formal contracts for the inauguration of the Leibniz Science Campus: Minister of Cultural Affairs of Saxony-Anhalt, Prof. Birgitta Wolff and President of the Leibniz Association, Prof. Karl Ulrich Mayer. (Photo: R. Honeit/ IAMO Halle)

Zusammenarbeit mit Universitäten und Forschungseinrichtungen

Ein wichtiger Aspekt im Hinblick auf die Weiterentwicklung des Forschungsprogramms ist die Vernetzung mit Forschungseinrichtungen. Hierbei sollen vor allem Komplementäreffekte (Know-how, technische Ausstattung) genutzt werden. Durch die enge Verbindung des Instituts mit den umliegenden Universitäten und Hochschulen soll, unter anderem, auch die Attraktivität des IPK als Ausbildungsstätte für den wissenschaftlichen Nachwuchs gesteigert werden.

Im Dezember 2010 wurde ein Kooperationsabkommen mit dem Julius Kühn-Institut (JKI) in Quedlinburg zur Formalisierung und Intensivierung der wissenschaftlichen Zusammenarbeit der beiden Einrichtungen unterzeichnet. Im Zuge der weiteren Intensivierung der Zusammenarbeit der Martin-Luther-Universität Halle mit den in der Region angesiedelten außeruniversitären Forschungseinrichtungen wurde 2011 der „Leibniz-WissenschaftsCampus“ gegründet (Abb. 4). In diesem sollen Forschungsarbeiten zur pflanzlichen Bioökonomie disziplinübergreifend durch die Zusammenführung von lebenswissenschaftlichen und wirtschaftswissenschaftlichen Ansätzen bearbeitet werden.

IPK scientists have given tuition at the Universities of Halle-Wittenberg, Potsdam, Kassel, Kiel, Jena, Greifswald, Western Australia (Perth), and the University of Applied Sciences in Bernburg and Köthen. In addition, our scientists have given several courses and run a number of workshops for the Institute's PhD student community. The size of the community reached 88 students by the end of 2011. IPK's PhD programme has been actively coordinated by the "PhD Student Board", which organized a student seminar series, hosted invited lectures given by external scientists, staged a "Plant Science Students' Conference" and provided various training events for the PhD student community. Thanks to a grant from the Leibniz Association, a graduate school themed "Yield formation in cereals – overcoming yield-limiting factors" will be established in 2012, together with the Martin Luther University, Halle. Further details of the IPK PhD programme can be found on page 155.

Wissenschaftler des Instituts führten Lehrveranstaltungen an oder in Zusammenarbeit mit den Universitäten Halle-Wittenberg, Potsdam, Kassel, Kiel, Jena, Magdeburg und Greifswald sowie der Hochschule Anhalt an den Standorten Bernburg und Köthen fort. Daneben boten Wissenschaftler Kurse und Praktika für Studierende am IPK an. Die Anzahl der am IPK betreuten Doktoranden wurde erheblich gesteigert. Ende 2011 waren 88 Doktoranden/-innen am IPK tätig. Das am IPK etablierte Doktorandenprogramm wird über weite Strecken durch das "PhD Student Board" entwickelt und betreut (s. S. 155). Zu den Aktivitäten zählen die Veranstaltungen in der Reihe der Doktorandenseminare, Einladungen von externen Wissenschaftlern zu Seminarvorträgen, die Organisation der "Plant Science Student Conference" sowie spezielle Fortbildungsveranstaltungen für Doktoranden. Im Zuge der weiteren Strukturierung des Doktorandenprogramms wird ab 2012 gemeinsam mit der MLU Halle eine Graduierten-Schule zum Thema „Yield formation in cereals – overcoming yield-limiting factors" anlaufen, welche aus Mitteln des Leibniz-Pakts für Forschung und Innovation gefördert wird.

Öffentlichkeitsarbeit und öffentliche Wirkung

Die Wahrnehmung des IPK innerhalb der wissenschaftlichen Gemeinde basiert zum größten Teil auf den oben aufgeführten wissenschaftlichen Publikationen. Ebenso stellen Vorträge auf internationalen Konferenzen bzw. Posterbeiträge (vgl. S. 165 ff.) einen wichtigen Baustein in der Kommunikation mit der Forschergemeinschaft dar.

Für die Darstellung in der breiten Öffentlichkeit spielen Medien- und Pressearbeit sowie Führungen von Besuchergruppen durch die Standorte des IPK eine besonders große Rolle. So konnten in den beiden Jahren über 1200 Besuchern während 71 Führungen durch das Institut in Gatersleben und die beiden Standorte der Genbank in Groß Lüsewitz und Malchow/Poel Informationen zum Institut und zur Pflanzenforschung allgemein vermittelt werden. Ein erheblicher Anteil der Führungen wurde – resultierend aus dem öffentlichen Interesse – von den Gruppen der Genbank in Gatersleben und an den beiden Standorten Groß Lüsewitz und Malchow/Poel übernommen.

Daneben wurde die Öffentlichkeit im Berichtszeitraum mit 20 Presseinformationen über aktuelle Entwicklungen am Institut und auf dem Biotech-Campus informiert. In diesem Zusammenhang standen Mitarbeiter des Instituts Medienvertretern für wissenschaftliche Fragestellungen bzw. zu am IPK erzielten Forschungsergebnissen zur Verfügung. Seitens der Medien waren das Thema Grüne Gentechnik sowie die Genbank von besonderem Interesse.

Gemeinsam mit den Partnern vor Ort veranstaltete das IPK sowohl in 2010 als auch in 2011 einen Tag der offenen Tür, welcher 2010 mit dem Fest der Begegnung fortgesetzt wurde. Letzteres erfreut sich in der Region großer Beliebtheit, da u. a. die ausländischen Mitarbeiter spezielle Angebote aus ihren Heimatländern bereit halten.

Public relations and public image

The recognition of IPK within the scientific community is shaped by its output of publications in international peer-reviewed scientific journals along with the talks and poster presentations made by the Institute's staff at national and international conferences. The visibility of IPK to the general public, in contrast, has to rely on contributions in the print, TV, radio and online media. This avenue of communication can be supplemented more locally by organizing open campus tours. Over the past two years, around 1,200 visitors have toured the Gatersleben headquarters and the two Genebank satellite stations in Groß Lüsewitz and Malchow/Poel. The same period has seen 20 press releases aimed to inform the public and media concerning recent developments at the Institute and the Biotech Campus. A number of IPK researchers took the opportunity to provide first-hand information to press and media representatives concerning a variety of scientific issues. Most of the interest has centred on the activity of the Genebank (biodiversity issues) and green biotechnology. Together with its campus partners, IPK organised an Open Day in both 2010 and 2011. In 2010, the Open Day was extended by providing a "Fest der Begegnung" ("Visitors' festival") which was well-received by the public.

IPK also had a presence at various international fairs, in particular Biotechnica in both 2010 and 2011. Two exhibits ("A biosensor designed to detect the presence of oestrogenic compounds in water samples" and "A DNA-based sensor able to detect the colonization of plant roots by Mycorrhiza") displayed on the joint (Saxony, Thuringia and Saxony-Anhalt) stand "Research for the Future" featured outcomes of IPK's biotechnology research. IPK scientists also presented talks at the BMBF innovation pavilion. The "A biosensor designed to detect the presence of oestrogenic compounds in water samples" exhibit was also displayed at the Analytica 2010 trade show in Munich.

On 4 October 2010, the "Gatersleben Research Award" was granted to Dr. Navreet Kaur (University of Zurich) for her doctoral thesis on the topic of resistance genes against powdery mildew in wheat.

Last, but not least, IPK continued its support of the activities of the "Gesellschaft zur Förderung der Kultur Gatersleben e.V." (The Gatersleben Society for Cultural Progress) which celebrated its twentieth anniversary in May 2011.

A comprehensive overview of the Institute's various PR activities is given on pages 231-248.

Auf der Biotechnica 2010 und 2011 in Hannover war das Institut mit Exponaten zu den Themen „Biosensor zum Nachweis östrogenwirksamer Substanzen im Wasser“ und „DNA-Sensor zum Nachweis mykorrhizierter Pflanzen“ auf dem Gemeinschaftsstand „Forschung für die Zukunft“ der Länder Sachsen, Sachsen-Anhalt und Thüringen vertreten. Darüber hinaus hielten Forscher des IPK Vorträge z. B. auf dem Innovations-Forum des BMBF. Ebenso stellte das IPK auf der Analytica 2010 in München das Exponat „Biosensor zum Nachweis östrogenwirksamer Substanzen im Wasser“ aus. Zur Vorbereitung dieser Messen und anderer Veranstaltungen führte das Institut seine Mitarbeit im Arbeitskreis „Messe“ des Landes Sachsen-Anhalt fort.

Im Rahmen des Institutstages wurde am 4. Oktober 2010 der durch die „Gemeinschaft zur Förderung der Kulturpflanzenforschung e.V.“ und das IPK gestiftete Gaterslebener Forschungspreis an Frau Dr. Navreet Kaur Bhullar von der Universität Zürich für ihre Dissertation zur Entdeckung von neuen Resistenzgenen gegen Weizenmehltau verliehen.

Neben den wissenschaftlichen Arbeiten unterstützt das IPK aktiv die kulturellen Aktivitäten der „Gesellschaft zur Förderung der Kultur Gatersleben e.V.“, die im Mai 2011 ihr 20-jähriges Bestehen feierte.

Eine Übersicht zu allen Öffentlichkeitsarbeit-relevanten Aktivitäten findet sich auf den Seiten 231-248.

Der Biotechnologiestandort Gatersleben

Als wissenschaftliches Zentrum ist das Institut auf vielfältige Weise an der Standortinitiative „Green Gate Gatersleben“ beteiligt und unterstützt die Weiterentwicklung des Biotechnologiestandorts (http://www.green-gate-gatersleben.de). Die Zusammenarbeit mit verschiedenen am Standort angesiedelten Firmen erfolgt in erster Linie durch die Bearbeitung gemeinsamer Forschungsprojekte. Die Ablehnung der Grünen Gentechnik in weiten Teilen der Gesellschaft und Politik sowie die unzulänglichen gesetzlichen Rahmenbedingungen, die einer Koexistenz zwischen gentechnisch veränderten und konventionellen Pflanzen entgegen stehen, erschweren den Erhalt bzw. die Weiterentwicklung des Biotechnologiestandorts Gatersleben erheblich. Umso erfreulicher war daher die Ansiedlung der Firma Bayer CropScience im Biotechpark, wo im Dezember 2011 mit dem Aufbau des europäischen Zentrums für Weizenzüchtung begonnen wurde.

Um das Interesse Jugendlicher an Lebenswissenschaften zu wecken, bietet das auf dem Campus angesiedelte „Grüne Labor“ ein breites Kursangebot. Dieses zielt in erster Linie auf den schulischen Bereich ab, wurde in den vergangenen zwei Jahren jedoch auch auf die berufliche Ausbildung ausgeweitet. Das Angebot stieß weiterhin auf sehr großes Interesse. Etwa 7.000 Schüler, Auszubildende und Lehrer nahmen in den vergangenen beiden Jahren an den Kursen und Veranstaltungen teil.

Gatersleben as a “Centre for Green Biotechnology”

As a scientific centre, the Institute is variously engaged in the local initiative “Green Gate Gatersleben”, and supports the development of the Biotechnology Campus (http://www.green-gate-gatersleben.de). Collaboration with private companies which share the campus is primarily conducted in the frame of joint research projects. The development of the Gatersleben Campus as a biotechnology hub is constrained by the opposition to GM technology which continues to be a feature of public and political opinion. A damaging result of this opposition has been a stalling in the establishment of a workable legal framework to regulate the co-existence of GM and non-GM plants. Against this backdrop, the decision of Bayer CropScience to establish its European headquarters for wheat breeding on the Gatersleben Biotechpark was particularly welcome.

To spur interest in life sciences amongst the young, the “Grünes Labor” (“Green laboratory”) has worked to develop an extensive curriculum. This has attracted an ever-increasing level of interest, as shown by the enrolment of over 7,000 people (mainly school-age children) in the various courses and events organized over the past two years.

Verwaltung und Infrastruktur/ Administration and Infrastructure

Personal/Staff

In den beiden Berichtsjahren 2010 und 2011 betrug der Gesamtpersonalbestand (zum jeweiligen Stichtag: 31. Dezember) 535 (2010) bzw. 550 (2011) Personen. Darunter befanden sich am 31. Dezember 2011 275 (2010: 272) Mitarbeiter/-innen auf Planstellen. Neben 155 (2010: 161) Drittmittelbeschäftigten waren 96 (2010: 81) Mitarbeiter/-innen über Annexstellen angestellt. (Abb. 5, S. 19)

Auch im Bereich der Berufsausbildung hat das Institut mit insgesamt 24 (2010: 21) Ausbildungsplätzen in verschiedenen Berufen und einem dualen Studenten das hohe Niveau halten können. Darunter drei Bürokaufleute, 11 Biologielaborant(en)/-innen, drei Fachinformatiker Systemintegration, eine Fachangestellte für Medien- und Informationsdienste, drei Gärtner/-innen für Gemüsebau und erstmalig ab 2010 zwei Köche im Casino des IPK.

Zum 30. September 2011 waren 339 Personen in einem befristeten Arbeitsverhältnis tätig. Von den 183 Wissenschaftler/-innen waren insgesamt 151 befristet beschäftigt. Von den 61 im Planstellenbereich beschäftigten Wissenschaftler/-innen hatten 29 eine befristete Anstellung. Die Abteilungen Genbank und Verwaltung und Zentrale Dienste verfügen über einen relativ hohen Anteil an Stellenplanpersonal im Vergleich zu den anderen drei wissenschaftlichen Abteilungen (Abb. 6, S. 19). Wissenschaftliche und technische Mitarbeiter der Genbank nehmen Daueraufgaben bei der Erhaltung und dem Management der in der Bundeszentralen *Ex-situ*-Genbank bewahrten Vielfalt wahr. Die Mitarbeiter der Abteilung Verwaltung und Zentrale Dienste unterstützen im gärtnerischen und technischen Bereich ganz unmittelbar die Forschungsarbeiten in den vier wissenschaftlichen Abteilungen.

GB	Abteilung Genbank
CYG	Abteilung Cytogenetik und Genomanalyse
MOG	Abteilung Molekulare Genetik
PZB	Abteilung Physiologie und Zellbiologie
VZD	Abteilung Verwaltung und Zentrale Dienste

Ein relativ hoher Personalanteil des Institutes ist im technischen und infrastrukturellen Bereich tätig (Abb. 7, S. 19). Dies ist wie bereits aufgeführt auf den großen gärtnerischen und technischen Betreuungsaufwand in der Pflanzenforschung bzw. im Vermehrungsanbau der Genbank zurückzuführen.

Budget

Seit der Einführung der Programmbudgets an Stelle der Wirtschaftspläne werden die Einnahmen und Ausgaben für die Programme ungeachtet der Mittelherkunft betrachtet. Dem IPK standen 2011 insgesamt 42.136 TEUR (2010: 42.144 TEUR) für eigene Ausgaben, d. h. ohne Einnahmen für Partner und ohne Einbehalte für Baumaßnahmen, zur Verfügung.
In 2011 betrugen die Zuwendungen im Rahmen der Grundfinanzierung 24.575 TEUR (2010: 24.547 TEUR). Darin enthalten waren 922 TEUR Betriebsmittel für die Projekte im Rahmen des wettbewerblichen Verfahrens der Leibniz-Gemeinschaft (SAW) (2010: 682 TEUR) (Abb. 8, S. 21).

Etwa 56 % der Gesamtausgaben entfielen auf den Personalbereich. Der Anstieg bei den Betriebsausgaben war vorrangig auf die Tariferhöhung im TV-L sowie auf die Kostensteigerung bei den Bewirtschaftungskosten zurückzuführen. Die Bauinvestitionen und die aus dem Konjunkturprogramm II der Bundesregierung (KP II) finanzierten Maßnahmen wurden 2010 abgeschlossen. Ferner erhielt das IPK im Rahmen des Gesetzes zur Umsetzung von Zukunftsinvestitionen der Kommunen und Länder/ Konjunkturpaket II Mittel für Geräteinvestitionen, die 2010 in einem Umfang von 2.130 TEUR eingesetzt wurden (Abb. 9, S. 21).

Drittmitteleinnahmen/Third Party Funding

Im Jahr 2011 wurden für 148 Projekte (2010: 150) Einnahmen (ohne Partner) in Höhe von insgesamt 10.623 TEUR (2010: 10.323 TEUR) erzielt (Abb. 10, S. 21). Hauptzuwendungsgeber waren das Bundesministerium für Bildung und Forschung (BMBF), die Deutsche Forschungsgemeinschaft (DFG) und das Land Sachsen-Anhalt. Außerdem erhielt das IPK Mittel von sonstigen Zuwendungsgebern in Höhe von 272 TEUR (Vorjahr 298 TEUR). Neben den Einnahmen für das IPK wurden 37 TEUR (Vorjahr 255 TEUR) für Partner eingenommen und weitergereicht.

Die Einnahmen vom BMBF resultierten überwiegend aus dem inzwischen abgeschlossenen Programm „GABI-FUTURE“ sowie aus der neuen Förderinitiative „Pflanzenbiotechnologie der Zukunft“. Der absehbare Rückgang bei den durch das BMBF geförderten Projekten konnte sowohl durch DFG-Mittel als auch Auftragsforschung für Wirtschaftsunternehmen mehr als ausgeglichen werden. Die Zusammensetzung der Drittmittelherkunft zeigt, dass die Umsetzung des Leibniz-Prinzips - exzellente Wissenschaft mit Anwendungsrelevanz - zu einem ausgewogenen Verhältnis zwischen Grundlagenforschung und angewandter Forschung am IPK führt.

Abb. 5
Personalentwicklung
(Stand: 30. September 2011)
Fig. 5
Development of staff
(as of 30th September 2011)

Abb. 6
Beschäftigte nach Abteilungen
(Stand: 30. September 2011)
Fig. 6
Staff per department
(as of 30th September 2011)

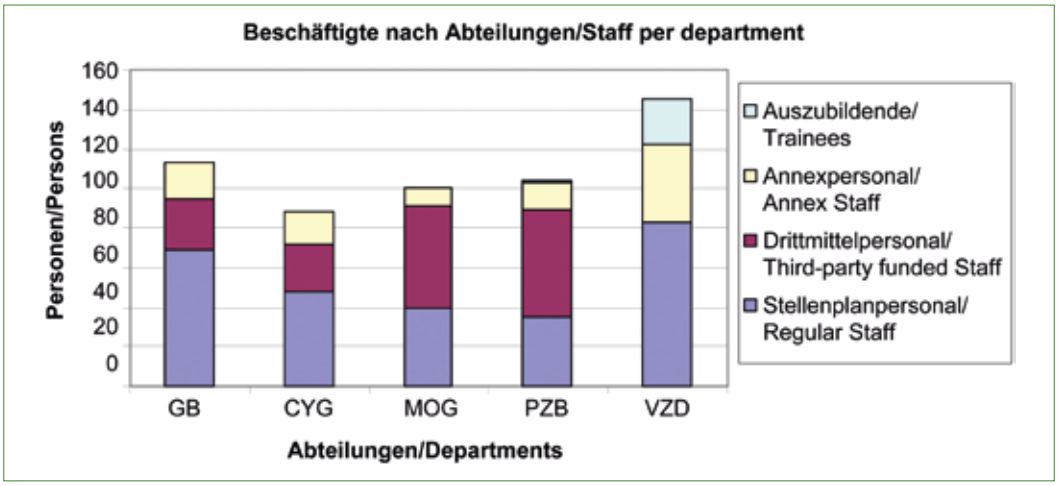
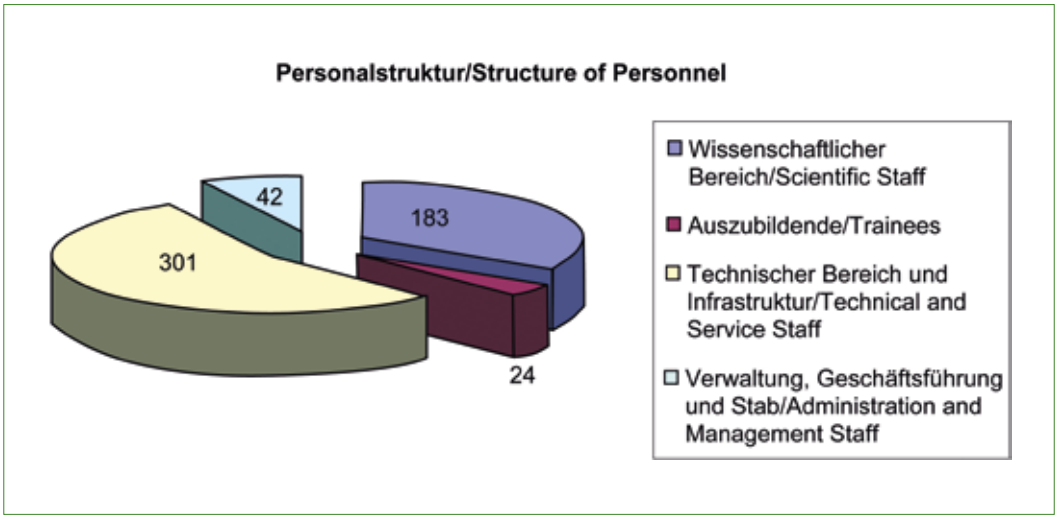


Abb. 7
Personalstruktur
(Stand 30. September 2011)
Fig. 7
Personnel structure
(as of 30th September 2011)



Technologietransfer/Technology Transfer

Im Jahr 2011 wurden 36 Erfindungen (2010: 5) durch Wissenschaftler des IPK gemeldet, von denen bis zum Jahresende 32 (2010: 2) vom Institut auch in Anspruch genommen worden sind. Im gleichen Zeitraum wurden drei neue Patentanmeldungen (2010: 1) durch das Institut vorgenommen.

Das IPK verfügte damit zum Jahresende 2011 über 22 Betriebsgeheimnisse (2010: 18) und war als alleiniger oder Mitanmelder an 28 Patentfamilien (2010: 26) mit Anmeldungen in Deutschland und im Ausland beteiligt. Daneben sind IPK-Erfinder an 28 Patentfamilien (2010: 22) beteiligt, die durch Industriepartner im Rahmen von FuE-Verträgen angemeldet wurden.

In 2011 ging das Institut insgesamt 20 projektorientierte Kooperationsverträge (einschließlich von vier Unteraufträgen und einem Werkvertrag) (2010: 20, einschließlich von vier Unteraufträgen und zwei Werkverträgen) ein und schloss neun Forschungs- und Entwicklungsverträge (2010: 8 und 3 Lizenzverträge sowie zwei Verwertungsvereinbarungen) ab. Außerdem wurden im Jahr 2011 63 Materialtransfer- und Geheimhaltungsvereinbarungen (2010: 106) (exklusive der Abteilung Genbank) mit in- und ausländischen Forschungseinrichtungen sowie Wirtschaftsunternehmen abgeschlossen.
Die Einnahmen aus der industriefinanzierten Auftragsforschung betrugen im Jahr 2011 rund 2,4 Mio. Euro (2010 insgesamt 1,8 Mio. Euro).

Raumprogramm und Baumaßnahmen/
Facilities and Constructions

Ausgehend von 14.714 m^2 Hauptnutzfläche (HNF) wurden dem IPK aufgrund erhöhten Platz- und Raumbedarfs für seine Arbeiten durch das Kultusministerium des Landes Sachsen-Anhalt weitere Flächen zur Nutzung bewilligt:

insgesamt **20.939 m^2 Hauptnutzfläche**
davon 15.703 m^2 HNF in Labor- und Bürogebäuden und
5.236 m^2 HNF in Gewächshäusern.

Dies war die Voraussetzung zum Bau des neuen Gewächshauskomplexes am Genomzentrum, zum Umbau von Flächen zur Aufnahme zusätzlicher Phytokammernkapazität sowie zur Sanierung des Technischen Servicegebäudes und zusätzlichen Räumlichkeiten für die Lagerung von Erntegut.

Wissenschaftliche Bibliothek/Scientific Library

Die Wissenschaftliche Bibliothek des IPK verfügt über einen Bestand von derzeit 78.695 Medieneinheiten zu den Sammelschwerpunkten Molekularbiologie, Genetik, Zytologie, Taxonomie und Kulturpflanzenforschung.

Durch die Beteiligung der Bibliothek am DFG-Projekt „Nutzung von Nationallizenzen" konnte das Angebot an elektronischen Literaturressourcen deutlich verbessert werden. So kann nunmehr jeder Wissenschaftler die Online-Archive von den Verlagen Springer und Elsevier nutzen, d. h. ältere Zeitschriftenartikel sind im Volltext zugänglich. Weiterhin wird für eine effektive Literaturrecherche die Fachdatenbank „ISI-Web of Knowledge" über ein Leibniz-Gemeinschaft-Konsortium erworben und bereitgestellt.

Um der geänderten wissenschaftlichen Nachfrage Rechnung zu tragen, wurde in 2010 eine Bestands- und Bedarfsanalyse im Bereich der Zeitschriften durchgeführt. Als Ergebnis ist das IPK zum 1. Januar 2011 dem Leibniz-Gemeinschaft/Springer-Konsortium beigetreten. Damit verbunden ist der Erwerb des Online-Paketes Lebenswissenschaften mit einem Umfang von ca. 500 Online-Zeitschriftentiteln. Bereits aktuell zu beobachten ist die vermehrte Nutzung des Onlineangebots verbunden mit einem Rückgang an Literaturanforderungen im Leihverkehr. Auch zukünftig sollen regelmäßige Analysen des Bedarfs und Nutzerverhaltens sowohl die Effizienz steigern als auch das Serviceangebot der Wissenschaftlichen Bibliothek anpassen.

Als öffentliche Bibliothek werden die Bestände auch über das IPK hinaus überwiegend von den auf dem Campus Gatersleben ansässigen Biotechnologiefirmen sowie von Praktikanten des „Grünen Labors" genutzt. Der Bibliotheksbestand ist in zahlreichen elektronischen Fachkatalogen, wie z. B. dem Gemeinsamen Bibliotheksverbund (GBV), dem Periodikabestand in der Zeitschriftendatenbank (ZDB) etc. bibliographisch nachgewiesen, womit die IPK-Bibliothek ihren Beitrag zur regionalen und überregionalen Literaturversorgung leistet.

Abb. 8
Entwicklung der Gesamteinnahmen
Fig. 8
Development of total revenues

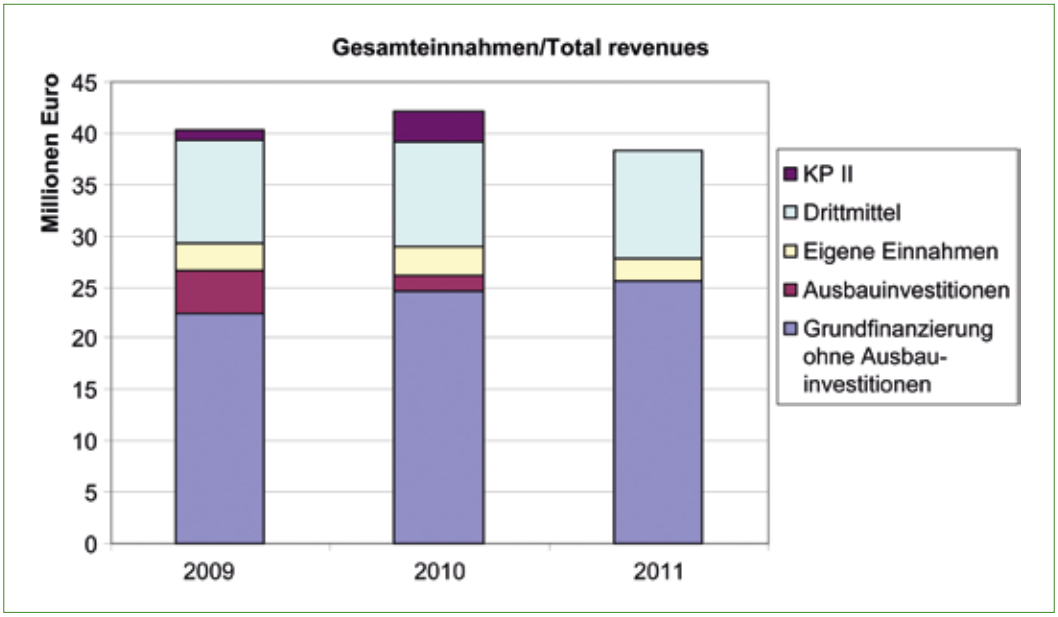


Abb. 9
Entwicklung der Gesamtausgaben
Fig. 9
Development of total expenditure

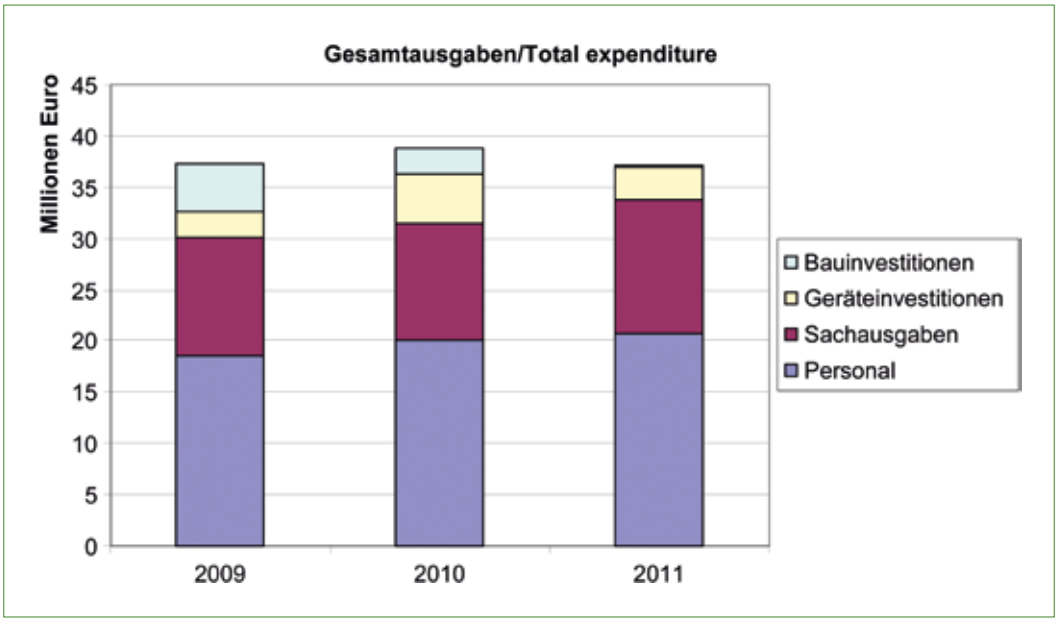
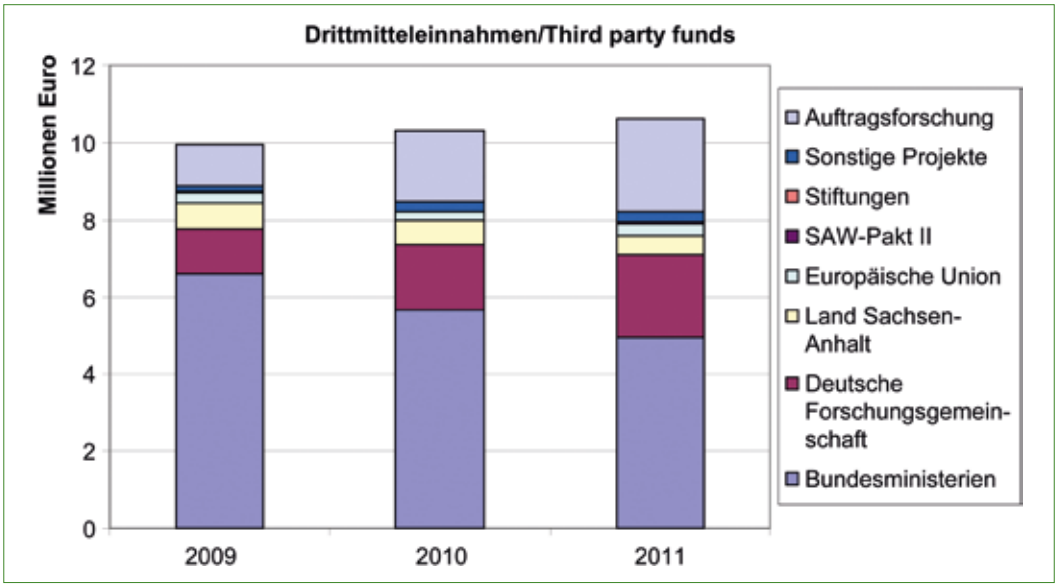
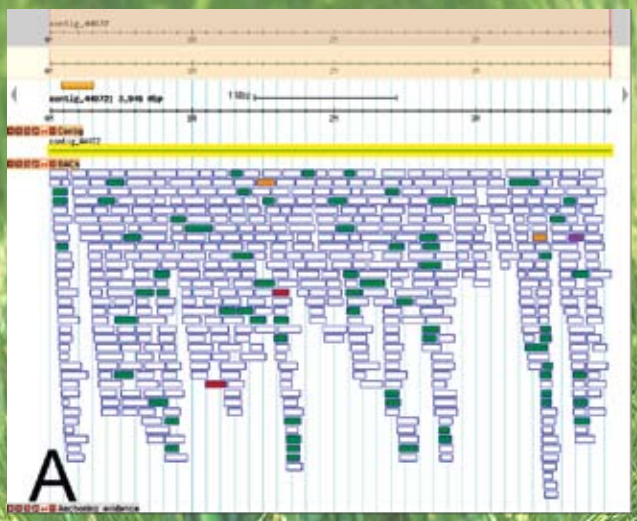
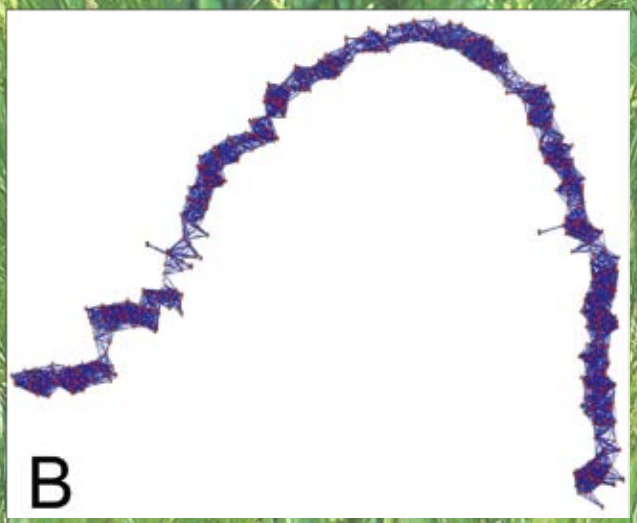


Abb. 10
Entwicklung der Drittmitteleinnahmen nach Mittelherkunft ohne Anteil für Partner
Fig. 10
Development of third party funds excl. partner shares (source of funds)



Abteilung Genbank/
Department of Genebank





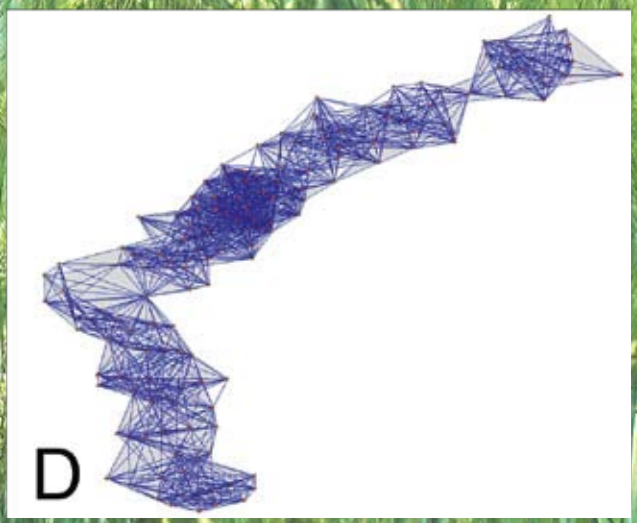


Abb. 11
Die Erstellung einer physikalischen Karte bildet die Grundlage für die kartengestützte Sequenzierung des Gerstengenoms. Das IPK (Ag Genomdiversität) erarbeitet gegenwärtig eine physikalische Karte des Gerstengenoms, durch sogenannte Fingerprintkartierung von BAC-Klonen aus genomischen DNA-Bibliotheken. BAC-Klone werden mit Restriktionsenzymen geschnitten, so dass definierte Fragmentmuster entstehen. Diese erlauben es, physikalisch überlappende Klone durch (zumindest teilweise) identische Fragmentmuster zu identifizieren. Aus überlappenden BAC-Klonen entstehen sogenannte Contigs. Abb. 11A zeigt eine klassische Darstellung des Contigs 44072, der eine Länge von ca. 4 Mbp besitzt. Dunkel markierte BAC-Klone sind in der genetischen Karte von Chromosom 3H verankert. Mit Hilfe der Software LTC (Frenkel et al. 2010, BMC Bioinformatics 11:584) lassen sich die wesentlich komplexeren Überlappungsbeziehungen der einzelnen BAC-Klone eines Contigs als Netzwerk darstellen (Abb. 11B-D) und auf ihre lineare Topographie hin überprüfen. Contig 44072 besitzt über die gesamte Länge von 4 Mbp eine vollständig lineare Topologie (Abb. 11B). (R. Ariyadasa, Z. Frenkel, A. Korol, N. Stein)

Fig. 11
A physical map is the foundation for map-based sequencing of the barley genome. IPK (Genome Diversity group) is developing a physical map by fingerprinting analysis of BAC clones of a genomic DNA library of barley. Cleavage by restriction enzymes is resulting in specific fragment patterns partially shared by overlapping BAC clones. This information can be utilised to form so-called contigs. A classical visualisation of a 4 Mbp large contig 44072 of the barley physical map is shown in Fig. 11A. BAC clones labeled in dark have been anchored to the genetic map of chromosome 3H. The new software LTC (Frenkel et al. 2010, BMC Bioinformatics 11:584) allows for an improved visualisation of the multidimensional relationships of BAC clones within contigs revealing the structure of a network (Fig. 11B-D). The analysis of the same contig 44072 by LTC indicated a completely linear topology of its entire length of 4Mbp (Fig. 11B). (R. Ariyadasa, Z. Frenkel, A. Korol, N. Stein)

Abteilung Genbank

Leiter: Prof. Dr. Andreas Graner

Allgemeine Forschungsziele

Die Bundeszentrale *Ex-situ*-Genbank für landwirtschaftliche und gartenbauliche Kulturpflanzen erhält eine der weltweit größten Sammlungen von pflanzengenetischen Ressourcen (PGR). Sie liefert wesentliche Beiträge zur Umsetzung der Nationalen Strategie zur Biologischen Vielfalt und des Nationalen Fachprogramms zur Erhaltung und nachhaltigen Nutzung pflanzengenetischer Ressourcen landwirtschaftlicher und gartenbaulicher Kulturpflanzen. Auf europäischer Ebene ist die Genbank darüber hinaus auf vielfältige Weise mit dem *European Cooperative Programme for Plant Genetic Resources* (ECPGR) verbunden. Die zentrale Aufgabe der Abteilung liegt in der Erhaltung der Sammlung und Bereitstellung von Material. In diesem Zusammenhang werden umfangreiche Dienstleistungen wie die Bereitstellung von Saat- und Pflanzgut sowie damit verbundenen Informationen erbracht. Die in der Abteilung bearbeiteten Forschungsthemen umfassen die fortgesetzte Optimierung des Erhaltungsmanagements, die Untersuchung von Artbildungs- und Anpassungsprozessen, die Aufklärung taxonomischer Zuordnungen innerhalb ausgewählter Kultur- und Wildpflanzengattungen sowie die (molekular)genetische Analyse agronomischer Merkmale.

Entwicklungen im Berichtszeitraum

Sammlungsmanagement

Im Zentrum des Sammlungsmanagements steht der Betrieb der Bundeszentralen *Ex-situ*-Genbank. Sie umfasst zum gegenwärtigen Zeitpunkt 151.002 Akzessionen aus 3.212 Arten und 776 Gattungen. Neben den Lebendsammlungen unterhält die Genbank als Referenzzentrum für taxonomische Arbeiten ein Herbarium mit über 420.000 Belegen sowie über 154.000 Referenzmustern von Getreideähren und Früchten.

Die Erhaltung der Sammlung erfolgte in Gatersleben (130.620 Akzessionen) und den beiden Außenstandorten Groß Lüsewitz (Kartoffelsortiment, 6.124 Akzessionen) und Malchow (Öl- und Futterpflanzen, 14.258 Akzessionen). Etwa 3.200 Akzessionen werden *in vitro* erhalten, hierunter befinden sich 2.900 Kartoffelakzessionen. Zur Absicherung der Lebendsammlung wird die Cryo-Sammlung von Kartoffel kontinuierlich ausgebaut und umfasst gegenwärtig 1.289 Akzessionen. Parallel hierzu wurde mit dem Aufbau einer Cryo-Sammlung für Knoblauch (*Allium sativum*) begonnen, die gegenwärtig 96 Akzessionen umfasst.

Etwa 4 % der Sammlung (6.658 Akzessionen) werden vegetativ erhalten, der Rest wird über Samen vermehrt. Der Vermehrungsanbau von 7.894 Akzessionen entspricht ca. 6 % der Samenträger, woraus sich eine mittlere Einlagerungszeit von etwa 17 Jahren ableiten lässt.

Zur Absicherung der weltweit in Genbanken gelagerten Saatgutbestände eröffnete der Global Crop Diversity Trust im Jahr 2008 im Permafrostboden von Spitzbergen ein Langzeitlager.

Department of Genebank

Head: Prof. Andreas Graner

General research goals

The Federal *ex situ* Genebank for agricultural and horticultural crops is one of the largest collections worldwide. It provides essential contributions to the implementation of the National Strategy for Biological Diversity and to the National Programme for the Conservation and Sustainable Utilisation of Plant Genetic Resources of Agricultural and Horticultural Crop Plants. At the European level, the Genebank is connected with the *European Cooperative Programme for Plant Genetic Resources* (ECPGR) in manifold ways. The overriding task of the department is the preservation and the characterisation of its genetic resources as well as the development of strategies aiming at their improved utilisation. In this context, comprehensive service activities are performed such as the allocation of seed, tuber and plant samples along with the corresponding information. Research topics of the department include the continued optimisation of the conservation management, investigation of biological processes involved in speciation and adaptation, clarification of taxonomic assignments within selected genera of crop and wild species and molecular genetic analysis of agronomically relevant characters and traits.

Developments in 2010 and 2011

Management of the ex situ collection

The Federal *ex situ* Genebank comprises 151,002 accessions from 3,212 species and 776 genera. Besides this living collection, the Genebank maintains a comprehensive herbarium which serves as reference centre for taxonomical studies and holds more than 420,000 voucher specimen as well as a collection representing 154,000 reference samples of spikes and fruits.

The collection is maintained in Gatersleben (130,620 accessions) and two satellite stations located at the Baltic Sea, Groß Lüsewitz (potato assortment, 6,124 accessions) and Malchow (oil and forage crops, 14,258 accessions). About 3,200 accessions are preserved *in vitro*, including 2.900 potato accessions. A cryo-collection of potato is continuously extended and currently comprises 1,289 accessions. It serves as a safety backup of the living collection. During the reporting period, a cryo-collection of garlic (*Allium sativum*) was initiated, presently comprising 96 accessions.

About 4 % of the collection (6,658 accessions) is propagated vegetatively, the rest is maintained as seeds. In the growing season 2010/2011 7,894 accessions were grown for seed multiplication, corresponding to about 6 % of the total collection, resulting in an average storage time per accession of about 17 years.

In order to increase the safety of the 7.4 million-odd seed samples maintained in genebanks across the world, the Global

Das IPK nutzt diese Möglichkeit zur Einlagerung von Sicherheitsduplikaten und hat seit der Eröffnung des **Global Seed Vault** nahezu 30.000 Samenmuster nach Spitzbergen geschickt. Die Genbank wird diese Aktivität fortsetzen, bis Sicherheitsduplikate aller Samenträger in den Kühllagern auf Spitzbergen deponiert wurden.

In den beiden vergangenen Jahren wurden insgesamt 21.788 bzw. 33.878 Muster abgegeben. Dies bedeutet einen erheblichen Anstieg gegenüber den Vorjahren. Die durchschnittliche Bearbeitungsdauer für Bereitstellung und Versand des Materials betrug 12 Tage ab dem Eingang der unterzeichneten Standard-Materialtransfer-Vereinbarung (SMTA). Sortimentsumfänge und Abgaben sind Tabelle 1, S. 25 zu entnehmen.

Im Berichtszeitraum stellten Privatpersonen mit insgesamt 23.260 Akzessionen die größte Nutzergruppe von Genbankmaterial dar, gefolgt von Forschungseinrichtungen (18.173) und Pflanzenzüchtern (7.901). Rund 23.000 Muster (41 %) wurden an Nutzer im Ausland abgegeben.

Seit 2007 verfügt die Genbank über ein Qualitätsmanagementsystem nach DIN EN ISO 9001:2008. Darin sind sämtliche Kernprozesse des Erhaltungsmanagements dokumentiert und durch Verfahrensregelungen und Arbeitsanweisungen unterlegt. Das Qualitätsmanagementsystem sichert Transparenz und Nachvollziehbarkeit der in der Genbank durchgeführten Arbeiten und liefert damit die Grundlage für die nachhaltige Sicherung des für die Sortimentserhaltung notwendigen Know-how. Zur Überprüfung des Qualitätsmanagementsystems sowie zur kontinuierlichen Verbesserung der Arbeitsprozesse werden in regelmäßigen Abständen interne Audits durchgeführt. Im Frühjahr 2010 wurde im Ergebnis eines externen Wiederholungsaudits der Zertifizierungsstatus um weitere drei Jahre verlängert.

Forschung

Die Abteilung Genbank ist in drei thematisch weitgehend kohärente Forschungsbereiche gegliedert: „Charakterisierung und Dokumentation", „Management und Evaluierung" sowie „Taxonomie und Evolution". In erster Annäherung lassen sich die Forschungsarbeiten in sammlungsbezogene und nutzungsbezogene Themen differenzieren. Das Ziel der sammlungsbezogenen Forschung ist ein verbessertes Erhaltungsmanagement. Die nutzungsbezogenen Forschungsarbeiten konzentrieren sich auf die Entwicklung von Ressourcen und Konzepten zur verbesserten Inwertsetzung der Gaterslebener Sammlung für die züchterische Anpassung von Kulturpflanzen. Hierbei stehen molekulargenetische Ansätze bei Getreide im Vordergrund. Eine Mittelstellung zwischen den beiden genannten Themen nehmen die Forschungsarbeiten zur Kulturpflanzentaxonomie und -evolution ein. Dort werden in erster Linie Fragestellungen aus dem Bereich der Gundlagenforschung bearbeitet.

Im Zentrum des Forschungsbereichs **„Taxonomie und Evolution"** stehen die Untersuchung von Artbildungsprozessen und die Aufklärung taxonomischer Beziehungen innerhalb ausgewählter Gattungen (*Hordeum, Allium, Hypericum*, u. a.). Hierbei ist die Gattung *Hordeum* aufgrund der großen Bedeutung der Kulturgerste (*Hordeum vulgare*) in der landwirtschaftlichen Praxis und für die Forschungsarbeiten am Institut von besonderem Interesse. Daneben zeichnet sich die 31 Arten umfassende Gattung durch eine

Crop Diversity Trust opened up a long-term storage facility established under permafrost conditions on the Norwegian island of Svalbard in 2008. IPK followed the invitation to store safety duplicates in the **Global Seed Vault** and has transferred by now some 30.000 seed samples. The Genebank will continue this effort in the years to come, until the whole collection will be secured in this way.

In the past two years, 21,788 and 33,878 samples were distributed, respectively. In comparison to previous years this represents a substantial increase. The average handling time amounts to 12 days from receipt of the signed Standard Material Transfer Agreement (SMTA) until dispatch of the seeds/tubers/plants. Further information on the collection and the distribution of accessions are presented in Table 1, p. 25.

In the reporting period, private individuals receiving a total of 23,260 accessions represented the largest user group, followed by research institutes (18,173) and plant breeders (7,901). About 23,000 accessions (41 %) were shipped abroad.

Since 2007 the Genebank deploys a Quality Management System (QM) according to standard DIN EN ISO 9001:2008. It documents and surveys all core processes pertaining to the conservation management. The QM warrants transparency and traceability of all relevant steps and provides the basis for the sustainable preservation of the ample know-how required for the conservation management. In 2010 the certificate was reconfirmed by an external audit.

Research

Research within the Genebank is structured into three coherent programmes: "Management and Evaluation", "Characterisation and Documentation" as well as "Taxonomy and Evolution". At first approximation the corresponding activities can be assigned on the one hand to research that is related to the collection proper and on the other hand to enhance the utilisation of plant genetic resources. The former aim at improvement of the conservation management of the collection whereas the latter aim at valorisation of plant genetic resources for the genetic improvement of crop plants. Major emphasis is put on implementation of molecular genetic approaches for cereal species, for trait mapping and gene discovery as well as research into evolution and domestication. In addition, research into taxonomy and evolution addresses mainly fundamental questions regarding speciation, adaptation and radiation of crop plants and their wild relatives.

The programme "**Taxonomy and Evolution**" deals with questions regarding the evolution of crop plants and related species (*Hordeum, Allium, Hypericum* etc.). The genus *Hordeum* has been used as a model for temperate grasses to gain insight into phylogenetic relationships, ecology and demographic history, because of the large significance of cultivated barley (*Hordeum vulgare*) both for agriculture and for research across all departments of the Institute. This genus, comprising 31 species, is characterised by an extraordinary diversity. It comprises both inbreeding and outbreeding species, diploid, tetraploid and hexaploid species, as well as annual and perennial forms. By means of phylogenetic and population genetic approaches as well as niche modelling, fundamental knowledge has been

Tabelle/Table 1:
Übersichten zum Bestand und zu den Transfers der Genbank nach Fruchtarten/Overview of collection and transfers from Genebank by crop species

Sortimente	Assortments	Bestand/ Accessions	Abgaben/Distribution 2010	2011
Getreide und Gräser	***Cereals and Grasses***	**65448**	**6725**	**7036**
Weizen	wheat	28111	3330	2932
Gerste	barley	23245	1571	1031
Hafer	oat	4835	315	119
Roggen	rye	2411	147	273
Triticale	Triticale	1581	8	26
Aegilops	*Aegilops*	1531	676	1549
Hirsen	millets	845	217	474
Mais	maize	1550	298	245
Gräser	grasses	1339	163	387
Leguminosen	***Legumes***	**28066**	**3470**	**3163**
Phaseolus	*Phaseolus*	9146	1421	776
Ackerbohnen	field beans	3283	399	344
Sojabohnen	soybeans	1514	176	70
Bohnen-Sonderkulturen	other beans	624	444	312
Erbsen	pea	5295	247	119
Kichererbsen	chickpea	531	80	799
Lathyrus	vetchling	524	30	64
Wicken	vetches	1878	223	383
Lupinen	lupins	2769	103	75
Linsen	lentils	475	113	101
Kleearten	clover species	1739	139	81
Sonstige	others	288	95	39
Cucurbitaceae	***Cucurbitaceae***	**2671**	**691**	**1311**
Kürbisse	pumpkins	1081	291	597
Melonen	melons	726	203	196
Gurken	cucumbers	709	126	459
Sonstige	others	155	71	59
Gemüse (+ Rüben)	***Vegetables***	**18794**	**3618**	**10838**
Tomaten	tomatoes	3544	680	2969
Paprika	pepper	1532	596	407
Eierfrüchte	eggplants	112	32	70
Beta	*Beta*	2320	254	100
Raphanus	*Raphanus*	750	178	89
Möhren	carrots	500	141	2804
Zichorie	chicory	690	98	164
Allium	*Allium*	3319	275	470
Brassica	*Brassica*	2184	411	262
Salat	lettuce	1130	146	399
Spinat	spinach	214	152	91
Sellerie	celery	252	50	508
Quinoa	*Quinoa*	957	11	1237
Sonstige	others	1290	594	1268
Öl-, Faser-, Farbpflanzen	***Oil, Fibre, Dye Plants***	**5526**	**1545**	**1844**
Lein	flax	2324	347	92
Sonnenblumen	sunflower	*691*	405	256
Farbpflanzen	dye plants	481	254	291
Faserpflanzen	fibre plants	187	65	185
Ölpflanzen	oil plants	557	234	488
Sonstige	others	1286	240	532
Arznei-, Gewürzpflanzen	***Medicinal, Spice Plants***	**8344**	**2370**	**5273**
Mohn	poppy	1149	141	239
Tabak	tobacco	590	61	145
Sonstige	others	6605	2168	4889
Mutanten	***Mutants***	**1771**	**51**	**108**
Tomaten	tomatoes	744	35	79
Soja	soybean	567	2	9
Antirrhinum	*Antirrhinum*	460	14	20
Kartoffeln	***Potatoes***	**6124**	**1981**	**1965**
Öl- und Futterpflanzen	***Oil and Forage Crops***	**14258**	**1327**	**2340**
Raps und Futterkohl	rapeseed and feeding kale	2472	714	1847
Gräser	grasses	10441	584	446
Rotklee und Luzerne	red clover and alfalfa	1345	29	47
Gesamt/Total		**151002**	**21778**	**33878**

außerordentliche Vielfalt aus. In ihr finden sich sowohl Selbst- als auch Fremdbefruchter, diploide, tetraploide und hexaploide Arten sowie einjährige und perennierende Formen. Durch den Einsatz phylogenetischer und populationsgenetischer Ansätze sowie mit Hilfe der Nischenmodellierung konnten in den vergangenen Jahren grundlegende Erkenntnisse über den räumlichen und zeitlichen Verlauf von Artbildung und Ausbreitung innerhalb der Gattung gewonnen werden. Darüber hinaus wurde gezeigt, dass die Entstehung polyploider *Hordeum*-Arten in der Mehrzahl auf die Hybridisierung diploider, teilweise bereits ausgestorbener Arten zurückzuführen ist. Nur bei einer Art konnte das Auftreten autopolyploider Formen nachgewiesen werden. Bei der Erarbeitung einer umfassenden Taxonomie für die ebenfalls durch große Vielfalt gekennzeichnete Gattung *Allium* konnten im Zuge von Sammelreisen in die natürlichen Verbreitungsgebiete in Zentralasien eine Reihe neuer Arten identifiziert werden. Ergänzend hierzu wurden wesentliche Fortschritte bei der Aufklärung der taxonomischen Beziehungen innerhalb der Untergattung *Melanocrommyum* erzielt.

Im Mittelpunkt der Forschungsarbeiten im Bereich **„Management und Evaluierung“** steht die weitere Verbesserung des Erhaltungsmanagements von vegetativ bzw. von über Samen vermehrten Genbankmustern. Im Hinblick auf die Erhaltung vegetativ vermehrter Pflanzenarten wurde an der weiteren Etablierung und Optimierung der Protokolle für Cryo-Konservierung von meristematischem Pflanzengewebe gearbeitet. Allerdings stellen samenvermehrte Akzessionen den weitaus größten Anteil der Sammlung dar. Dementsprechend ist die Lagerdauer von Saatgutproben ein wichtiger Faktor für die Effizienz des Erhaltungsmanagements. Einen weiteren Forschungsschwerpunkt in diesem Bereich stellt daher die Aufklärung der Prozesse, die zum Abbau der Keimfähigkeit von Saatgut führen, dar. Hieraus werden längerfristig wichtige Hinweise zur Verbesserung der Langlebigkeit von Saatgut erwartet. In diesem Zusammenhang wurden im Rahmen genetischer Untersuchungen bei Gerste und Weizen erste QTL für dieses Merkmal identifiziert. Des Weiteren konnte gezeigt werden, dass das Verhältnis von oxidiertem zu reduziertem Glutathion einen geeigneten Indikator für die Lebensfähigkeit von Gerstensaatgut darstellt.

Der Forschungsbereich **„Charakterisierung und Dokumentation“** befasst sich mit der molekulargenetischen Charakterisierung von Genbankmaterial auf DNA-Ebene sowie mit der Entwicklung und Pflege von Datenbanken zur Speicherung und Bereitstellung von genbankbezogenen Daten. Ein zentrales Element für die Speicherung und Verwaltung akzessionsbezogener Informationen stellt das Genbankinformationssystem (GBIS) dar. In dem System sind sämtliche Prozesse des Erhaltungsmanagements und des Bestellwesens abgebildet. Es erfolgt eine kontinuierliche Weiterentwicklung im Hinblick auf die Implementierung neuer Funktionalitäten, wie z. B. einem Modul für die Verwaltung von Charakterisierungs- und Evaluierungsdaten. Das System stellt zudem die Schnittstelle für den Datenexport zur Aktualisierung nationaler und internationaler Datenbanken zu pflanzengenetischen Ressourcen dar.

Wichtige Voraussetzung für die verbesserte Nutzbarmachung der in den Sammlungen vorhandenen genetischen Diversität sind Informationen zur Position, Struktur und Funktion von

gained regarding spatio-temporal processes of speciation and radiation within this species. Moreover, it could be shown that the emergence of polyploid species mainly results from interspecific hybridisation events, as all but one of the polyploid species are alloploids. In the context of elaborating a comprehensive taxonomy for the genus *Allium*, which is likewise coined by an extraordinary amount of diversity, several new species were collected and described in the context of research in Central Asia, which represents the natural range for many species in this genus. Furthermore substantial progress was made regarding the elucidation of the taxonomic structure with the subgenus *Melanocrommyum*.

Research within the programme “**Management and Evaluation**” focuses on further optimisation of the conservation management. In this context, the maximum storage duration for seeds is an important parameter regarding the economy and efficiency of the conservation management. As mentioned above, seed borne accessions make up for the vast majority of the collection and each increase in the average seed longevity would represent an important contribution to the improvement of the efficiency of the conservation management. Hence, genetic and physiological processes are investigated that lead to a decrease in the germination ability of seeds. Elucidation of these processes may provide important clues regarding the improvement of seed longevity. In this regard, genetic analyses in wheat and barley resulted in identifying first QTLs for this trait. Moreover, it could be demonstrated that the ratio of oxidised to reduced glutathion is a useful indicator of seed longevity.

The programme “**Characterisation and Documentation**” comprises the characterisation of genetic resources at the DNA level as well as the development and curation of databases for storage and provision of genebank-related data. In this regard, the Genebank Information System (GBIS) acts as a central hub for both storage and provision of accession-based data. The system has implemented all steps of the conservation management and purchase order processing. It is continuously updated regarding the implementation of new functionalities, such as a module for the administration of characterisation and evaluation data. In addition the system serves as an interface for the export of data into national and international databases on plant genetic resources.

To further improve the valorisation of plant genetic resources, information is required on position, structure and function of genes involved in the expression of agricultural characters and traits. In this context, research into trait mapping and gene isolation is mainly focused on barley and wheat. Genetic mapping increasingly targets quantitative traits and trait components by employing genome-wide linkage disequilibrium mapping using SNP marker chips for high-throughput genotyping, which have been developed together with partners from the public and the private sector. Gene isolation is still focused on monogenic traits such as spike morphology (row-type, branching, compactness) and virus resistance. Research activities focusing on the development of a genomic sequence of barley have been initiated back in 2006 in the frame of the International Barley Sequencing Consortium (IBSC). Even when employing the most advanced sequencing technologies only small runs

Genen, welche an der Ausprägung agronomischer Merkmale beteiligt sind. Die in diesem Zusammenhang in der Abteilung durchgeführten Forschungsarbeiten zur Merkmalskartierung und Genklonierung konzentrieren sich auf Gerste und Weizen. Bei den Kartierungsarbeiten steht in zunehmendem Umfang die Erfassung quantitativer Merkmalsvariation mit Hilfe der genomweiten Assoziationskartierung im Vordergrund. Hierbei werden SNP-Marker-Chips für die Hochdurchsatz-Genotypisierung eingesetzt, an deren Entwicklung das Institut beteiligt war. Weiterführende Arbeiten zur Genklonierung konzentrieren sich auf monogen vererbte Merkmale, wie Ährenmorphologie (Zeiligkeit, Verzweigung, Kompaktheit) und Virusresistenzen.

Eine wesentliche Beschleunigung und Erleichterung der zeit- und ressourcenaufwändigen kartengestützten Klonierung agronomisch relevanter Gene stellt die Verfügbarkeit einer genomischen Sequenz dar. Technologische Fortschritte auf den Gebieten der DNA-Fragmentanalyse und -sequenzierung sowie in der Bioinformatik haben die Entschlüsselung komplexer Nutzpflanzengenome in den Bereich des Machbaren gerückt. Entsprechende Arbeiten zur Sequenzierung des Genoms der Kulturgerste (*Hordeum vulgare*) wurden bereits im Jahr 2006 im Rahmen eines durch das Institut ins Leben gerufenen internationalen Konsortiums (IBSC) aufgenommen. Da sich jedoch auch mit modernsten Sequenziertechnologien immer nur kleine DNA-Abschnitte entschlüsseln lassen, deren Assemblierung durch hochredundante, repetitive DNA-Fragmente häufig verhindert wird, stellt die Entwicklung einer physischen Karte eine wichtige Voraussetzung für die Erstellung einer kohärenten genomischen Sequenz dar. Bei dem Aufbau einer solchen Karte wurden die sieben Gerstenchromosomen durch ein Gerüst überlappender, in bakterielle Plasmidvektoren klonierter DNA-Fragmente (BAC-Klone) rekonstituiert (Abb. 11, S. 22). Einzelne Chromosomenbereiche können nun durch Auswahl entsprechender, überlappender BAC-Klone systematisch sequenziert und assembliert werden. Auch wenn auf dem Weg zu einer qualitativ hochwertigen Genomsequenz noch einige Hindernisse überwunden werden müssen, lieferten die bereits verfügbaren Sequenzen, in denen nahezu alle Gene der Gerste erfasst sind, wichtige Erkenntnisse zur Evolution dieses Nutzpflanzengenoms. Sie ermöglichten darüber hinaus die Entwicklung einer Vielfalt analytischer Ressourcen für die Genomanalyse. Diese werden in absehbarer Zeit die systematische Resequenzierung umfangreicher Genbankkollektionen einleiten und damit neue Wege für die weitere Erforschung und die wissensbasierte Inwertsetzung pflanzengenetischer Ressourcen eröffnen.

Weitere Einzelheiten zu den aufgeführten Forschungsthemen und damit verbundenen Projekten sind den nachfolgenden Berichten der einzelnen Arbeitsgruppen zu entnehmen.

Andreas Graner, November 2011

of DNA can be deciphered (although by the billions). The assembly of such sequence fragments is strongly compromised by repetitive DNA, which is highly abundant in cereal genomes. The availability of a physical map represents an important prerequisite to reduce the complexity of the DNA fragments to be sequenced in order to facilitate assembly of a coherent genomic sequence. Towards the construction of a physical map of the barley genome the seven barley chromosomes were reconstituted by a scaffold of overlapping DNA fragments cloned into bacterial plasmid vectors (BAC clones, Fig. 11, p. 22). This allows for sequencing and assembly of defined chromosomal regions by selecting a corresponding set of overlapping BACs forming a so-called minimum tiling path. Even though there are still obstacles to be negotiated on the way to a high quality genomic sequence of barley, the presently available sequence information comprises nearly all barley genes and yielded important findings about the evolution of this genome. The sequence information also facilitated the development of manifold analytical resources such as SNP markers and DNA arrays. In the foreseeable future these will usher in the systematic re-sequencing of genebank collections and thereby blaze the trail for a thorough investigation and a knowledge-based valorisation of plant genetic resources. Further details of the mentioned and many other research and service activities of the department will be found in the subsequent reports of the individual research groups.

Andreas Graner, November 2011

PROGRAMME: CHARACTERISATION AND DOCUMENTATION
Research Group: Genome Diversity

Head: Prof. Andreas Graner, Dr. Nils Stein

Scientists

IPK financed
Ariyadasa, Ruvini Tharanga, Dr. (Pakt für Forschung und Innovation, since 01.07.2011)
Himmelbach, Axel, Dr. (Pakt für Forschung und Innovation, 01.05.2010-31.10.2011)
Kilian, Benjamin, Dr. (till 28.02.2014)
Pasam, Raj Kishore (0.50, since 01.07.2011)
Poursarebani, Naser (0.50 Pakt für Forschung und Innovation, 01.07.-31.12.2011)
Sharma, Rajiv (0.50, since 30.06.2011)

Grant Positions
Ariyadasa, Ruvini Tharanga, Dr. (BMBF, till 30.06.2011)
Dhanagond, Sidram (0.50 BMBF, since 17.11.2011)
Himmelbach, Axel, Dr. (BMBF, since 01.11.2011)
Jost, Matthias (0.50 DFG, 01.07.-31.10.2011; 0.50 BMBF, since 01.11.2011)
Neumann, Kerstin (0.50/1.00 BMBF, since 01.09.2010)
Pasam, Raj Kishore (0.50 BMBF, till 30.06.2011)
Poursarebani, Naser (0.50 BMBF, till 30.06.2011)
Saal, Bernhard, Dr. (BMBF, 01.01.-30.04.2010)
Schmutzer, Thomas (0.50 BMBF, till 31.12.2010)
Sharma, Rajiv (0.50 DFG, till 29.06.2011)
Yang, Ping (0.50 BMBF, since 01.09.2010)
Zhou, Ruonan, Dr. (0.50 BMBF, till 30.06.2011; 0,50 EU)

Visiting Scientists/Scholars
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Bartos, Jan, Dr. (self-financed, 22.03.-26.03.2010)
Filatenko, Anna, Dr. (DFG, 22.05.-31.10.2011)
Fricano, Agostino (BMBF, 22.03.-26.03.2010)
Gottwald, Sven, Dr. (self-financed, till 28.02.2011)
Gradin, Therese (Södertörn University, 01.02.-28.02.2010)
Imri, Ben-Israel (IPK and self-financed, 19.06.-26.06.2011)
Konovalov, Fedor A., Dr. (DFG, 01.03.-31.05.2010; self-financed, 18.11.-18.12.2010; IPK, 04.06.-19.06.2011)
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Maccaferri, Marco, Dr. (University Bologna, 22.03.-26.03.2010)
Manninen, Outi, Dr. (self-financed, 22.03.-26.03.2010)
Moisy, Cedric, Dr. (self-financed, 22.03.-26.03.2010)
Obidiegwo, Oskar (University of Hohenheim and IPK, 28.08.-02.09.2011)
Paquariello, Marianna, Dr. (self-financed, 15.03.-30.05.2010 and 28.08.-27.09.2011)
Perovic, Dragan, Dr. (JKI Quedlinburg, 01.01.-30.04.2010 and 01.06.-31.12.2010)
Schulte, Daniela, Dr. (self-financed, 01.02.-31.12.2010)
Shaaf, Salar (Iranian government, 11.02.-25.09.2010)
Shi, Bu-Jun, Dr. (University of Adelaide, 27.02.-02.03.2011)
Turktas, Minne, Dr. (self-financed, 22.03.-26.03.2010)
Yang, Ping (self-financed, 24.08.-31.08.2010)

Goals

Development of genomics-based approaches to valorise plant genetic resources of barley (*Hordeum vulgare*) to facilitate the understanding of structural and functional principles that impinge on variation in agronomic and adaptive traits as well as identification of the effects of evolutionary and selective forces that shape the genome of this species.

Research Report

Knowledge about the structure and function of genes that underlie agronomic traits forms a prerequisite for the systematic analysis and exploitation of the genetic resources of a given crop plant. Against this backdrop the research programme connects **phenotypic analysis, trait mapping and structural genomics** to conduct both hypothesis-driven and explorative research aiming at the identification and validation of genes with agricultural relevance. Genomics resources are being developed with special focus on barley (*Hordeum vulgare*) and comprise high-density genetic marker maps, a physical BAC-contig map and a genomic sequence. Activities with regard to trait mapping include the analysis of biparental progenies to develop high-resolution maps for selected characters and the analysis of quantitative traits based on whole genome association mapping. To facilitate an in-depth analysis of quantitative traits, a phenotyping project has been started to analyse plant growth over time using automated image capture and image analysis systems.

In order to characterise the extent of linkage disequilibrium (LD) 1,536 SNPs were interrogated to genotype a comprehensive panel of accessions representing three different gene pools: (i) 282 European spring and 112 European winter barley cultivars (HVCC), (ii) 322 landrace accessions from Syria and Jordan (LRC) and (iii) 216 wild barley (*Hordeum vulgare* ssp. *spontaneum)* accessions from Israel (HSC). Genome-wide LD decay was found to be within the range of 7-10 cM in HVCC, <5 cM in LRC and <1 cM in HSC. In collaboration with the research group Transcriptome Analysis all gene pools were screened for quantitative resistance to powdery mildew (*Blumeria graminis* f.sp. *hordei*) using poly-virulent pathotypes. Moreover, twenty agronomical traits were scored in eight European environments from 2008 till 2010 in collaboration with an EU-wide consortium. Using **genome-wide association (GWA) analysis** significant

SNP associations were found for a series of agronomic characters and traits including plant height, heading date and internode length (R. Sharma, A. Graner, B. Kilian). In a similar approach, a panel of 224 spring barley accessions was analysed based on 918 informative SNPs and 1,037 DArT markers 57 novel QTL were detected (R. Pasam, B. Kilian, A. Graner).

The two studies revealed that despite the high extent of LD in cultivated barley the insufficient redundancy of SNP markers severely limits the genetic power of GWA mapping. Therefore, a **high-density SNP chip** (iSELECT, Illumina) has been developed in a collaborative effort with the James Hutton Institute, Scotland and Trait Genetics GmbH. The array contains 7,864 bi-allelic SNPs that were previously validated in a broad range of barley accessions to maximise marker information content and to minimise ascertainment bias. Fig. 12 shows the massive increase in significant effects, when increasing the number of SNP markers from 918 to 5,600 (R. Pasam, B. Kilian).
Landraces are unexplored resources of allelic diversity and contain useful alleles for crop improvement. In order to capture the genetic and phenotypic diversity, a large collection of spring barley landraces has been selected from the genebank. This set of 1,491 purified landraces originating from 40 countries from 5° N to 62.5° N and 16° W to 71° E, was genotyped with 45 SSR markers to assess the genetic diversity and population structure. A total of 372 alleles were detected among which 152 are rare alleles. Given the genetic and geographic diversity, this **landrace collection forms a resource for future association studies** (R. Pasam, A. Graner, B. Kilian).

Being a member of the network of excellence in agricultural and nutrition research funded by the BMBF, non-invasive **sensor technologies were applied for systematic phenotyping**. Using a LemnaTec HTS-Scanalyzer 3-D system, plant growth has been monitored under various stress conditions via automated image analysis. Plants were phenotyped on a daily basis using top and side cameras to capture images at different wavelengths. Phenotypic data were analysed in collaboration with the research group Image Analysis. Correlations of fresh weight and digital biomass were sufficient (R^2 >0.95) to estimate the accumulation of above ground biomass by using image data (K. Neumann, A. Graner, B. Kilian).

The construction of a generic physical map is a central task of the internationally coordinated effort towards sequencing the whole barley genome (International Barley Sequencing Consortium, IBSC, http://barleygenome.org). To this end, an automated fingerprint assembly was generated based on about

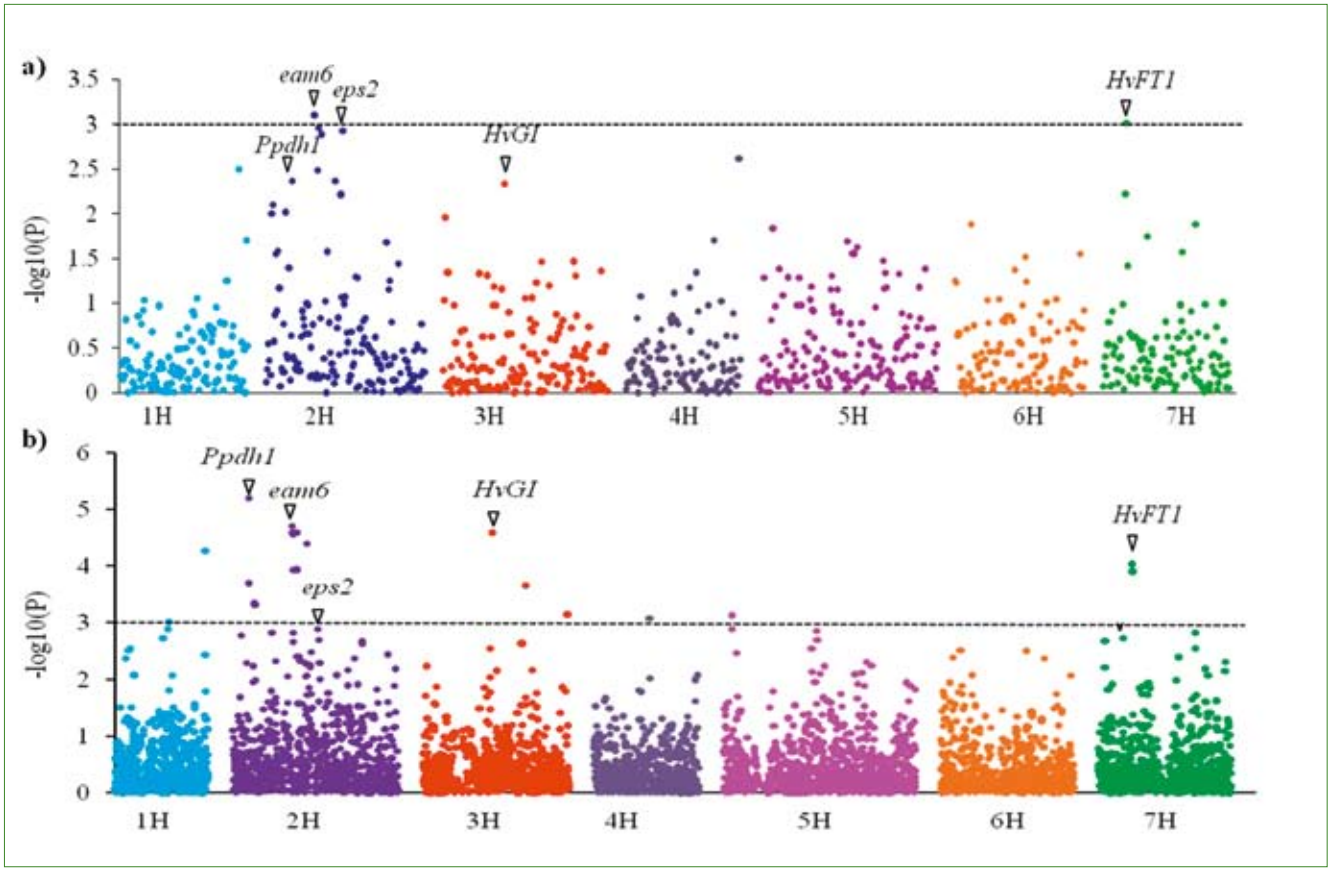

Fig. 12
Effects of marker density on genome-wide association analysis of heading date in a panel of 224 spring barley accessions. Associations were computed using a Mixed Linear Model using the kinship coefficient (K) to account for population structure. The K-matrix was based on 918 informative SNP markers. In the upper panel (a) the same 918 markers were employed for association analysis while in the lower panel (b) 5,600 SNP markers were analysed. The y-axis gives the significance level for each marker and the dashed line indicates the significance threshold of log P = 10^{-3}. SNP markers are represented as dots with different colors representing the individual barley chromosomes (1H-7H). Markers are ordered according to their position on the genetic map, with the short arm of each barley chromosome pointing to the left. Approximate genetic positions of known genes for flowering time are indicated by arrowheads. Higher significance levels were attained in b) due to increased number of SNP markers (i) located in close vicinity to and (ii) in linkage disequilibrium with the marked flowering time genes (R. Pasam).

13-fold haploid genome coverage of BAC clones originating from 5 different BAC libraries of the barley cultivar 'Morex'. This resulted in less than 10,000 BAC contigs representing 99 % of the barley genome. Anchoring of the draft contig map to the genetic map of barley could build on diverse datasets of marker/gene information obtained by different partners of the IBSC consortium (IPK/Gatersleben, Helmholtz Center/ Munich, Leibniz Institute of Age Research/Jena, James Hutton Institute/Dundee, University of California/Riverside, Kansas State University/Manhattan). This included on the one hand genes/markers assigned to BAC addresses by PCR/array-based screening of multidimensional BAC pools. On the other hand, genetic marker information was integrated by *in silico* sequence comparison between BAC end sequences, sequenced BAC clones, Whole-Genome Shotgun Assembly sequence and Genotyping-by-Sequencing signatures (D. Schulte, R. Ariyadasa, R. Zhou, N. Poursarebani, N. Stein).

A Minimum Tiling Path (MTP) of the physical map comprising 70,000 BACs was defined as a major deliverable during physical map construction. The MTP was rearrayed in a chromosome-wise manner at CNRGV Toulouse, France, and is readily available for being utilised in any attempt of map-based sequencing the barley genome. A project funded by the Leibniz "Pakt für Forschung und Innovation" is taking advantage of this new resource while heading for **sequencing barley chromosome 3H**. Based on previous experience of shotgun sequencing BAC clones on the Roche/454 GSFLX Titanium platform, more than 3,000 BAC clones (40 %) of the chromosome 3H Minimum Tiling Path will be sequenced and assembled to Phase I status (A. Himmelbach, N. Stein).

Next Generation Sequencing (Roche/454) of sorted barley chromosomes allowed gathering information of the overall gene content and gene-order of barley chromosome 1H in a first pilot study. Subsequently, all further 12 barley chromosome arms were shotgun sequenced to ~1-fold coverage and the resulting sequence information was used in frame of a close collaboration with the Helmholtz Center/Munich, the James Hutton Institute/Dundee and the Institute of Experimental Botany/Olomouc for developing **linear gene order maps ("genome-zippers") of the entire barley genome**. The same approach was used to sequence the homoeologous wheat chromosomes 1A, 1B and 1D and is further explored for sequencing all rye chromosomes (N. Stein).

Besides the efforts of unlocking the barley genome for whole genome sequencing, the genomic resources developed for barley are being used for map-based cloning of genes underlying important economical or developmental/ morphological traits. Emphasis is put on the elucidation of the genetic basis of *Bymovirus* resistance in barley. After the successful cloning of the gene *rym*4/5 resistance gene in 2005, we made, in collaboration with the Julius Kühn-Institute/ Quedlinburg, substantial progress in the **map-based isolation** of a second recessive resistance gene. The value of the available genomics resources is highlighted by the fact that this project did not require any attempt of chromosome walking, since the physical map provided direct access to a physical BAC contig comprising the closest flanking markers on either side of the gene. While functional characterisation of the gene is in progress, high-resolution mapping of three additional recessive resistance loci is underway (P. Yang, A. Graner, N. Stein).

Publications

Peer Reviewed Papers

2010

Cockram, J., J. White, D.L. Zuluaga, D. Smith, J. Comadran, M. Macaulay, Z. Luo, M.J. Kearsey, P. Werner, D. Harrap, C. Tapsell, H. Liu, P.E. Hedley, N. Stein, D. Schulte, B. Steuernagel, D.F. Marshall, W.T. Thomas, L. Ramsay, I. Mackay, D.J. Balding, T.A. Consortium, R. Waugh & D.M. O'Sullivan: Genome-wide association mapping to candidate polymorphism resolution in the unsequenced barley genome. Proc. Natl. Acad. Sci. U.S.A. 107 (2010) 21611-21616.

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Haseneyer, G., S. Stracke, H.P. Piepho, S. Sauer, H.H. Geiger & A. Graner: DNA polymorphisms and haplotype patterns of transcription factors involved in barley endosperm development are associated with key agronomic traits. BMC Plant Biol. 10 (2010) 5.

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Özer, S., T. Karaköy, F. Toklu, F.S. Baloch, B. Kilian & H. Özkan: Nutritional and physicochemical variation in Turkish kabuli chickpea (*Cicer arietinum* L.) landraces. Euphytica 175 (2010) 237-249.

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Wang, G., I. Schmalenbach, M. von Korff, J. Léon, B. Kilian, J. Rode & K. Pillen: Association of barley photoperiod and vernalization genes with QTLs for flowering time and agronomic traits in a BC2DH population and a set of wild barley introgression lines. Theor. Appl. Genet. 120 (2010) 1559-1574.

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Yediay, F.E., F.S. Baloch, B. Kilian & H. Özkan: Testing of rye-specific markers located on 1RS chromosome and distribution of 1AL.RS and 1BL.RS translocations in Turkish wheat (*Triticum aestivum* L., *T. durum* Desf.) varieties and landraces. Genet. Resour. Crop Evol. 57 (2010) 119-129.

2011

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Books and Book Chapters

2010

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Graner, A., A. Kilian & A. Kleinhofs: Barley genome organization, mapping and synteny. In: Ullrich, S.E. (Ed.): Barley: Production, Improvement, and Uses. Blackwell Publishing Ltd., Oxford/UK (2011) 63-84.

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Other Papers

2010

Graner, A.: Research along the value chain of biodiversity. Public Service Review. Sci. Technol. 7 (2010) 160-161.

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2011

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PhD and Diploma Theses

2011

Jost, M.: Genetische Kartierung der Ährenmorphologie – Mutante *laxatum.a* in Gerste. (Diploma Thesis) Martin-Luther-Universität Halle-Wittenberg, Halle/S. (2011) 69 pp.

Weissgerber, W.: Evolution der Spindelbrüchigkeit bei Gerste. (Diploma Thesis) Martin-Luther-Universität Halle-Wittenberg, Halle/S. (2011) 152 pp.

Additional Publications *2009*

Turuspekov, Y., I. Honda, Y. Watanabe, N. Stein & T. Komatsuda: An inverted and micro-colinear genomic region of rice and barley carrying the *cly1* gene for cleistogamy. Breed. Sci. 59 (2009) 657-663.

Patents

2010

Gottwald, S. & N. Stein: "Six-row-type barley". WO 2010/076279; Anmeldetag: 02.01.2009, Offenlegung: 07.07.2010, IPK Nr. 2008/08.

Research Group: Genebank Documentation

Head: Dr. Helmut Knüpffer

Scientists

IPK financed
Oppermann, Markus
Stephanik, Andreas (till 31.01.2010)

Visiting Scientists/Scholars
Jinjikhadze, Tamar (Tbilisi Botanical Garden, 19.03.-29.03.2011)
Stephanik, Andreas (self-financed, 01.02.-31.12.2010)

Goals

Development and maintenance of information systems for plant genetic resources (PGR) with the aim to provide information on PGR to researchers, breeders and other users, and to support the management of genebank material.

Research Report

The group's activities were focused on the continuous maintenance, development and extension of the **Genebank Information System (GBIS)**. GBIS is being developed in an Oracle environment.
(1) **GBIS/M**, the internal genebank management system, offers numerous functions supporting the day-to-day genebank activities. The module for handling characterisation and evaluation (C&E) data of genebank accessions was completed. This includes interaction with the pocket PCs used for C&E data recording in the field (**GBIS/B**), as well as visualisation, editing and searching C&E data via GBIS/M (A. Stephanik, M. Oppermann). The development of the *in vitro* storage module (Fig. 13) and the complete integration of the Groß Lüsewitz potato collection (Satellite Collections North) in GBIS started in 2010 (C. Dittmann, M. Oppermann, cooperation with K. Dehmer). The *Allium* Taxonomic Reference Collection of the research group Taxonomy of Plant Genetic Resources (R. Fritsch) was fully integrated in GBIS (M. Oppermann).
The developers' (technical) documentation for GBIS/M and the user manual are updated annually. Bugfixing, the implementation of change requests, and improving the user-friendliness of GBIS are continuously carried out. The data base was increased and further consolidated, and the data quality was improved (M. Oppermann, H. Knüpffer).

(2) **GBIS/I**, the internet portal for searching and ordering genebank accessions (http://gbis.ipk-gatersleben.de/gbis_i/), provides online access to 148,500 accessions of the IPK Genebank collections at Gatersleben, Malchow and Groß Lüsewitz. It is being used by 75 % of the users for material requests.
Integration of IPK data in information networks. Passport data of genebank accessions were repeatedly exported and submitted to the German National Inventory of PGR (PGRDEU),

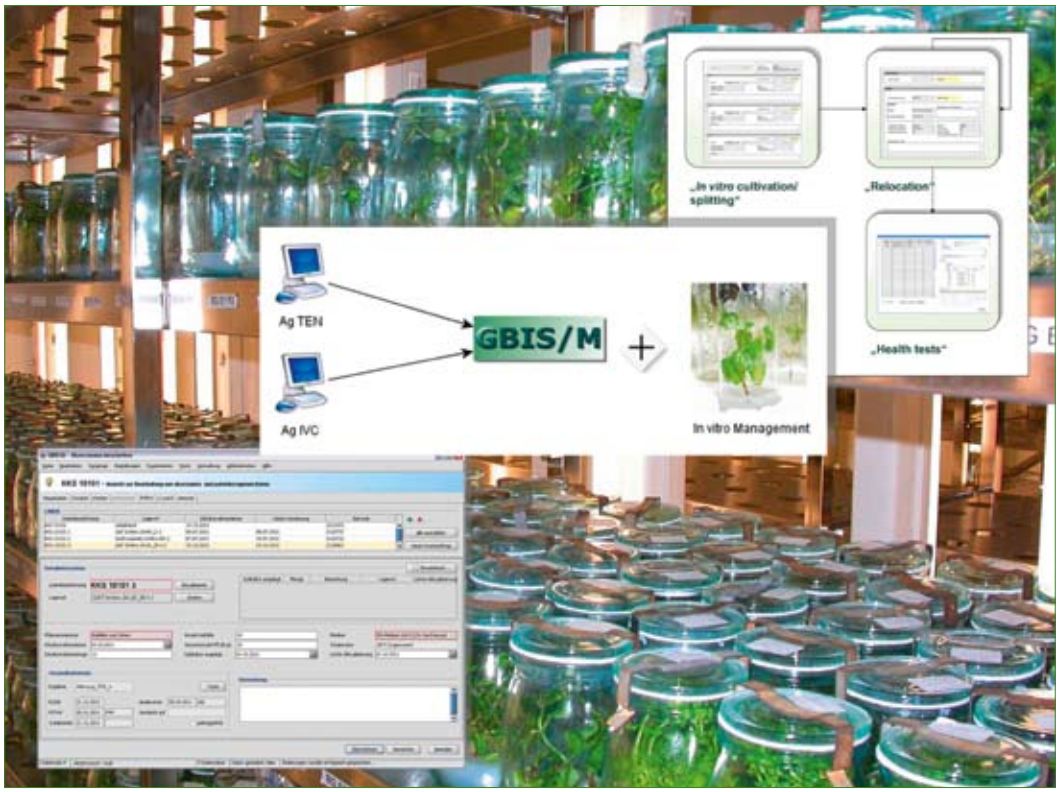

Fig. 13
The GBIS/M project "*In vitro* Management" aims at integrating the *in vitro* preservation activities of the research groups *In vitro* Storage und Cryopreservation and Satellite Collections North into the Genebank Information System GBIS/M. The background figure depicts an *in vitro* storage room. The image on the bottom left shows the extended management system of GBIS/M. On the right side, the three daily work processes, i.e. "*In vitro* cultivation/Splitting", "Relocation" and "Health tests" are shown (Photo: IPK Gatersleben/C. Dittmann).

the European Central PGR Search Catalogue (EURISCO), and numerous ECPGR European Central Crop Databases. GBIF (Global Biodiversity Information Facility) is accessing IPK's passport data via a web service.

The group is presently updating the **European Barley Database** (EBDB) (H. Knüpffer, M. Oppermann) and it is maintaining the **European *Poa* Database** of the European Cooperative Programme for Plant Genetic Resources (ECPGR), the latter together with E. Willner (Satellite Collections North). Via an interface, passport and observation data from GBIS are accessed by the **Garlic and Shallot Core Collection Database** (GSCC) (J. Keller, research group *In vitro* Storage and Cryopreservation, in cooperation with research group Bioinformatics and Information Technology) and by the **Diversity Studies Toolkit 2** (DISTo2) developed by the research group Bioinformatics and Information Technology for the *Lolium* collection.

The group is also maintaining other databases: **Mansfeld's World Database of Agricultural and Horticultural Crops** (http://mansfeld.ipk-gatersleben.de) and the in-house **Database for Checklists of Cultivated Plants** (not online) (M. Oppermann, H. Knüpffer).

The **automatic IPK weather stations** in Gatersleben and Malchow (since 2011) are operated by the group, and the data generated are made publicly accessible via the IPK website (M. Oppermann).

Publications

Peer Reviewed Papers

2010

Knüpffer, H.: The Balkan Collections 1941-1942 of Hans Stubbe in the Gatersleben Gene Bank. Czech J. Genet. Plant Breed. 46 (2010) S27-S33.

van Hintum, T. & H. Knüpffer: Current taxonomic composition of European genebank material documented in EURISCO. Plant Genet. Resour. 8 (2010) 182-188.

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Other Papers

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2011

Endresen, D.T.F. & H. Knüpffer: The Darwin Core extension for genebanks opens up new opportunities for sharing genebank datasets. In: Endresen, D.T.F.: Utilization of plant genetic resources. A lifeboat to the gene pool. (PhD thesis) Faculty of Life Sciences, Univ. Copenhagen (2011) 121-142.

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2010

Höppner, F. & H. Knüpffer: Status report on the German collections of flax and hemp. Report, ECP/GR Fibre Crops (Flax and Hemp) Working Group 1st meeting, Wageningen, The Netherlands, 14 – 16 June 2006. http://www.ecpgr.cgiar.org/Workgroups/Flax_Hemp/Flax%20Presentations%202006/Germany_Country_report_final.pdf (2010).

Oppermann, M., J. Keilwagen, H. Knüpffer, S. Friedel & A. Börner: Validation, analysis and aggregation of long-term trait observation data of genebank material. In: Weitzmann, A.L. (ed.), Proceedings of TDWG (2010). Woods Hole, Massachusetts, USA (2010) 52-53. http://www.vliz.be/imisdocs/publications/215525.pdf (2010).

Weise, S., N. Biermann, S. Flemming, J. Vorwald, T. van Hintum, H. Knüpffer & I. Grosse: Proposal for improvement of PGR data exchange through XML. Proceedings of the EPGRIS Final Conference, 11-13 September 2003, Prague, Czech Republic. International Plant Genetic Resources Institute (IPGRI). http://www.ecpgr.cgiar.org/Networks/Info_doc/FinalMeeting Presentations/Papers/Bierman_IPK_v0.14.doc (2010).

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2011

Knüpffer, H., L. Maggioni, M. Jalli, A. Kolodinska, D. Fasoula & E. Lipman: Report of a working group on barley. Seventh meeting, 10-12 May 2011, Nicosia, Cyprus. Bioversity International, Rome, Italy. ii+43 pp. http://www.ecpgr.cgiar.org/fileadmin/www.ecpgr.cgiar.org/NW_and_WG_UPLOADS/Barley_7_Cyrpus/Barley_7_Cyprus_revised210911.pdf, (2011)

Maggioni, L., A. Katsiotis, H. Knüpffer, G. Kleijer & E. Lipman: Report of a Cereals Network. Second Meeting, 21-24 April 2008, Foça, Turkey. May 2011. Bioversity International, Rome, Italy (2011) iv+64 pp. http://www.ecpgr.cgiar.org/fileadmin/bioversity/publications/pdfs/1437_Report%20of%20a%20cereals%20network%20second%20meeting%2021-24%20April%202008%20Fo%C3%A7a%20Turkey.pdf?cache=1304494577 (2011).

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Additional Publications 2009

Hovhannisyan, N., M.E. Dulloo, A. Yesayan, M.S. Röder, H. Knüpffer, A. Amri & A.M. Danielian: Wild relatives of wheat as sources of useful genes. In: In Vitro Cellular & Developmental Biology-Animal. Vol. 45, Springer, New York (2009) S82-S83.

Research Group: Plant Architecture

Head: Dr. Thorsten Schnurbusch

Scientists

IPK financed
Seidensticker, Tina (0.50)

Grant Positions
Alqudah, Ahmad Mohammad (0.65 DFG, since 28.09.2010)
Bini, Federica, Dr. (0.75/0.50 BMBF, 01.02.-31.12.2010; 0.25/0.50 Overhead, 01.11.2010-30.06.2011)
Gawroński, Piotr (0.50 DFG)
Koppolu, Ravi (0.50 DFG, since 16.03.2010)
Youssef, Helmy Mohamed, Dr. (0.50 Overhead, 01.02.-31.05.2011)

Visiting Scientists/Scholars
Bini, Federica, Dr. (self-financed, since 01.09.2011)
Fazeli, Arash (Ministry of Science, Research and Technology, Iran, 13.04.-12.10.2011; self-financed, 13.10.-31.12.2011; IPK, 01.01.-29.02.2012)
Shavrukov, Yuri, Dr. (self-financed, 19.05.-21.05.2010)
Youssef, Helmy Mohamed, Dr. (DAAD, 09.05.-09.07.2010)

Goals

Elucidating the developmental and molecular genetics of spike development in small grain cereals wheat and barley.

Research Report

Cereal grains are produced in specific plant organs called ears or spikes. Spike development of cereal crop plants, such as barley (*Hordeum vulgare* L.) or wheat (*Triticum aestivum* L.), is one of the important determinants of reproductive success and is measurable as grain yield. Modern wheat cultivars typically have a 10 to 15 cm long spike with 17 to 25 spikelets attached to the rachis. Each spikelet - the actual inflorescence - is able to produce two to six seeds; each seed contained in florets. Cereal grains contributed more than 50 % of all food calories worldwide in 2006 (FAO Statistics 2008) and bread wheat represents the major cereal crop in Germany, where it is usually cultivated on more than 3 Mio ha annually. However, despite these facts our understanding of the developmental genetics of central features such as spike morphology and development is very limited. Functional knowledge of genes, which regulate key morphological and developmental traits such as inflorescence architecture, spikelet initiation or abortion, rachis internode length, or total number of rachis internodes is almost completely lacking in most of our cereal crops.

In the BMBF-funded project (GABI-FUTURE Start: T. Schnurbusch; T. Seidensticker) we are performing **detailed phenotypic analyses of spike mutants in wheat and barley** with a specific interest in spikelet formation and identity, as well as spike branching. The latter feature can be classified into three

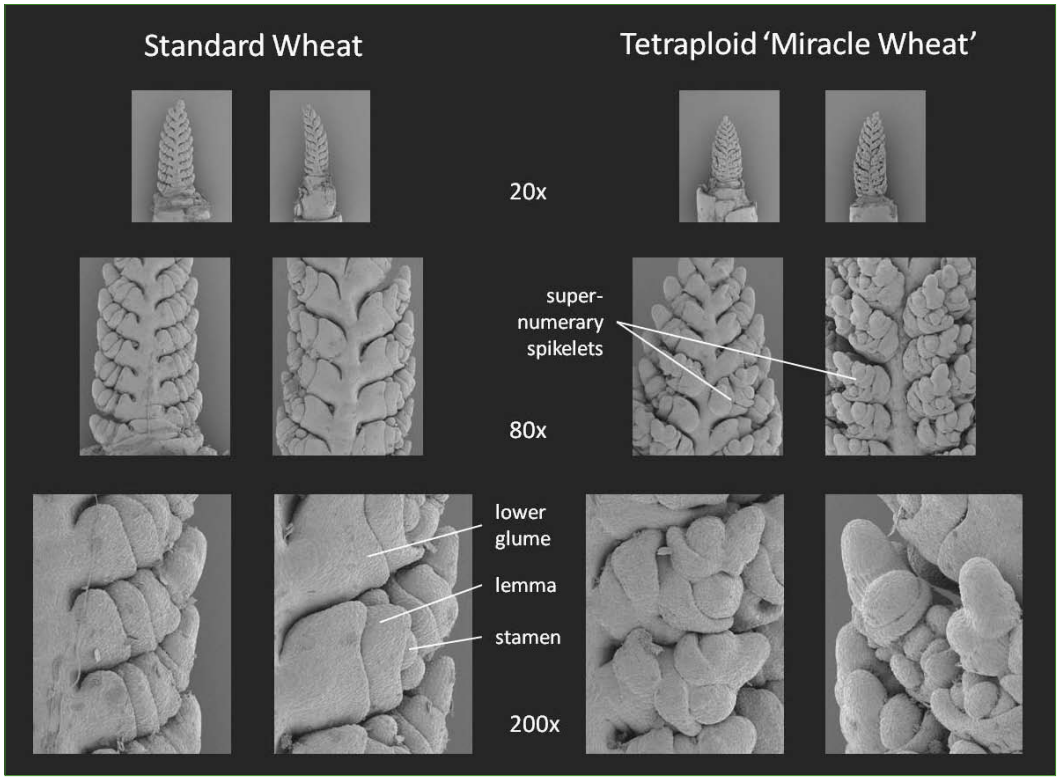

Fig. 14
Spikelet development in standard wheat and 'Miracle Wheat', including the development of supernumerary spikelets at floret primordium stage (Photo: IPK Gatersleben).

phenotypic classes based upon their corresponding branching phenotypes: (I) the hetero-branched spike possess two or more fully developed spikes which jointly emerge from the top of the peduncle; however, such mutant form is not part of our collection; (II) the pseudo-branched spike is a distinct feature of hexaploid *T. vavilovii* (Tumanian) Jakubz. and shows an extension of rachilla internodes; and (III) the branched spike, mainly occurring in tetraploid wheats (*T. turgidum* L. convar. *compositum* (L.f.) A. Filat.) and sometimes also known as "Miracle" or "Egyptian Wheat", "Wunderweizen" or "Blé d'Osiris", develops first order branches with additional, completely fertile spikelets preferentially at the base of the spike (Fig. 14, p. 35). Depending on the genotype and environmental conditions, the degree of branching can be reduced, and hence, only additional spikelets develop from one rachis node showing so called double, twin or supernumerary spikelets. The branched-spike phenotype is of particular interest to our research group since it might deliver one approach for increasing spikelet numbers per spike in wheat by modulating an important grain yield component. Developmentally, grain yield potential in current wheat cultivars is primarily influenced through the floret fertility per spikelet, i.e. whether two, three, four or more grains per spikelet develop. During the life cycle of wheat plants, the number of spikelets per spike is rather early determined, namely once the terminal spikelet has been formed. After terminal spikelet formation, no additional spikelets are formed, and thus, grain yield potential is mainly regulated through floret fertility. However, in the branched wheats this determinacy of spikelet development is usually not seen; a terminal spikelet develops only occasionally. Additional spikelets are still being formed on first order branches, hence commonly increasing total grain number *per spike* but in turn reducing the number of grains *per spikelet and* grain size. Nevertheless, elucidating the genetic and molecular factors, influencing **spikelet development and spike branching in "Miracle Wheats"** is one central goal of our research group.

The appearance of the *six-rowed spike* phenotype in barley is one of the important developmental processes that promoted barley domestication owing to its increased grain yield. Until today, five different loci have been identified which can convert two-rowed barley to six-rowed barley; they include *vrs1* (2HL), *vrs2* (5HL), *vrs3* (1HL), *vrs4* (3HS) and *int-c* (5HS). Komatsuda et al. (PNAS 2007, 104:1424–1429) identified the *Vrs1* gene as being an HD ZIP transcription factor and recently Ramsay et al. found *int-c* as the barley orthologue of maize *Teosinte Branched1* (Nat. Genet. 2011, 43:169-172). Among other *vrs* loci (*vrs2* and *vrs3*) *vrs4* is known to produce a prominent six-rowed phenotype with many fully fertile, long awned lateral spikelets. In our present DFG-funded project (R. Koppolu) we mapped the ***vrs4* locus** in two bi-parental mapping populations (Barke × *vrs4.k* and *vrs4.k* × Golden Promise; 96 individuals in each), using SNP-based CAPS and VeraCode markers, thereby applying the following research approach. The phenotype showed linkage to markers derived from chromosome 3HS. The corresponding marker-phenotype interval comprised 27 genes in *Brachypodium*, annotations of which revealed an important transcription factor involved in inflorescence development. Re-sequencing of the transcription factor in *vrs4.k* and its wild type MFB 104 showed a unique deletion in the *vrs4.k* mutant, resulting in a truncated gene product. Hence, we re-sequenced the gene in 18 *vrs4* mutant alleles available from NordGen, Sweden and USDA, USA; most of them showed nucleotide changes in the coding region, but also in upstream or downstream regions of the gene. Fine mapping and the establishment of a physical contig for the *vrs4* locus is already underway. Tissue localisation of *vrs4* gene expression through *in situ* hybridisations, its genetic networks by microarray analysis and a working model for the *six-rowed spike* pathway, involving *vrs4*, will soon become available.

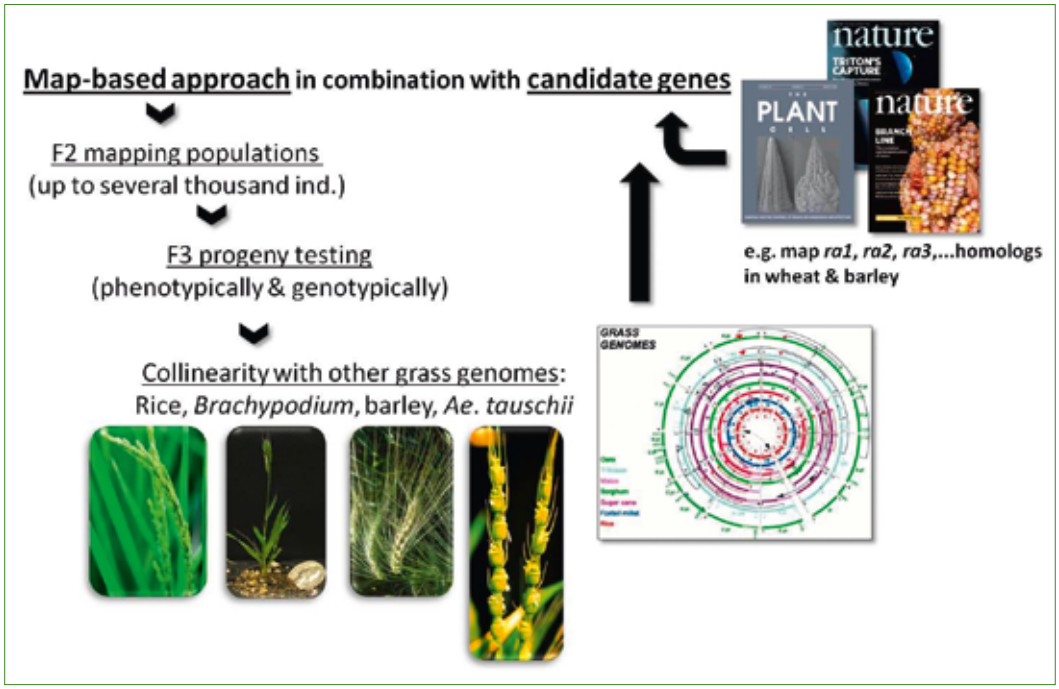

Fig. 15
Predominantly applied research approach within the research group Plant Architecture during the gene isolation process.

In cereal breeding, optimal adaptation to a given environment and subsequently high yield potential is mainly determined by the time of flowering. **Flowering time**, however, is commonly affected by a complex interplay between three determinants: photoperiodic and vernalisation requirements as well as the intrinsic capability of a cultivar/genotype to flower. In temperate grasses, such as wheat and barley, *earliness per se* (*Eps*) is understood as the intrinsic difference in flowering time of fully vernalised plants grown under long day conditions. In the current DFG-funded project (P. Gawroński), two einkorn wheat lines, RIL25 (early) and RIL71 (late), were selected from a RILWA1 population (*Triticum monococcum* L. × *T. boeoticum* Boiss.) to generate a new F2 population for **fine mapping of the *Eps-3A^m* locus**. About 650 F2 individuals were screened for genetic recombinations and new markers were added utilising the physical map from barley chromosome 3H. The locus could be delimited to ca. 350 kb and contained only two putative genes. Moreover, both genes were found to be deleted in the mutant parent of the RILWA1 population KT3-5 (*T. monococcum* L.) as well as in RIL25. One of the two genes deleted in the KT3-5 mutant belonged to the circadian clock which is known to regulate the photoperiodic flowering pathway. Therefore, two experiments were performed to verify whether circadian clock distortions could be observed: (i) results received from delayed fluorescence measurements indicated that the mutant KT3-5 had indeed an affected rhythm of the chloroplastic clock compared with wild type line KT3-1. And (ii) secondly, obtained gene expression data from a time-course qRT-PCR experiment on two key nuclear clock genes, Tm*TOC1* (*timing of CAB2 expression 1*) and Tm*LHY* (*late elongated hypocotyl*), supported our hypothesis that the *Eps-3A^m* locus had been affected in a gene belonging to the circadian clock.

Publications

(The publication with a "*" is based on work that has been carried out when Thorsten Schnurbusch was at the University of Adelaide, Australian Centre for Plant Functional Genomics, Australia).

Peer Reviewed Papers

2010

*Schnurbusch, T., J. Hayes, M. Hrmova, U. Baumann, S.A. Ramesh, S.D. Tyerman, P. Langridge & T. Sutton: Boron toxicity tolerance in barley through reduced expression of the multifunctional aquaporin HvNIP2;1. Plant Physiol. 153 (2010) 1706-1715.

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PROGRAMME: MANAGEMENT AND EVALUATION
Research Group: Resources Genetics and Reproduction

Head: Dr. Andreas Börner

Scientists

IPK financed
Lohwasser, Ulrike, Dr.
Nagel, Manuela, Dr. (0.50, till 30.06.2011)

Grant Positions
Nagel, Manuela, Dr. (ICARDA / GTZ, 01.07.-30.11.2011)
Pochepnya, Nadezhda (0.50 ICARDA / GTZ, 18.10.-31.12.2010)

Visiting Scientists/Scholars
Allam, Mai (DAAD, since 04.04.2011)
Danesh-Shahraki, Abdolrazagh, Dr. (University of Shahrekord, 13.07.-29.07.2010)
Daniel, Isaac, Dr. (Humboldt Foundation, 01.07.-26.09.2011)
Dobrovolskaya, Oxana, Dr. (DFG, 02.03.-03.04.2010; 31.10.-31.12.2010)
Jantassov, Serik (GIZ Bonn / Eschborn, 11.09.-17.09.2011)
Kruppa, Klaudia (Agricultural Research Institute Martonvásár, 10.01.-09.04.2011)
Neumann, Kerstin (self-financed, till 31.08.2010)
Rehman Arif, Mian Abdur (DAAD)
Stimolo, Lucia (self-financed, 23.08.-27.08.2010)
Tikhenko, Natalia, Dr. (self-financed, 04.04.-14.04.2010)
Weidner, Annette, Dr. (self-financed, till 30.06.2010)
Zaynali Nezhad, Khalil (Iranian Government, till 30.09.2010)

Goals

Long-term seed storage; reproduction, distribution, evaluation and genetic characterisation of genebank collections.

Research Report

The total number of accessions maintained at the Gatersleben site comprises 130,620 samples, of which 123,147 are preserved in the cold store. Safety duplicates are available for 29,963 accessions (ca. 20% of the whole collection). They are stored at the Global Seed Vault, Svalbard, Norway. In the reporting period **germination tests** were performed for 21,122 samples (S. Pistrick). 48,043 accessions (excluding the Satellite Collections North) were distributed to users. During the **regeneration** seasons 2009/2010 and 2010/2011 totals of 8,819 and 10,654 accessions were cultivated, respectively, including 772 and 523 samples grown for evaluation only (M. Grau, M. Kotter, K. Krusch, R. Kurch, B. Schmidt in collaboration with P. Schreiber, Experimental Fields and Nurseries). A taxonomic classification was performed for 8,588 accessions. Descriptor lists were created or revised for species of the genera *Anethum, Apium, Brassica, Crambe, Pastinaca, Phaseolus, Raphanus, Sinapis* and *Vicia* (U. Lohwasser).

The studies of the collection-related research on **seed longevity** in **barley** were continued. In cooperation with the research group Genome Diversity (N. Stein, B. Kilian) a highly saturated bi-parental mapping population together with an association mapping panel were investigated by exploiting experimental ageing tests following the rules of the International Seed Testing Association (M. Nagel, M. Gäbler, I. Daniel). The studies revealed loci which are assumed to be responsible for the disruption of the cellular homeostasis that enhances the production of reactive oxygen species. The major antioxidant glutathione (GSH) is generally affected by these stresses and was analysed in 26 accessions which were maintained in parallel at cold (0 °C) and ambient (20 °C) storage up to 15 years. Further six of them (harvested in 2008) were experimentally aged with low (13 %) and high (18 %) seed moisture content (smc). In all storage treatments, a general depletion of the total glutathione pool and a shift towards more oxidising conditions, expressed by the oxidised glutathione (GSSG), were seen with ageing (see Fig. 16A, p. 39). The drier seeds of ambient and cold storage had a higher GSSG concentration than the moister seeds exposed to artificial ageing, suggesting that enzymes were not active in the dry state to reduce GSSG to GSH. Ageing at 18 % smc was less destructive and enzymes could synthesise further GSH. Comparing six barley genotypes over different storage and ageing treatments showed that genotypes maintained germination but with different concentrations of total GSH which is assumed to be specific to the genotype and may depend on the pre-harvest conditions. Therefore highly significant correlations over all treatments were not found for GSH but for percentage of GSSG of the total glutathione pool and the half-cell reduction potential ($E_{GSSG\ /\ 2GSH}$) which both represent **good viability markers**. Testing the same material on tocopherols, (see Fig. 16B) and storage compounds namely oil content, starch and proteins (see Fig. 16C) revealed that these metabolites were not affected by ageing treatments (M. Nagel; collaboration with H. Rolletschek, research group Heterosis).

Recently the genetic studies on **seed longevity** were extended to **wheat** and oilseed rape (M.A. Rehman Arif, M. Allam). For wheat an association mapping approach was initiated using long-term stored (35 years) accessions. The variation of seed germination (longevity) ranged between 0 and 94 %. The accessions were regenerated and experimentally aged in order to compare loci for seed longevity detected after long-term storage and accelerated ageing approach. Only a few common loci were discovered. It was concluded that different deterioration mechanisms may be involved in experimental ageing and conventional long-term cold storage.

Research to improve the utilisation of the cereal genebank collection is focused on agronomic traits but mainly **abiotic**

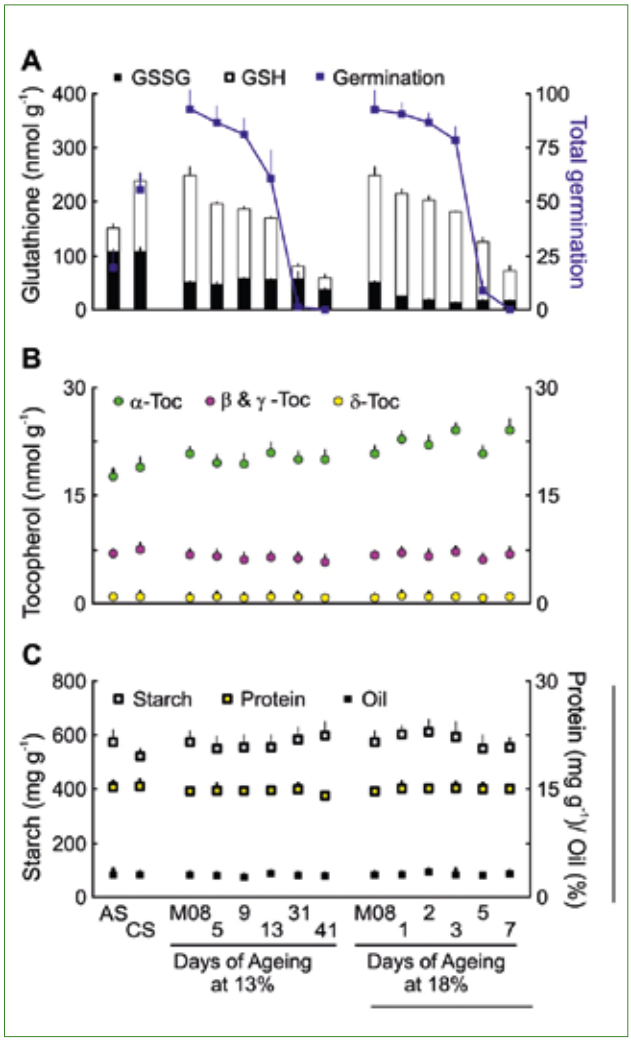

Fig. 16
Relationship between antioxidants, storage compounds and seed longevity. A) Glutathione (GSH, white bars) and the redox partner glutathionedisulphide (GSSG, black bars), are shown in relation to total germination (blue squares). B) α (green dot) β & γ purple dot) and δ (yellow dot). Tocopherol contents are shown and do not undergo changes during storage and artificial ageing. C) Seed storage reserves of protein (yellow square), oil (black square) and starch (grey square) did not change significantly in response to any treatment (M. Nagel).

stress tolerance (drought, pre-harvest sprouting) in barley and wheat. Loci determining the traits of interest were detected on different chromosomes via segregation (collaboration with M. Röder, research group Gene and Genome Mapping) and association mapping. For **drought tolerance** loci (marker trait associations) were detected on barley chromosomes 3HL, 4HL, 5HL and 6HS in regions carrying dehydrin (*Dhn*) genes. The dehydrin multigenes are known as regulatory genes for cold and drought stress tolerance (K. Neumann). Loci for **pre-harvest sprouting/dormancy** were detected on all seven homoeologous groups of wheat and on the chromosomes 2H, 3H, 5H, 6H, and 7H of barley. Already known regions on chromosomes 3A and 4A for wheat and 5H for barley were confirmed. Candidates as *viviparous1* gene on chromosome 3A, a protein belonging to the aquaporin family on chromosome 4A and the *aleurain* gene on chromosome 5H may be responsible for the characters investigated (U. Lohwasser, M.A. Rehman Arif, A. Marlow, S. Thumm).

Activities on **characterisation and evaluation** directed to *Petroselinum* were continued. The taxonomic classification based on morphological characters was verified. Using molecular markers root parsleys form a cluster together with some smooth leaf types. The other smooth and curled parsleys appear in a second cluster. Analysing essential oil compounds the content of myrcene and β-pellandrene are correlated with root and leaf parsley, respectively (R. Kurch, U. Lohwasser). A **European Project** on conservation and utilisation of leafy vegetables (*Lactuca, Spinacia, Cichorium, Valerianella, Eruca, Diplotaxis*) was successfully completed. The European-wide activities on regeneration and characterisation were coordinated by IPK (S. Thumm, K. Krusch, U. Lohwasser).

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Daniel, I.O., M. Kruse, G. Muller & A. Börner: A MS Excel implementation of the seed viability equation for managing gene bank collections of *Solanum melongena* and *Capsicum annuum*. Proceedings of the XIVth EUCARPIA Meeting on Genetics and Breeding of Capsicum & Eggplant, 30.08.-01.09.2010 Valencia, Spain, Universidad Politécnica de Valencia, Valencia, Spain (2010) 37-47.

Landjeva, S., U. Lohwasser & A. Börner: Mapping QTL for germination, seed vigour and longevity on wheat D genome. Berichte der Gesellschaft für Pflanzenbauwissenschaften, Bd. 5 (2010) 104-107.

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Nagel, M., I. Kranner & A. Börner: Langlebigkeit von Getreidesamen und deren genetische Ursachen. Berichte der Gesellschaft für Pflanzenbauwissenschaften, Bd. 5 (2010) 7-10.

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Rosenhauer, M., M. Nagel, E. Willner, F.-G. Schröder, R. Snowdon, W. Friedt & A. Börner: Genetische Untersuchungen des Merkmals Langlebigkeit von Saatgut der Spezies *Brassica napus* L. Berichte der Gesellschaft für Pflanzenbauwissenschaften, Bd. 5 (2010) 108-111.

Thumm, S., M.-L. Graichen, A. Börner & U. Lohwasser: Zwölf Institutionen aus zehn Ländern an Europa-Projekt zur Blattgemüse-Züchtung beteiligt - Netzwerk für Resistenzzüchtung bei Salaten im Aufbau. Gemüse 8 (2010) 20-22.

Ulrich, D., H. Budahn, T. Struckmeyer, F. Marthe, H. Krüger & U. Lohwasser: Diversity of volatile patterns in a genebank collection of parsley (*Petroselinum crispum* [Mill.] Nyman). Proceedings of the 12th International Weurman Flavour Research Symposium "Expression of Multidisciplinary Flavour Science", Juli 2008, Interlaken, Switzerland (2010) 383-386.

Yang, Q., A. Börner & M. Kruse: Bestimmung der optimalen Lagerungsbedingungen für die ultra-dry Saatgutlagerung von Zwiebel (*Allium cepa* L.), Weizen (*Triticum aestivum* L.) und Raps (*Brassica napus* L.). Berichte der Gesellschaft für Pflanzenbauwissenschaften, Bd. 5 (2010) 16-19.

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Börner, A., E.V. Antonova, H.J. K, E.K. Khlestkina, B. Kobiljski, S. Kollers, U. Lohwasser, M. Nagel, K. Neumann, M.A. Rehman-Arif, N. Tikhenko, K. Zaynali Nezhad & M.S. Röder: Items from Germany. Ann. Wheat Newsl. 57 (2011) 12-15.

Kik, C., R. van Treuren, D. Pink, D. Astley, P. Coquin, V. Cadot, A. Börner, U. Lohwasser, S. Thumm, A. Lebeda, E. Kristkova, S. Solberg, K. Antonius, B. Maisonneuve, F. Lerch, P. Sumption, F. D'Antuono, V. Meglic & B. Bartha: Leafy vegetables GENRES project successfully completed! Newsl. Europe 42 (2011) 12.

Lohwasser, U. & A. Börner: Saatgut im Wandel der Zeit. Getreide Magazin 4 (2011) 66.

Electronic Publications

2010

Oppermann, M., J. Keilwagen, H. Knüpffer, S. Friedel & A. Börner: Validation, analysis and aggregation of long-term trait observation data of genebank material. In: Weitzmann, A.L. (Ed.), Proceedings of TDWG (2010). Woods Hole, Massachusetts, USA (2010) 52-53. http://www.vliz.be/imisdocs/publications/215525.pdf (2010).

PhD and Diploma Theses

2010

Börner, M.: Langlebigkeit von Saatgut: Assoziationsgenetische Studie anhand einer künstlich gealterten Kollektion der Gerste (*Hordeum vulgare* L.). (Bachelor) Martin-Luther-Universität Halle-Wittenberg, Halle/S. (2010) 58 pp.

Brathuhn, A.: Blütenbiologische Untersuchungen an Kulturen im Freiland und in Kleingewächshäusern der Genbank des IPK Gatersleben. (Bachelor) Fachhochschule Wiesbaden, Standort Geisenheim (2010) 40 pp.

Rosenhauer, M.: Genetische Untersuchungen des Merkmals Langlebigkeit von Saatgut an der Spezies *Brassica napus* L. (Diploma Thesis) Hochschule für Technik und Wirtschaft, Fachbereich Landbau/Landespflege, Dresden (2010) 126 pp.

Zaynali Nezhad, K.: Genetic linkage map construction and identification of Quantitative Trait Loci (QTLs) determining postanthesis drought tolerance and other agronomic traits in bread wheat. (PhD Thesis) Martin-Luther-Universität Halle-Wittenberg, Naturwissenschaftliche Fakultät, Halle/S. (2010) 267 pp.

2011

Nagel, M.: Seed survival in genebanks - genetic and biochemical aspects of seed deterioration in barley. (PhD Thesis) Georg-August-Universität, Göttingen (2011) 121 pp.

Neumann, K.: Genomweite Assoziationsstudie zur Identifizierung von Loci für juvenile und adulte Trockentoleranz in Gerste. (PhD Thesis) Martin-Luther-Universität Halle-Wittenberg, Halle/S. (2011) 113 pp.

Additional Publications *2009*

Asch, F. & A. Weidner: Klimawandel und Pflanzenzüchtung: Eine transdisziplinäre Herausforderung. Vortr. Pflanzenzücht. 81 (2009) 25-40.

Research Group: *In vitro* Storage and Cryopreservation

Head: Dr. Joachim Keller

Scientists

IPK financed
Zanke, Christine, Dr. (01.04.-31.05.2011)

Grant Positions
Zanke, Christine, Dr. (EU, till 31.03.2011)

Visiting Scientists/Scholars
Olas-Sochacka, Marta (COST Action 871, 19.10.-18.11.2010)
Pelc, Malgorzata, Dr. (COST Action 871, 07.04.-28.05.2010)

Goals

In vitro maintenance of vegetatively propagated genebank accessions, cryopreservation of potato, garlic, and mint. Research on tissue water conditions and cold adaptation connected with influence of ultra-low temperatures on plant organs. Integration of new cryopreservation strategies, such as pollen storage, into germplasm management.

Research Report

Accessions of the genera ***Allium, Antirrhinum, Artemisia, Brassica, Dioscorea, Mentha, Orthosiphon,* and *Sechium*** are in *in vitro* maintenance in total comprising **368 clones of 339 genebank accessions**. For distribution to the users **96 samples of mint and yams accessions were provided** (M. Grübe, D. Büchner, A. Senula).
The **cryo-collection of potato** was increased to **1,289 clones. For distribution to the users 10 samples** were provided to the Satellite Collections North (M. Grübe).

The *Allium* collection established in **cryopreservation** amounts to **101 accessions, amongst them 96 of garlic**, 2 of *Allium* hybrids and 3 of *A. obliquum*. The transfer of **virus-free garlic** material into protected greenhouse and field conditions was continued. Virus-free material was provided to the cryopreservation routine (A. Senula, D. Büchner, J. Keller).

The droplet vitrification method was further used routinely for cold-hardened plants of mint. **Seventy-one accessions from 15 species** are kept in cryopreservation with 200 explants each. Regeneration rates varied between 30 and 98 %. The cryopreservation method has been optimised by using donor *in vitro* plantlets directly from medium-term cold storage at 10 °C. This results in a shorter duration of the preparative phase prior to introduction into liquid nitrogen and does not allow accumulation of endophytes. As a result, better regeneration rates were achieved (A. Senula).

Based on results of previous measurements by Differential Scanning Calorimetry, the cryopreservation protocol of shallots was modified by omission of preculture and shorter pretreatments in cryoprotectant solutions. Two methods were compared, namely droplet vitrification and encapsulation vitrification. The latter did not lead to improved results and was not followed further.

Pollen cryopreservation was successfully applied in the two model species *Allium cepa* and *A. obliquum*. In the latter species, seed set after fertilisation with cryopreserved pollen was successfully tested (A. Senula, D. Büchner, J. Keller).

The project EURALLIVEG funded by the European Commission DG Agriculture under the Council Regulation No 870/2004 was finalised. Within this project a documentation of a garlic and shallot core collection was completed including the regeneration rates of the cryopreserved garlic accessions. The Tripartite Garlic Cryobank was established including safety duplication between the three partner genebanks of Czech Republic, Germany and Poland. AFLP analysis was done on 219 garlic and 63 shallot accessions. SNP analysis was performed in the laboratory of the company Trait Genetics on 24 garlic accessions. The results were used to develop new markers. A total of 220 accessions, 67 of them from IPK, were completely cryopreserved consisting either of 100 explants with regeneration rates better than 30 % or of 200 explants with regeneration rates between 10 and 30 %. Virus elimination, performed in the frame of EURALLIVEG was supported by training courses and plant material. The project website is permanently updated and will be continuously updated (C. Zanke, J. Keller, F. Blattner, A. Senula). Within the AEGIS strategy of the European Cooperative Programme for Plant Genetic Resources (ECPGR), a project was completed on cryopreservation of young inflorescence bases in bolting garlic for germplasm storage. This system has the advantage that the material is cleaner than bulbs, the procedure is shorter than use of *in vitro* donor material and the combination of this method used in summer with bulbil cryopreservation in winter increases cryopreservation efficiency (C. Zanke, J. Keller). In the frame of the EU-funded COST Action 871 two Short Term Scientific Missions were organised and supervised. First tests on the influence of ascorbic acid as antioxidant were done on mint and garlic (A. Senula, C. Zanke, M. Pelc, M. Olas-Sochacka). Furthermore, the influence of abscisic acid has been tested on mint cryopreservation (A. Senula, M. Muminova). A study on the costs of garlic cryopreservation was completed. Data on various field culture and cryopreservation strategies were compared and efficiency aspects were discussed (A. Breuing, see Fig. 17, p. 44).

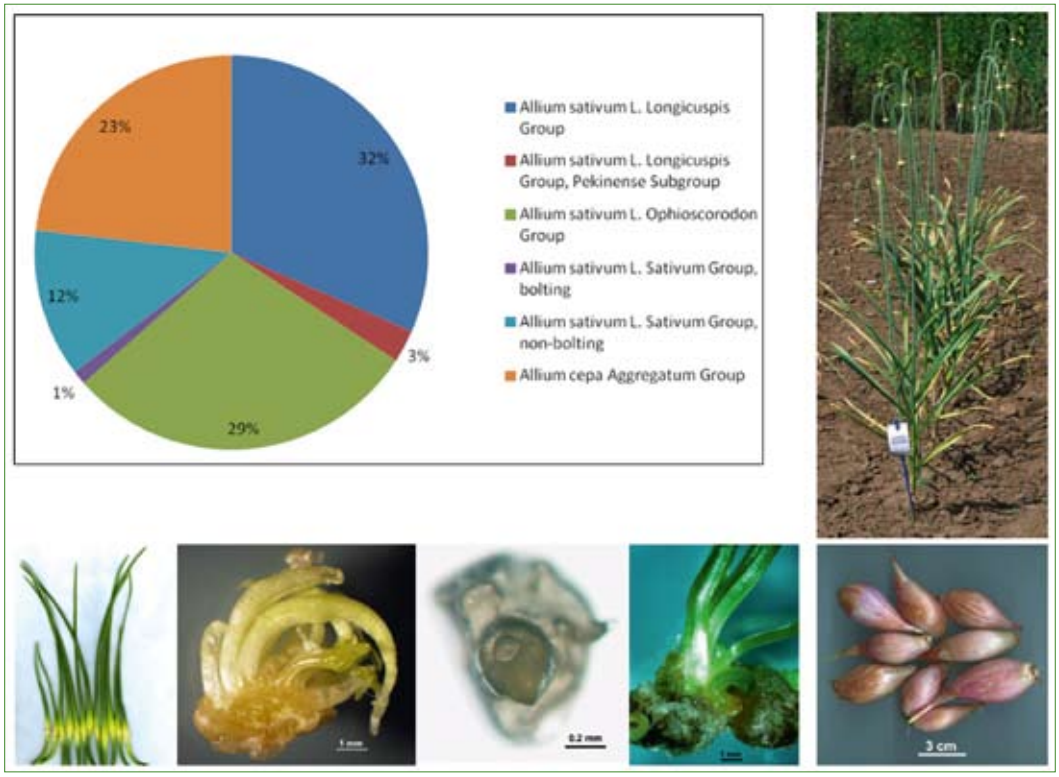


Fig. 17
Overview on activities for cryopreservation and virus elimination. Diagram: Distribution of taxa in the EURALLIVEG collection of 263 accessions. Right side: target plants of EURALLIVEG garlic (above) and shallot (below). Lower row from left to right: Donor organs for the AEGIS project on unripe inflorescences and regeneration from inflorescence explants 14 days after rewarming, meristem explants of garlic as needed to be used for virus elimination and regeneration stage in shallot experiments after pretreaments with cryoprotectants without cryopreservation (Photos: J. Keller, A. Senula, C. Zanke).

Publications

Peer Reviewed Papers

2010

Kaczmarczyk, A., A. Houben, E.R.J. Keller & M.F. Mette: Influence of cryopreservation on the epigenetic state of potato. CryoLetters 31 (2010) 380-391.

Lynch, P., G. Souch, S. Trigwell, E.R.J. Keller & K. Harding: Plant Cryopreservation: From laboratory to genebank. Asia Pac. J. Mol. Biol. Biotechnol. 18 (2010) 239-242.

2011

Kaczmarczyk, A., V.-M. Rokka & E.R.J. Keller: Potato shoot tip cryopreservation, a review. Potato Res. 54 (2011) 45-79.

Kaczmarczyk, A., C. Zanke, A. Senula, M. Grübe & E.R.J. Keller: Thermal analyses by differential scanning calorimetry for cryopreservation of potato shoot tips. 1st Int. Symp. of ISHS Cryopreservation in Horticultural Species, Leuven/Belgium, 5-8 April 2009. Acta Horticult. 908 (2011) 39-46.

Keller, E.R.J., A. Senula & C. Zanke: *Alliaceae* in cryopreservation, achievements and constraints. 1st Int. Symp. of ISHS Cryopreservation in Horticultural Species, Leuven/Belgium, 5-8 April 2009. Acta Horticult. 908 (2011) 495-508.

Senula, A. & E.R.J. Keller: Cryopreservation of mint – routine application in a genebank, experience and problems. 1st Int. Symp. of ISHS Cryopreservation in Horticultural Species, Leuven/Belgium, 5-8 April 2009. Acta Horticult. 908 (2011) 467-475.

Zanke, C., E.R.J. Keller, T. Kotlińska, M. Olas & J. Zámečník: Cryopreservation of vegetative garlic for the establishment of a European core collection. 1st Int. Symp. of ISHS Cryopreservation in Horticultural Species, Leuven/Belgium, 5-8 April 2009. Acta Horticult. 908 (2011) 431-438.

Books and Book Chapters

2010

Keller, E.R.J. & A. Senula: Cryopreservation of plant germplasm. In: Davey, M.R. & P. Anthony (Eds.): Plant Cell Culture: Essential Methods. Wiley (2010) 131-152.

2011

Keller, E.R.J., D. Astley, A. Tsivelikas, J. Engels & E. Lipman (Eds.): Report of a Working Group on *Allium*. 7th Meeting, 6-8 September 2011, Perea, Thessaloniki/Greece. Bioversity International, Rome, Italy (2011) 32 pp.

Other Papers

2010

Keller, E.R.J.: COST Action "CRYOPLANET" meets Society of Low Temperature Biology in Germany. Biovers. Newsl. Europe 40 (2010) 15.

Maggioni, L., M.C. Daunay, W. van Dooijeweert, D. Astley, N. Bas, F. Branca, M.J. Díez Niclós, E. Geoffriau, E.R.J. Keller, T. Kotlińska, K. Smékalová, R. van Treuren & E. Lipman (Eds.): Report of a Vegetables Network, 3rd Meeting, 10-12 November 2009, Catania/Italy. Bioversity International, Rome, Italy (2010) 59 pp.

2011

Keller, E.R.J., C.D. Zanke, T. Kotlinska, M. Olas-Sochacka, A. Reis & A.M. Barata: Broadening the spectrum of usable organ sources for cryopreservation of garlic – An AEGIS project report. Biovers. Newsl. Europe 53 (2011) 9.

Electronic Publications

2010

Colmsee, C., C. Zanke, T. Funke, S. Weise, E.R.J. Keller & U. Scholz: The Garlic and Shallot Core Collection (GSCC). http://www.ipk-gatersleben.de/databases/genetic_resources/gscc (2010).

Keller, E.R.J. & T. Funke: Die Knoblauch-Kernkollektion des IPK - IPK's Core Collection of Garlic. http://pgrc-35.ipk-gatersleben.de/apps/gcc/index.htm (2010).

Keller, E.R.J., C. Zanke & U. Scholz: EURALLIVEG - Vegetative Allium, Europe's Core Collection, Safe and Sound http://euralliveg.ipk-gatersleben.de (2010).

2011

Colmsee, C., C. Zanke, T. Funke, S. Weise, E.R.J. Keller & U. Scholz: The Garlic and Shallot Core Collection (GSCC). http://www.ipk-gatersleben.de/databases/genetic_resources/gscc (2011).

Keller, E.R.J. & T. Funke: Die Knoblauch-Kernkollektion des IPK - IPK's Core Collection of Garlic. http://pgrc-35.ipk-gatersleben.de/apps/gcc/index.htm (2011).

Keller, E.R.J., C. Zanke & U. Scholz: EURALLIVEG - Vegetative Allium, Europe's Core Collection, Safe and Sound http://euralliveg.ipk-gatersleben.de (2011).

PhD and Diploma Theses

2010

Breuing, A.: Einschätzung der Kosteneffektivität verschiedener Strategien der Langzeiterhaltung von Knoblauch (*Allium sativum* L.) in der Genbank Gatersleben. (Master Thesis) Leibniz-Universität Hannover, Naturwissenschaftliche Fakultät, Institut für Zierpflanzen- und Gehölzwissenschaften, Hannover (2010) 186 pp.

Additional Publications 2009

Astley, D. & E.R.J. Keller: Working Group on Allium. In: Astley, D., N. Bas, F. Branca, M.C. Daunay, M.J. Diez, E.R.J. Keller, W. van Dooijeweert, R. van Treuren, L. Maggioni & E. Lipman (Eds.): Report of a Vegetables Network. 2nd Meeting, June 2007, Olomouc/Czech Republic. Bioversity International, Rome/Italy (2009) 8-13.

Research Group: Satellite Collections North

Head: Dr. Klaus J. Dehmer

Scientists

IPK financed
Nehrlich, Stephanie (0.50, since 01.10.2010)
Willner, Evelin (till 30.09.2010; 0.50, since 01.10.2010)

Grant Positions
Diekmann, Kerstin, Dr. (BMELV, since 01.02.2010)
Gernand-Kliefoth, Dorota, Dr. (BMELV, till 30.04.2011)
Gerson, Lydia (0.50 Bayerische Landesanstalt für Landwirtschaft)
Schlichting, Andre, Dr. (0.25 BMELV, 01.01.-30.04.2010)
Witter, Steffi (0.50 BMELV/FNR, since 01.11.2010)

Goals

Collection, conservation, evaluation, distribution and research regarding plant genetic resources of potatoes, oil and fodder crops.

Research Report

The **Groß Lüsewitz Potato Collections** (GLKS; K.J. Dehmer) include a total of **6,124 accessions** from **140 tuber bearing *Solanum* species** within three separate collections. They comprise 2,849 accessions of 139 wild and cultivated species from Southern and Central America (WKS, sexually propagated), 2,736 *Solanum tuberosum* ssp. *tuberosum* cultivars, landraces or breeding lines (KKS, vegetatively propagated) and clonally propagated genotypes of Andean or equatorial origin (AKS; 539 entries, mainly seven cultivated species).

In 2010 and 2011, 292 WKS accessions (152; 140) were multiplied in the greenhouse, while a total of 171 AKS (79; 92) and 1,287 KKS accessions (617; 670) were cultivated in the field with 10 plants each and characterised for 15 traits. Via *in vitro* culture with a microtuber storage step, 2,361 KKS and 539 AKS accessions are maintained. More than 1,250 KKS accessions are kept as cryopreserved safety duplicates at IPK Gatersleben (research group *In vitro* Storage and Cryopreservation). **Germination rates** were determined for **1,600 WKS entries**. **3,890 potato accessions** (2010: 1,925; 2011: 1,965) were distributed in the context of **523 requests** (222; 301).

According to the respective ELISA tests, **2,744 *in vitro* samples** (95 %) are **free of** the six most common **potato viruses**. The State Plant Protection Offices at Hannover and Rostock tested potato accessions of the GLKS for quarantine viruses (293 accs.), quarantine bacteria (945), and PSTVd (2,144).
Evaluations were carried out for resistance to ***Globodera pallida*** (174 WKS accessions/804 genotypes, State Plant Protection Office Rostock), ***Phytophthora infestans*** on leaves (299 WKS accessions; Julius Kühn-Institute (JKI), Institute for Breeding Research on Agricultural Crops) and tubers (150 WKS accessions/885 genotypes; JKI) and ***Synchytrium endobioticum*** (10 AKS, 36 KKS accessions; JKI/Institute for **Plant Protection in Field Crops and Grassland**). For all pests, complete resistance was observed in several instances, for WKS entries both on the genotype and even on the accession level. Tubers of 94 entries (16 AKS; 78 KKS) were cultivated for the **evaluation of** their **taste**, while **starch content** was determined in tubers of 161 accessions. For a **project on the evaluation of potato tuber quality**, tubers produced from 80 KKS accessions, 77 AKS accessions and 42 WKS genotypes were evaluated at the University of Rostock and at Steinbeis Transfer Center (STZ) Soil Biotechnology, and a large variability was detected for most traits investigated (A. Schlichting). Research on degree of diversity and duplication within the clonal collections, as well as on genetic stability under different regeneration regimes and wild species taxonomy was conducted using retro transposon-based markers (K. Diekmann). In potato, these proved equally informative as the well established SSR markers, even with lower numbers of markers applied.

The Malchow/Poel **Oil Plants and Fodder Crops Collections** (E. Willner, S. Nehrlich) consist of 10,441 samples of (fodder) grasses, 2,472 oil plants and 1,345 forage legumes (total **14,258 accessions**).

In 2010 and 2011, a total of 2,780 (1,093; 1,687) accessions were cultivated, either for multiplication and characterisation (1,779) or evaluation (1,001; Fig. 18, p. 47). **Germination tests** were conducted for 12,670 accessions (2010: 6,506; 2011: 6,164). According to FAO genebank standards, **76 %** of the whole Malchow collection is **stored as an active and base collection with safety duplicates** at the Svalbard Global Seed Vault (9,248 accessions, 64 % of total Malchow stocks), while 82 % of the whole collection is available for seed requests. A total of **3,666 samples** (1,325; 2,341) **were provided to 228 users** (88; 140).
Characterisations for 15 traits were performed on 1,947 grass accessions (620; 1,327), 275 crucifers (121; 154) and 301 legumes (123; 178) for an initial description of their morphological and phenotypical traits as well as for the confirmation of their botanical classification. **Field evaluations** were carried out for *Lolium perenne* (46 accessions as recently bred material in cooperation with Agricultural Research Institute Mecklenburg, West Pomerania), which were compared to standard varieties in a three-year trial for trait variability and green matter yield.

The **European Central *Poa* Database** (http://poa.ipk-gatersleben.de) was developed further. Progress was made in the identification of "Originality" (98 % of the entries) and "Primary Holder" (86 % of the accessions) matters, which will allow to avoid unnecessary regenerations and to improve the sharing of responsibilities.

Fig. 18
Multi-purpose building and greenhouse of IPKs Fodder and Oil Crops Collections at Malchow (Photo left, S. Nehrlich) and multiplication of accessions of different grass genera in an isolation plot on Poel island (Photo right, K. Ploen).

Genebank and breeding material from the three **grass genera *Dactylis, Lolium*** and ***Phleum*** was examined in **diversity and introgression studies** (D. Gernand-Kliefoth). Here, SSR markers facilitated the identification of interspecific hybrids, while GISH experiments proved the presence of introgressed donor chromatin even after several backcross generations. In cooperation with an external partner (Bavarian State Research Center for Agriculture), **the complex trait 'persistence'** was analysed in ***Lolium perenne*** (L. Gerson), while the elucidation of **heterotic groups for biomass production in *Lolium* hybrids** (S. Witter) and **drought tolerance in *Lolium*** were in the scope of two further research projects.

Publications

Peer Reviewed Papers

2010

Michalski, S.G., W. Durka, A. Jentsch, J. Kreyling, S. Pompe, O. Schweiger, E. Willner & C. Beierkuhnlein: Evidence for genetic differentiation and divergent selection in an autotetraploid forage grass (*Arrhenatherum elatius*). Theor. Appl. Genet. 120 (2010) 1151-1162.

Schubiger, F.X., J. Baert, B. Bayle, P. Bourdon, B. Cagas, V. Cernoch, E. Czembor, F. Eickmeyer, U. Feuerstein, S. Hartmann, H. Jakesova, D. Johnston, B. Krautzer, H. Leenheer, H. Lellbach, C. Persson, W. Pietraszek, U.K. Posselt, M. Romani, L. Russi, S. Schulze, M.C. Tardin, F. VanHee, L. van Kruijssen, P. Wilkins, E. Willner, L. Wolters & B. Boller: Susceptibility of European cultivars of Italian and perennial ryegrass to crown and stem rust. Euphytica 176 (2010) 167-181.

van de Wiel, C.C.M., T. Sretenovic Rajicic, R. van Treuren, K.J. Dehmer, C.G. van der Linden & T.J.L. van Hintum: Distribution of genetic diversity in wild European populations of prickly lettuce (*Lactuca serriola*): implications for plant genetic resources management. Plant Genet. Resour. 8 (2010) 171-181.

2011

Beierkuhnlein, C., D. Thiel, A. Jentsch, E. Willner & J. Kreyling: Ecotypes of European grass species respond differently to warming and extreme drought. J. Ecol. 99 (2011) 703-713.

Nestmann, S., T. Sretenovic Rajicic, K.J. Dehmer, M. Fischer, J. Schumacher & C. Roscher: Plant species diversity and composition of experimental grasslands affect genetic differentiation of *Lolium perenne* populations. Mol. Ecol. 20 (2011) 2188-2203.

Walter, J., L. Nagy, R. Hein, U. Rascher, C. Beierkuhnlein, E. Willner & A. Jentsch: Do plants remember drought? Hints towards a drought-memory in grasses. Environ. Exp. Bot. 71 (2011) 34-40.

Books and Book Chapters

2010

Willner, E., S. Hünmörder & K.J. Dehmer: Towards an enhanced utilization of plant genetic resources in grass breeding by characterization and evaluation trials. In: Huyghe, C. (Ed.): Sustainable Use of Genetic Diversity in Forage and Turf Breeding. Springer, The Netherlands (2010) 173-180.

Other Papers

2010

Rosenhauer, M., M. Nagel, E. Willner, F.-G. Schröder, R. Snowdon, W. Friedt & A. Börner: Genetische Untersuchungen des Merkmals Langlebigkeit von Saatgut der Spezies *Brassica napus* L. Berichte der Gesellschaft für Pflanzenbauwissenschaften, Bd. 5 (2010) 108-111.

2011

Schlichting, A., P. Leinweber & K.J. Dehmer: Innovative Analysen von Inhaltsstoffen und Qualitätsparametern. Kartoffelbau 9 (2011) 46-47.

Electronic Publications

2010

Maggioni, L., M. Veteläinen, E. Willner & E. Lipman: Report of a Working Group on Forages. Tenth Meeting, 28-29 April 2010, Poel Island, Germany. http://www.ecpgr.cgiar.org/networks/forages/forages_wg_germany_2010.html (2010).

PROGRAMME: TAXONOMY AND EVOLUTION
Research Group: Experimental Taxonomy

Head: Dr. Frank Blattner

Scientists

IPK financed
Baier, Christina, (0.50, till 31.08.2010)
Benor, Solomon (0.50, 01.10.-26.11.2011)
Ekhvaia, Jana (0.50, 01.09.-30.11.2010)
Gurushidze, Maia, Dr. (0.50, 01.04.-30.09.2011)
Jakob, Sabine, Dr. (till 31.12.2011)
Nürk, Nicolai Matthias (0.50, 01.09.2010-31.08.2011)

Grant Positions
Harpke, Dörte, Dr. (0.50 DFG, since 01.05.2010)
Herrmann, Katja (0.65 DFG, since 01.08.2011)
Bernhardt, Nadine (0.65 DFG, since 01.06.2011)
Brassac, Jonathan (0.65 DFG, since 01.02.2010)
Nürk, Nicolai Matthias (DFG, till 31.08.2010)

Visiting Scientists/Scholars
Bachmann, Konrad, Prof. (self-financed, till 31.05.2011)
Baier, Christina (self-financed, 01.09.2010-31.03.2011; 01.07.-31.12.2011)
Benor, Solomon (DAAD, till 30.09.2011)

Goals

Phylogenetic classification and analysis of **evolution** of crops and their wild relatives. Experimental studies to link **molecular markers** and **phylogenetic data** with **ecological** and **morphological traits**, and to analyse **plant–environment interdependency** on and below the species level in an evolutionary framework.

Research Report

The major aim of the group is to understand mechanisms resulting in **speciation** processes in specific plant groups. This involves the study of the **distribution** of species, populations and genotypes **in time and space** together with the analysis of character state changes involved in **environmental adaptation** and **reproductive isolation**. These characters (e.g., abiotic stress tolerance, flowering time) influence the ecological niches of organisms and are often also **important agronomic traits**.

In the barley genus ***Hordeum*** we analyse all aspects related to phylogeny, speciation and ecological adaptation. During the last two years we analysed the evolution of ecological niches in the diploid South American *Hordeum* species and combined these data with population genetic approaches. We inferred that population demography influences the ability of species to change or maintain their ecological niches. In a pilot study on polyploid evolution in wall barley (*H. murinum*) we could show that two extinct diploid taxa together with subsp. *glaucum* were involved in the formation of extant tetra- and hexaploid subspecies of this taxon. Similar analyses are currently conducted on all polyploid species of *Hordeum* within a DFG-funded project. Also through DFG funding a study on the influence of flowering time differences on species stability in sympatric geographical settings in Patagonia could be started (within the DFG Priority Programme on flowering time) and analyses of Central Asian species of the genus continued (S. Jakob, J. Brassac, K. Herrmann).

In the DFG-funded project on ***Hypericum*** systematics we finished analyses of molecular and morphological characters including more than 450 species of the genus plus representatives of other genera of the family Hypericaceae. Through this analysis we were able to evaluate earlier theories of character evolution, geographic origin and taxonomic treatment of the genus. We could show that *Hypericum* originated during the Miocene in Laurasia from tropical progenitors, when cooling climate conditions resulted in expanding temperate habitats. Apomictic species evolved independently in at least three different clades of the genus (see Fig. 19, p. 49). The project is part of cooperation with the Natural History Museum London, and connected to projects on *Hypericum* in the groups of T. Sharbel and H. Bäumlein at the IPK and M. Koch's group at the University of Heidelberg (N. Nürk).

Species of the Euphorbiaceae genus ***Macaranga*** are important Southeast Asian pioneer shrubs and trees of areas where the rainforest was freshly logged. Many of these species co-occur with mutualistic ants. In cooperation with the universities in Kassel and Würzburg we study speciation processes, probably driven by co-evolution between plants and their ant partners. In population genetic and phylogeographic analyses of two widespread Bornean *Macaranga* species, one a myrmecophyte (ant-plant), the other without ant mutualists, we studied the influence of mutualistic ants on dispersal abilities of their host plant species. We found clear differences between the genepools on the Malayan Peninsula and Borneo, and also within Borneo a separation of populations in the northeast from genotypes occurring in the southwest of the island, indicating partly long-term isolation of these areas. In comparison to the non-myrmecophyte, populations of the myrmecophytic species were genetically much more differentiated, indicating restricted gene flow in this species. This probably results from the need of the plant to co-disperse with its ant partner, as seedlings not readily colonised by the ants will soon die (C. Baier).

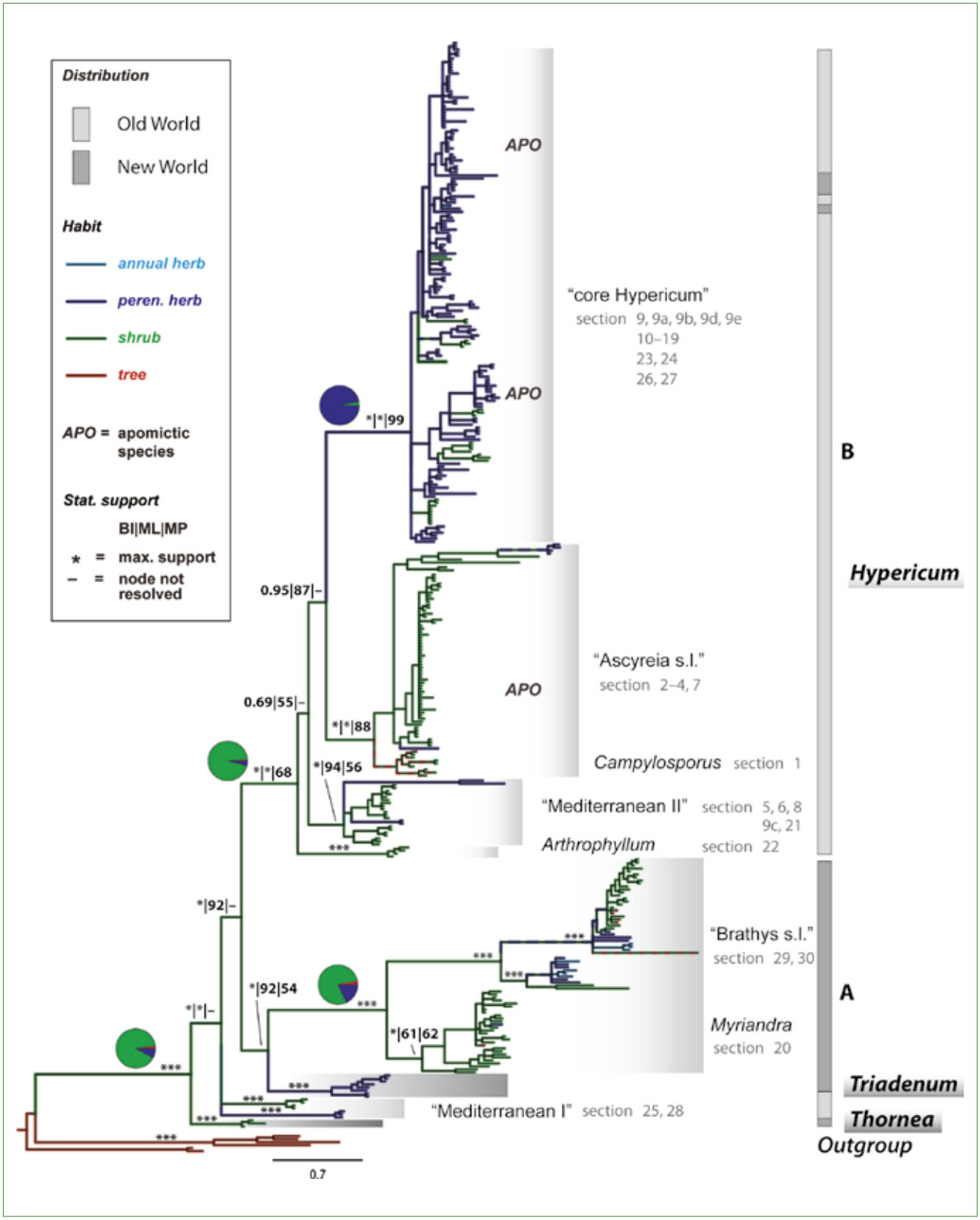


Fig. 19
Bayesian tree from the analysis of nrDNA ITS sequence data, showing relationships of 194 *Hypericum* and 12 outgroup species, represented by 366 accessions. A light-grey background highlights clades of *Hypericum*, dark-grey other taxa of Hypericaceae. Asterisks indicate maximum statistical support for branches. Occurrence of apomixis (APO) is marked on the tree. Evolution of habit, shrubs (in green), trees (red), perennial (dark blue) and annual herbs (light blue), is depicted by colour of branches. The four pie charts display the proportion of character states reconstructed over 1000 trees at a certain node (N. Nürk).

Several species of the **jute** genus *Corchorus* (Malvaceae s.l.) are used in African countries as vegetables or salad in addition to their properties as fibre plants. These species are so-called neglected crops. Ethnobotanical data on the Ethiopian species were collected and detailed molecular and morphological studies of *C. olitorius* were conducted. The analyses prove an African origin of cultivated jute and provide evidence for Ethiopia as an important genotype reservoir for jute breeding. Phylogenetic analysis of the genus inferred several intercontinental long-distance dispersals out of Africa to Australasia and South America (S. Benor).

The genus ***Crocus*** consists of about 80 species distributed from Western Europe to the western-most parts of China. Many *Crocus* species are used as ornamentals. In a DFG-funded project we constructed a phylogeny of the genus based on two nuclear marker regions. We were able to resolve species relationships, trace the evolution of chromosome numbers in the genus, and could show that many of the different subspecies of *C. biflorus* occurring on mountaintops in Anatolia merit species rank. We now use these results as basis for phylogeographic and population genetic analyses of the Anatolian *C. biflorus* taxon complex to infer modes of speciation on sky islands in this area (D. Harpke).

Recently a project aiming at clarifying the phylogeny of **Triticeae** was approved by DFG. Although relationships in this important group of grasses were analysed for nearly a century, up to now no conclusive hypothesis could be reached. This might partly be due to occasional gene flow among species belonging even to different genera. In this project we will use next generation sequencing to compare gene regions in a genome-wide approach among all diploid species of the tribe to understand reasons for inconsistencies among the published studies and to arrive at a comprehensive phylogeny for the group (N. Bernhardt).

Publications

Peer Reviewed Papers

2010

Benor, S., F.R. Blattner, S. Demissew & K. Hammer: Collection and ethnobotanical investigation of *Corchorus* species in Ethiopia: potential leafy vegetables for dry regions. Genet. Resour. Crop Evol. 57 (2010) 293-306.

Fritsch, R.M., F.R. Blattner & M. Gurushidze: New classification of *Allium* L. subg. *Melanocrommyum* (Webb & Berthel.) Rouy (Alliaceae) based on molecular and morphological characters. Phyton 49 (2010) 145-220.

Gurushidze, M., R.M. Fritsch & F.R. Blattner: Species-level phylogeny of *Allium* subgenus *Melanocrommyum*: Incomplete lineage sorting, hybridization and *trnF* gene duplication. Taxon 59 (2010) 829-840.

Jakob, S.S. & F.R. Blattner: Two extinct diploid progenitors were involved in allopolyploid formation in the *Hordeum murinum* (Poaceae: Triticeae) taxon complex. Mol. Phylogenet. Evol. 55 (2010) 650-659.

Jakob, S.S., C. Heibl, D. Rodder & F.R. Blattner: Population demography influences climatic niche evolution: evidence from diploid American *Hordeum* species (Poaceae). Mol. Ecol. 19 (2010) 1423-1438.

Kotseruba, V., K. Pistrick, F.R. Blattner, K. Kumke, O. Weiss, T. Rutten, J. Fuchs, T. Endo, S. Nasuda, A. Ghukasyan & A. Houben: The evolution of the hexaploid grass *Zingeria kochii* (Mez) Tzvel. (2n=12) was accompanied by complex hybridization and uniparental loss of ribosomal DNA. Mol. Phylogenet. Evol. 56 (2010) 146-155.

Marchelli, P., C. Baier, C. Mengel, B. Ziegenhagen & L. Gallo: Biogeographic history of the threatened species *Araucaria araucana* (Molina) K. Koch and implications for conservation – a case study with organelle DNA markers. Conserv. Genet. 11 (2010) 951-963.

Nürk, N.M. & F.R. Blattner: Cladistic analysis of morphological characters in *Hypericum* (Hypericaceae). Taxon 59 (2010) 1495-1507.

Peterson, A., D. Harpke, L. Peruzzi, J.-M. Tison, H. John & J. Peterson: *Gagea bohemica* (Liliaceae), a highly variable monotypic species within *Gagea*. Plant Biosystems 144 (2010) 308-322.

Schallau, A., F. Arzenton, A.J. Johnston, U. Hähnel, D. Koszegi, F. Blattner, L. Altschmied, G. Haberer, G. Barcaccia & H. Bäumlein: Identification and genetic analysis of the APOSPORY locus in *Hypericum perforatum* L. Plant J. 62 (2010) 773-784.

Weigend, M., M. Gottschling, H.H. Hilger & N.M. Nürk: Five new species of *Lithospermum* L. (Boraginaceae tribe Lithospermeae) in Andean South America – another radiation in the Amotape-Huancabamba Zone. Taxon 59 (2010) 1161-1179.

2011

Benor, S., J. Fuchs & F.R. Blattner: Genome size variation in *Corchorus olitorius* (Malvaceae s.l.) and its correlation with elevation and phenotypic traits. Genome 54 (2011) 575-585.

Bordbar, F., M.R. Rahiminejad, H. Saeidi & F.R. Blattner: Phylogeny and genetic diversity of D-genome species of *Aegilops* and *Triticum* (Triticeae, Poaceae) from Iran based on microsatellites, ITS and *trnL-F*. Plant Syst. Evol. 291 (2011) 117-131.

Guicking, D., B. Fiala, F.R. Blattner, F. Slik, M. Mohamed & K. Weising: Comparative chloroplast DNA phylogeography of two tropical pioneer trees, *Macranga gigantea* and *M. pearsonii* (Euphorbiaceae). Tree Genet. Genomes 7 (2011) 573-585.

Karimi Ashtiyani, R., A.M. Banaei Moghaddam, V. Schubert, T. Rutten, J. Fuchs, D. Demidov, F.R. Blattner & A. Houben: AtHaspin phosphorylates histone H3 at threonine 3 during mitosis and contributes to embryonic patterning in *Arabidopsis*. Plant J. 68 (2011) 443-454.

Nürk, N.M. & S.L. Crockett: Morphological and phytochemical diversity among *Hypericum* species of the Mediterranean basin. Med. Aromat. Plant Sci. Biotechnol. 5 (2011) 14-28.

Peruzzi, L., Peterson, A., Tison, J.-M. & D. Harpke: New light on phylogeny and taxonomy of the Eurasian *Gagea villosa-G. fragifera* complex (Liliaceae). Nord. J. Bot. 29 (2011) 722-733.

Peterson, A., I.G. Levichev, J. Peterson, D. Harpke & M. Schnittler: New insights into phylogeny and taxonomy of Chinese species of *Gagea* (Liliaceae) - Speciation through hybridization. Organisms Divers. Evol. 11 (2011) 387-407.

Books and Book Chapters

2010

Blattner, F.R., T. Pleines & S.S. Jakob: Rapid radiation in the barley genus *Hordeum* (Poaceae) during the pleistocene in the Americas. In: Glaubrecht, M. (Ed.): Evolution in Action. Springer, Heidelberg (2010) 17-34.

Weising, K., D. Guicking, C. Fey-Wagner, T. Kröger-Kilian, T. Wöhrmann, W. Dorstewitz, G. Bänfer, U. Moog, M. Vogel, C. Baier, F.R. Blattner, H. Feldhaar & B. Fiala: Mechanisms of speciation in Southeast Asian ant-plants of the genus *Macaranga* (Euphorbicaceae). In: Glaubrecht, M. (Ed.): Evolution in Action. Springer, Heidelberg (2010) 169-191.

Other Papers

2011

Harpke, D. & A. Peterson: Molekulare Systematik und Taxonomie in der Gattung *Mammillaria*. Mitteilungsblatt Arbeitskreis für Mammillarienfreunde 1 (2011) 2-11.

Nürk, N.M.: Johanniskraut – von seiner Wirkung zum Namen und zur Botanik. Aromareport 5 (2011) 8-10.

PhD and Diploma Theses

2011

Al-Hodali, K.Y.: Systematic revision of the genus *Tulipa* (Liliaceae) in Jordan. (Master Thesis) University of Jordan, Amman (2011) 139 pp.

Baier, C.: Comparative phylogeographic and population genetic analyses of three tropical pioneer trees, *Macaranga winkleri*, *M. winkleriella* and *M. tanarius* (Euphorbiaceae). (PhD Thesis) Martin-Luther-Universität Halle-Wittenberg, Halle/S. (2011) 156 pp.

Benor, S.: Phylogeny of the genus *Corchorus* (Malvaceae s.l.) and diversity analyses in selected species: evidence from morphology, flow cytometry, and molecular data. (PhD Thesis) Universität Kassel, Kassel (2011) 125 pp.

Nürk, N.: Phylogenetic analyses in St. John's wort (*Hypericum*) - inferring character evolution and historical biogeography. (PhD Thesis) Freie Universität Berlin, Berlin (2011) 129 pp.

Research Group: Taxonomy of Plant Genetic Resources

Head: Dr. Frank Blattner (provisional)

Scientists

IPK financed
Pistrick, Klaus, Dr.

Visiting Scientists/Scholars
Filatenko, Anna, Dr. (self-financed, 15.02.-10.03.2010)
Fritsch, Reinhard, Dr. (DFG)

Goals

Curatorial management of living and archive **taxonomic collections**, investigation of morphological, karyological and anatomical characters resulting in phylogenetic and taxonomic conclusions, and **nomenclaturally suitable treatments** of taxa. The studies target general questions of the **taxonomy of crop plants** and are performed in close cooperation with the research group Experimental Taxonomy.

Research Report

The **custodial management of the taxonomic reference collections** is a continuous activity of the research group. During 2010 and 2011 7,693 herbarium sheets, 1,955 fruit and seed samples, and more than 1,056 cereal spike samples were added to the collection. Apart of employees of the IPK the collections were used by many visitors of the IPK facilities, and vouchers were sent abroad in the frame of national and international herbarium exchange. This part of the work involves also taxonomical determination of genebank materials from a wide variety of plant families (K. Pistrick).

A general review of the **nomenclatural relationships** between diverging recent taxonomic treatments of ***Triticum***- and ×***Triticosecale*** variability, following broad versus narrow species concepts, has been performed. In *Triticum* a detailed infraspecific system has been supported for stable classification, better estimation of genetic erosion and suitable management of wild and cultivated *Triticum* accessions in genebanks. It is proposed to maintain ×*Triticosecale* Wittm. as a nothogenus, with ×*T. rimpaui* Wittm. for octoploid races, ×*T. neoblaringhemii* A. Camus for hexaploid races and ×*T. semisecale* (Mac Key) K. Hammer et A. Filat. for tetraploid races (K. Hammer, A.A. Filatenko, K. Pistrick).

The actual situation of **plant genetic resources** in southeastern **Georgia** has been studied together with staff members of the Botanical Garden and Institute of Botany, Tbilisi in July 2010. 294 accessions of local cereals, pulses, spices and medicinal plants could be collected, despite of increased genetic erosion, especially in field crops. Variable landraces of *Triticum aestivum* L. are still cultivated in several villages of Mescheti. Nine

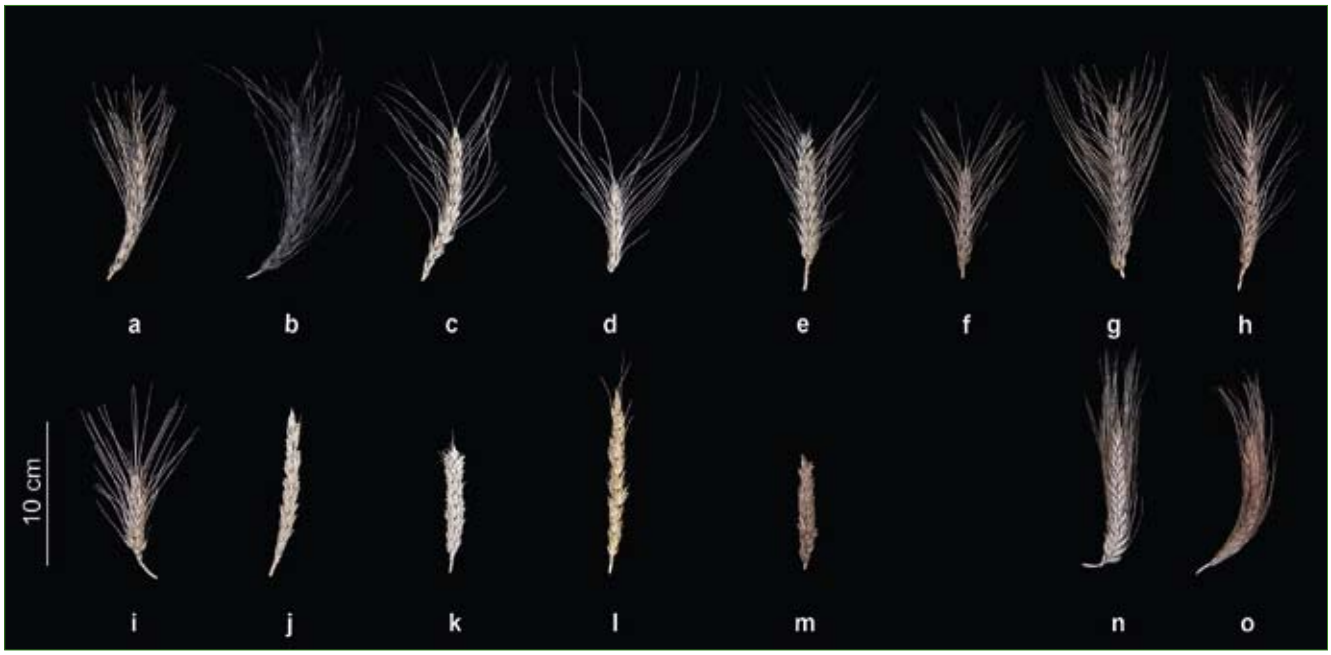


Fig. 20
Spikes of different *Triticum* and ×*Triticosecale* accessions collected in Mescheti (southeastern Georgia) 2010: **a** – *Triticum carthlicum* Nevski var. *stramineum* Zhuk.; **b** – *T. carthlicum* Nevski var. *carthlicum*; **c** – *T. aestivum* L. var. *pseudoerythrospermum* (Kudr.) A. Filat.; **d, e** – different types of *T. aestivum* L. var. *aestivum*; **f, g** – different types of *T. aestivum* L. var. *variabile* (Kudr.) A. Filat.; **h** – *T. aestivum* L. var. *ferrugineum* (Alef.) Mansf.; **i** – *T. aestivum* L. var. *ferrugineumcompactoides* (Kob.) Mansf.; **j** – *T. aestivum* L. var. *pulchrum* (Kudr.) A. Filat.; **k** – *T. aestivum* L. var. *lutescens* (Alef.) Mansf.; **l** – *T. aestivum* L. var. *uzbekistanicum* (Kudr.) A. Filat.; **m** – *T. aestivum* L. var. *milturum* (Alef.) Mansf.; **n**, **o** – different types of ×*Triticosecale neoblaringhemii* A. Camus (M. Akhalkatsi, J. Ekhvaia, K. Pistrick).

different varieties of subspecies *aestivum*, as well as of subsp. *hadropyrum* (Flaksb.) Tzvel. have been recorded in the fields (see Fig. 20, p. 52). Relic crops, such as *Pisum sativum* L. (pod vegetable), *Glycine max* (L.) Merr. (coffee substitute and cattle-food) or *Brassica oleracea* L. var. *viridis* (leaf vegetable) could be collected in Atčara (M. Akhalkatsi, J. Ekhvaia, K. Pistrick).

During several DFG-funded research missions in Iran new *Allium* materials were collected and incorporated in the living ***Allium* reference collection** of the IPK. Analyses of these plants resulted in the detection of several new species. The phylogenetic positions of these newly discovered taxa could all be determined by molecular markers. For a part of these species taxonomic descriptions and determination keys were already published (R. Fritsch).

Formerly published molecular phylogenies of the members of ***Allium* subgenus *Melanocrommyum*** based on nuclear rDNA internal transcribed spacer sequences were supplemented by additional materials from Central Asia, West Asia, and Near East. This work resulted in further clarification of relationships in subgenus *Melanocrommyum*. Several taxonomic groups were already newly described, and a modern conspectus of subg. *Melanocrommyum* was published. An illustrated key for determination of all sections and subsections of this subgenus is ready for publication, and description of several new species from Near East is in preparation (R. Fritsch, M. Gurushidze).

Publications

Peer Reviewed Papers

2010

Fritsch, R.M., F.R. Blattner & M. Gurushidze: New classification of *Allium* L. subg. *Melanocrommyum* (Webb & Berthel.) Rouy (Alliaceae) based on molecular and morphological characters. Phyton 49 (2010) 145-220.

Fritsch, R.M. & H. Maroofi: New species and new records of *Allium* L. (Alliaceae) from Iran. Phyton 50 (2010) 1-26.

Gurushidze, M., R.M. Fritsch & F.R. Blattner: Species-level phylogeny of *Allium* subgenus *Melanocrommyum*: Incomplete lineage sorting, hybridization and *trnF* gene duplication. Taxon 59 (2010) 829-840.

Hoffmann, M.H., H. Schmuths, C. Koch, A. Meister & R.M. Fritsch: Comparative analysis of growth, genome size, chromosome numbers and phylogeny of *Arabidopsis thaliana* and three cooccurring species of the Brassicaceae from Uzbekistan. J. Bot. 2010 (2010) Article ID 504613, 8 pages, doi:10.1155/2010/504613.

Kotseruba, V., K. Pistrick, F.R. Blattner, K. Kumke, O. Weiss, T. Rutten, J. Fuchs, T. Endo, S. Nasuda, A. Ghukasyan & A. Houben: The evolution of the hexaploid grass *Zingeria kochii* (Mez) Tzvel. (2n=12) was accompanied by complex hybridization and uniparental loss of ribosomal DNA. Mol. Phylogenet. Evol. 56 (2010) 146-155.

2011

Gladis, T. & K. Pistrick: *Chaerophyllum byzantinum* Boiss. and *Trachystemon orientalis* (L.) G. Don – recently introduced from Turkish wild flora as new crop species among other interesting findings from immigrant gardens in western Germany. Genet. Resour. Crop Evol. 58 (2011) 165-174.

Hammer, K., A.A. Filatenko & K. Pistrick: Remarks on *Triticum* L. and ×*Triticosecale* Wittm. – Genet. Resour. Crop Evol. 58 (2011) 3-10.

Kusterer, J., R.M. Fritsch & M. Keusgen: *Allium* species from Central and Southwest Asia are rich sources of marasmin. J. Agr. Food Chem. 59 (2011) 8289-8297.

Pistrick, K. & K. Hammer: Peter Hanelt 80. Genet. Resour. Crop Evol. 58 (2011) 1-2.

Razyfard, H., S. Zarre, R.M. Fritsch & H. Maroofi: New species of *Allium* L. sect. *Acanthoprason* Wendelbo (Alliaceae) from Iran. Ann. Bot. Fenn. 48 (2011) 352-360.

Books and Book Chapters

2011

Pistrick, K.: Kulturpflanzen. In: Jäger, E. (Ed.): Rothmaler Exkursionsflora von Deutschland. Gefäßpflanzen: Grundband. 20., neu bearbeitete und erweiterte Auflage. Spektrum Akad. Verlag, Heidelberg (2011) 930 pp.

Other Papers

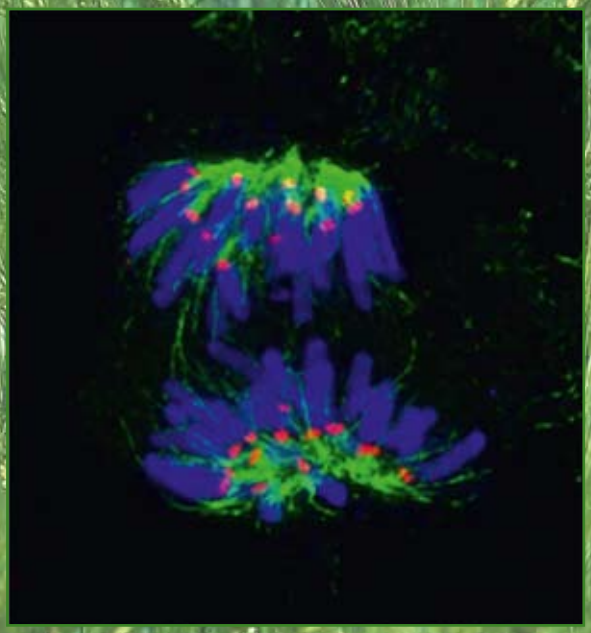
2010

Pistrick, K., M. Akhalkatsi, M. Girgvliani & T. Shanshiashvili: Sammlung von Saat- und Pflanzgut pflanzengenetischer Ressourcen in Svanetien und Lečchumi (Georgien, Kaukasus) 2009. Berichte der Gesellschaft für Pflanzenbauwissenschaften, Bd. 5 (2010) 123-127.

Additional Publications 2009

Fritsch, R.M. & M. Gurushidze: Phylogenetic relationships of ornamental species in *Allium* L. subg. *Melanocrommyum* (Webb et Berthel.) Rouy (Alliaceae). Isr. J. Plant Sci. 57 (2009) 287-295.

Abteilung Cytogenetik und Genomanalyse/
Department of Cytogenetics and Genome Analysis



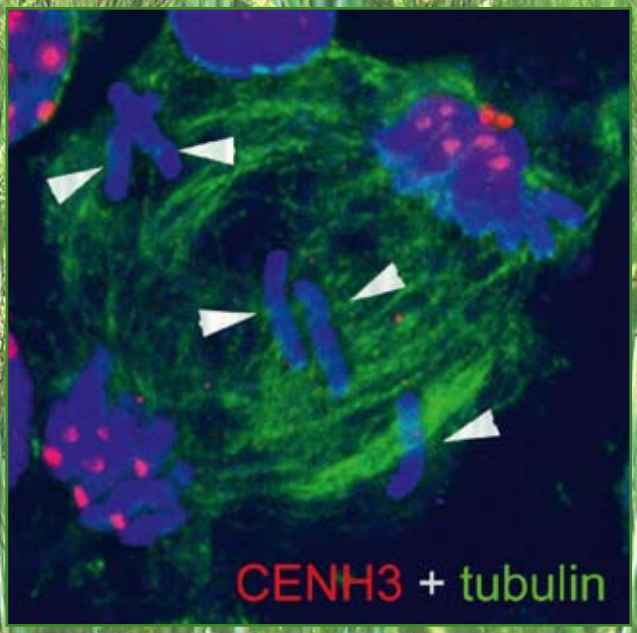


Abb. 21
Anaphase-Chromosomen eines stabilen (links) und eines instabilen (rechts) *Hordeum vulgare* × *H. bulbosum* Hybridembryos nach Immunmarkierung mit anti-CENH3- und anti-Tubulin-Antikörpern. In instabilen Hybriden sind die Zentromeren der nicht verteilten Chromosomen (Pfeilspitze) frei von CENH3 und somit inaktiv. Diese Chromosomen werden nicht in die Tochterkerne integriert, bilden stattdessen Kleinkerne und werden abgebaut. Im Ergebnis dessen entstehen haploide Pflanzen (M. Sanei, R. Pickering, A. Houben).

Fig. 21
Anaphase chromosomes of a stable (left) and an unstable (right) *Hordeum vulgare* × *H. bulbosum* hybrid embryo after immunostaining with anti-CENH3 and anti-tubulin. In the unstable hybrid, the centromeres of lagging chromosomes (arrowed) are CENH3-negative which indicates centromere inactivity. The lagging chromosomes are not integrated into daughter nuclei, form micronuclei and undergo degradation. As a result, a haploid plant is formed (M. Sanei, R. Pickering, A. Houben).

Abteilung Cytogenetik und Genomanalyse

Leiter: Prof. Dr. Ingo Schubert

Allgemeine Forschungsziele

Die Forschungsschwerpunkte der Abteilung sind die Genomdynamik auf molekularer und mikroskopischer Ebene unter evolutionären, ontogenetischen und experimentellen Gesichtspunkten (vor allem Bereich Cytogenetik) sowie die Genetik pflanzlicher Leistungen unter Einbeziehung genomweiter, vorwärts- und revers-genetischer sowie bioinformatischer Ansätze (vor allem Bereich Genomanalyse).

Folgende Themenbereiche werden gruppen-/abteilungsübergreifend bearbeitet:

Bereich Cytogenetik (Leiter: Prof. Dr. Ingo Schubert)

- Evolution von Gen- und Chromosomenbeständen im Zusammenhang mit Polyploidisierung, Artbildungsprozessen und sexuellen *versus* asexuellen Reproduktionswegen (Arbeitsgruppen Karyotypevolution, Chromosomenstruktur und -funktion, Genomplastizität, Epigenetik und Apomixis sowie Pflanzliche Reproduktionsbiologie - Abt. Physiologie und Zellbiologie);
- Erzeugung von Minichromosomen und von künstlichen Zentromeren sowie Ansätze zum gezielten Gentransfer in Gerste (Arbeitsgruppen Chromosomenstruktur und -funktion, Karyotypevolution und Epigenetik sowie Pflanzliche Reproduktionsbiologie - Abt. Physiologie und Zellbiologie);
- Mechanismen und funktionelle Bedeutung epigenetischer Prozesse (v. a. DNA-Methylierung und Histon-Modifikationen) für die Assemblierung kompetenter *versus* inkompetenter Chromatinzustände, z. B. Heterochromatin, Zentromer (Arbeitsgruppen Epigenetik, Karyotypevolution, Chromosomenstruktur und -funktion, Genomplastizität und Apomixis, sowie Dateninspektion - Abteilung Molekulare Genetik);
- Entwicklungsabhängige und experimentell (Mutanten, DNA-Schäden) erzeugte Genomdynamik (z. B. hinsichtlich der Interphasechromatinanordnung oder chromosomaler Strukturumbauten) und deren biologische Konsequenzen (Arbeitsgruppe Karyotypevolution).

Bereich Genomanalyse (Leiter: Dr. habil. Patrick Schweizer)

- Molekulare Identifikation von Genen bzw. Allelen für agronomisch bedeutsame Eigenschaften in Getreide (Arbeitsgruppen Transkriptomanalyse, Gen- und Genomkartierung, Bioinformatik und Informationstechnologie);
- Gen- und Allel-Phänotypbeziehungen sowie Genexpressionsmuster in Getreidepflanzen, die unter (a)biotischem Stress leiden, Resistenzen aufweisen oder sich in anderen ertragsrelevanten Merkmalen unterscheiden (Arbeitsgruppen Transkriptomanalyse, Gen- und Genomkartierung, Bioinformatik und Informationstechnologie);

Department of Cytogenetics and Genome Analysis

Head: Prof. Ingo Schubert

Research Goals

The research topics of the Department are focused on genome dynamics at the molecular and the microscopic level under evolutionary, developmental and experimental aspects (in particular Programme Cytogenetics) as well as on the genetic dissection of crop plant's performances using forward and reverse genetic as well as bioinformatic approaches (predominantly Programme Genome Analysis).

The Department's research groups are working on the following topics:

Programme Cytogenetics (Head: Prof. Ingo Schubert)

- Evolution of genes and chromosome complements in the context of polyploidisation, speciation and sexual *versus* asexual propagation (research groups Karyotype Evolution, Chromosome Structure and Function, Genome Plasticity, Epigenetics, Apomixis, and at the Dept. Physiology and Cell Biology the group Plant Reproductive Biology).
- Generation of minichromosomes as gene transfer vehicles and of artificial centromeres, as well as approaches for gene targeting in barley (research groups Chromosome Structure and Function, Karyotype Evolution, Epigenetics, and the Dept. Physiology and Cell Biology the group Plant Reproductive Biology).
- Mechanisms and functional importance of epigenetic processes (e.g. DNA methylation and histone modifications) for the assembly of competent *versus* incompetent chromatin states (heterochromatin, centromere etc.) (research groups Epigenetics, Karyotype Evolution, Chromosome Structure and Function, Genome Plasticity, Apomixis and of the Dept. Molecular Genetics the group Data Inspection).
- Developmental and experimentally induced (mutants; DNA damage) genome dynamics and its biological consequences (altered interphase chromatin arrangement; chromosome rearrangements) (research group Karyotype Evolution).

Programme Genome Analysis (Head: Dr. Patrick Schweizer)

- Identification and exploitation of the natural genetic diversity for improvement of agriculturally important traits in cereals (research groups Transcriptome Analysis, Gene and Genome Mapping, Bioinformatics and Information Technology).
- Analysis of gene- and allele-phenotype relationships and of gene expression patterns in cereals for (a)biotic stress resistance and other yield-related traits (research groups Transcriptome Analysis, Gene and Genome Mapping, Bioinformatics and Information Technology).

– Etablierung von Ontologien bzw. kontrollierten Vokabularien zur Strukturierung, Integration und Vernetzung diverser Datenbanken, Assemblierung und Annotation genomischer Sequenzen (Arbeitsgruppe Bioinformatik und Informationstechnologie).

Im Mittelpunkt der Arbeiten stehen neben Erkenntnisgewinn die Schaffung von Voraussetzungen für eine gezielte Modifikation pflanzlicher Genome sowie die Etablierung und Verbreiterung biotechnologisch und züchterisch nutzbarer Techniken und Ressourcen. Diese Arbeiten finden zu einem wesentlichen Teil im Rahmen des **Pflanzengenom-Ressourcen-Centrums (PGRC)** statt, einer abteilungsübergreifenden Forschungs- und Dienstleistungsplattform. Im PGRC-Dienstleistungsbereich, der in den Arbeitsgruppen Transkriptomanalyse, Bioinformatik und Informationstechnologie verankert ist, werden u. a. DNA-Sequenzierung und bioinformatischer Service angeboten.

Im Rahmen der gruppenspezifischen Forschungsarbeiten wird die Erhaltung und Weiterentwicklung von Spezialsortimenten v. a. der Ackerbohne, der Gerste u. a. Gramineen mit modifizierten Gen- und Chromosomenbeständen betrieben (Arbeitsgruppen Chromosomenstruktur und -funktion, Gen- und Genomkartierung, Karyotypevolution).

Entwicklung im Berichtszeitraum

Mit Eintritt der Leiterin in den Ruhestand wurde die Arbeitsgruppe ‚*In vitro*-Differenzierung' zum 31.12.2010 geschlossen. Mehrere Projekte werden in der Junior-Forschergruppe „Stammzell-Forschung" am Institut für Anatomie und Zellbiologie der Martin-Luther-Universität Halle-Wittenberg weitergeführt, die von der früheren IPK-Mitarbeiterin Dr. Insa Schroeder geleitet wird.

In den Jahren 2010/2011 wurden eine Habilitation, acht Dissertationen, eine Diplomarbeit und zwei Bachelorarbeiten erfolgreich abgeschlossen.

Für die abteilungsinterne, die institutsweite und die institutsübergreifende Zusammenarbeit spielten auch 2010/2011 lasergestützte Durchflusszytometrie, Fluoreszenzmikroskopie, transiente Hochdurchsatz-RNAi und Bioinformatik eine wesentliche Rolle. Alle Gruppen der Abteilung kooperierten innerhalb und außerhalb des IPK, z. B. im Rahmen von GABI, des „Paktes für Forschung und Innovation" der *WGL*, des Exzellenz-Netzwerks des Landes Sachsen-Anhalt, des ERA-NET Plant Genomics und von KBBE-Projekten. Für die vielfältig verflochtene Zusammenarbeit zwischen den Gruppen der Abteilung, innerhalb des IPK und darüber hinaus siehe die Berichte der jeweiligen Arbeitsgruppen und deren Publikationsverzeichnisse.

Unter den in 2010/2011 erbrachten Forschungsleistungen seien die folgenden besonders hervorgehoben:

– Establishing of ontologies and controlled vocabularies for structuring, integration and linking of diverse databases; assembly and annotation of genomic sequences (research group Bioinformatics and Information Technology).

In addition to obtaining basic knowledge, it is intended to establish the prerequisites for directed modification of plant genomes and to provide technological platforms and resources for biotechnology and breeding purposes. These efforts are largely integrated within the frame of the **Plant Genome Resources Centre (PGRC**) involving all departments of the IPK. PGRC services such as DNA sequencing and bioinformatics services are provided by the research groups Transcriptome Analysis and Bioinformatics and Information Technology.

Special germplasm collections (barley, field bean, and other crops) with gene and chromosome mutations are developed, characterised and maintained within the framework of the research programmes of the research groups Chromosome Structure and Function, Gene and Genome Mapping and Karyotype Evolution.

Developments in 2010 and 2011

Due to retirement of the group leader, the group '*In vitro* Differentiation' has been closed on 31.12.2010. Several projects are continued in the Junior Research Group "Stem Cell Research" at the Institute of Anatomy and Cell Biology, University Halle, led by the former group member Dr. Insa Schroeder.

In 2010 and 2011 one habilitation, eight dissertations (PhD), one Diploma thesis and two Bachelor theses have been finished successfully.

Besides PGRC services, flow-cytometry, fluorescence microscopy, high-throughput transient RNAi and bioinformatic approaches were important issues for collaboration within the Department and with other groups at and beyond IPK during the last two years. All groups of the Department collaborated with internal and external partners within the frame of large national and international research networks such as GABI (BMBF), "Pakt für Forschung und Innovation" (*WGL*), Excellence network (Saxony-Anhalt), ERA-NET Plant Genomics and KBBE projects. For the multiple cooperative links of the individual groups see their detailed reports and publication records.

The following scientific achievements are considered as highlights of the Department in 2010/2011:

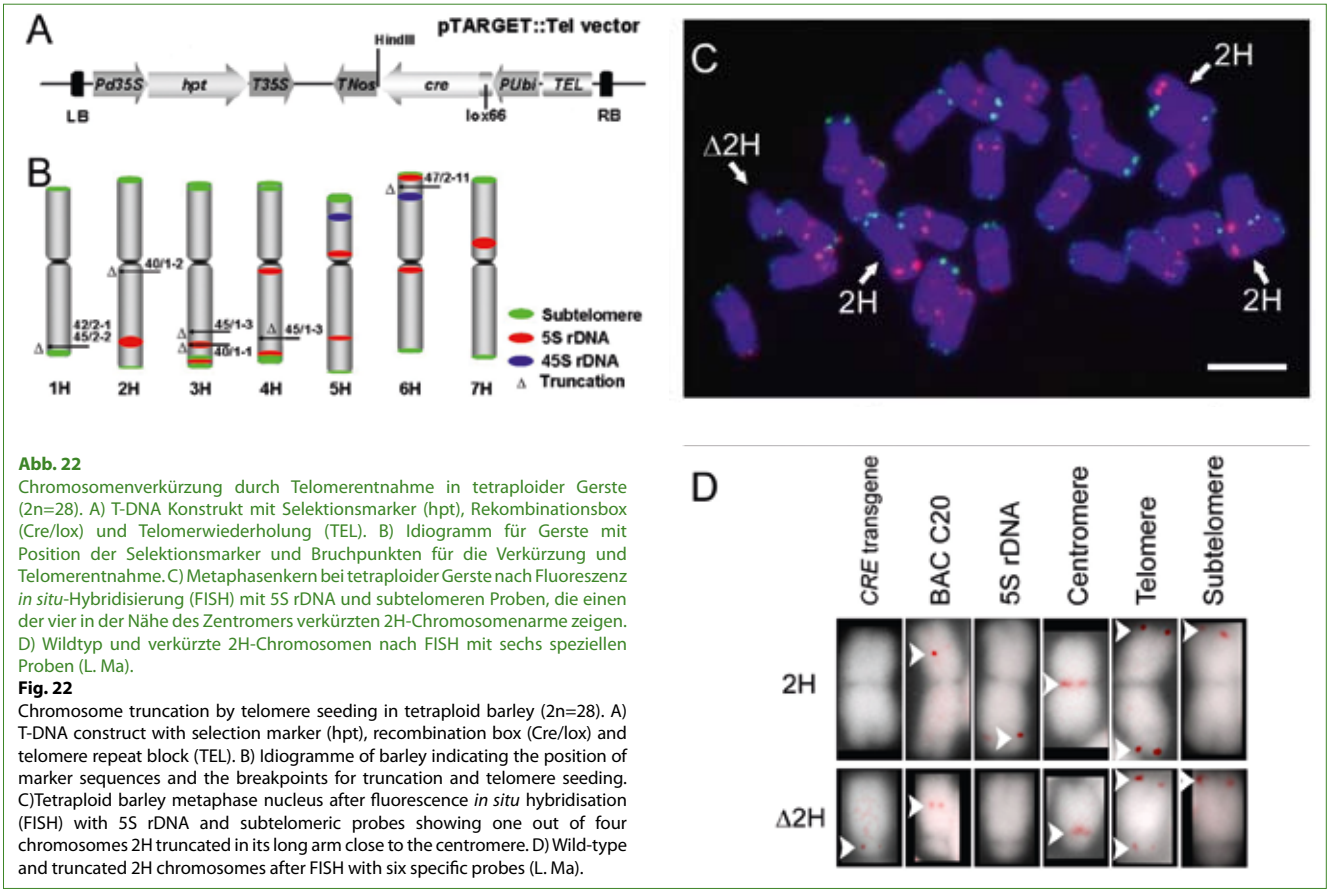


Abb. 22
Chromosomenverkürzung durch Telomerentnahme in tetraploider Gerste (2n=28). A) T-DNA Konstrukt mit Selektionsmarker (hpt), Rekombinationsbox (Cre/lox) und Telomerwiederholung (TEL). B) Idiogramm für Gerste mit Position der Selektionsmarker und Bruchpunkten für die Verkürzung und Telomerentnahme. C) Metaphasenkern bei tetraploider Gerste nach Fluoreszenz *in situ*-Hybridisierung (FISH) mit 5S rDNA und subtelomeren Proben, die einen der vier in der Nähe des Zentromers verkürzten 2H-Chromosomenarme zeigen. D) Wildtyp und verkürzte 2H-Chromosomen nach FISH mit sechs speziellen Proben (L. Ma).

Fig. 22
Chromosome truncation by telomere seeding in tetraploid barley (2n=28). A) T-DNA construct with selection marker (hpt), recombination box (Cre/lox) and telomere repeat block (TEL). B) Idiogramme of barley indicating the position of marker sequences and the breakpoints for truncation and telomere seeding. C)Tetraploid barley metaphase nucleus after fluorescence *in situ* hybridisation (FISH) with 5S rDNA and subtelomeric probes showing one out of four chromosomes 2H truncated in its long arm close to the centromere. D) Wild-type and truncated 2H chromosomes after FISH with six specific probes (L. Ma).

Erfolgreiche Manipulation von Pflanzenchromosomen

Im Rahmen eines gemeinsamen „Pakt für Forschung und Innovation"-Projektes der Leibniz-Gemeinschaft generierten die Gruppen Epigenetik, Karyotypevolution, Chromosomenstruktur und -funktion und Pflanzliche Reproduktionsbiologie (Abt. Physiologie und Zellbiologie) verkürzte Chromosomen in *Arabidopsis thaliana* und in Gerste über Agrobakterium-vermittelten Transfer von Telomersequenz-haltigen Konstrukten. Telomersequenz-bedingte Chromosomenverkürzung wurde nur in tetraploiden Pflanzen gefunden. Offenbar ist der Verlust chromosomaler Segmente nur in polyploidem Hintergrund tolerierbar. Die verkürzten Chromosomen sind mitotisch stabil und sexuell übertragbar, obwohl die Übertragungsrate durch männliche wie weibliche Gameten geringer ist als nach den Mendelschen Regeln zu erwarten (C.H. Teo, L. Ma, E. Kapusi, G. Hensel, I. Schubert, J. Kumlehn, A. Houben, M.F. Mette; Plant Journal 2011; E. Kapusi, L. Ma, C.H. Teo, G. Hensel, A. Himmelbach, I. Schubert, M.F. Mette, J. Kumlehn, A. Houben; Chromosoma 2011; Abb. 22).

Successful generation of engineered plant chromosomes

In frame of a joined "Pakt für Forschung und Innovation" project, the research groups Epigenetics, Karyotype Evolution, Chromosome Structure and Function, and Plant Reproductive Biology (Dept. of Physiology and Cell Biology) generated engineered minichromosomes of *Arabidopsis thaliana* and barley. Following a top-down approach, truncated endogenous chromosomes were obtained by *Agrobacterium*-mediated transfer of T-DNA constructs containing telomere sequences. Telomere seeding connected to chromosome truncation was found in tetraploid plants only, indicating that genetic redundancy facilitates recovery of shortened chromosomes. Truncated chromosomes were transmissible in sexual reproduction, but were via male and female gametes inherited at rates lower than expected according to Mendelian rules. However, more studies are required to develop tools for a targeted shortening of chromosome arms (C.H. Teo, L. Ma, E. Kapusi, G. Hensel, I. Schubert, J. Kumlehn, A. Houben, M.F. Mette; Plant Journal 2011; E. Kapusi, L. Ma, C.H. Teo, G. Hensel, A. Himmelbach, I. Schubert, M.F. Mette, J. Kumlehn, A. Houben; Chromosoma 2011; Fig. 22).

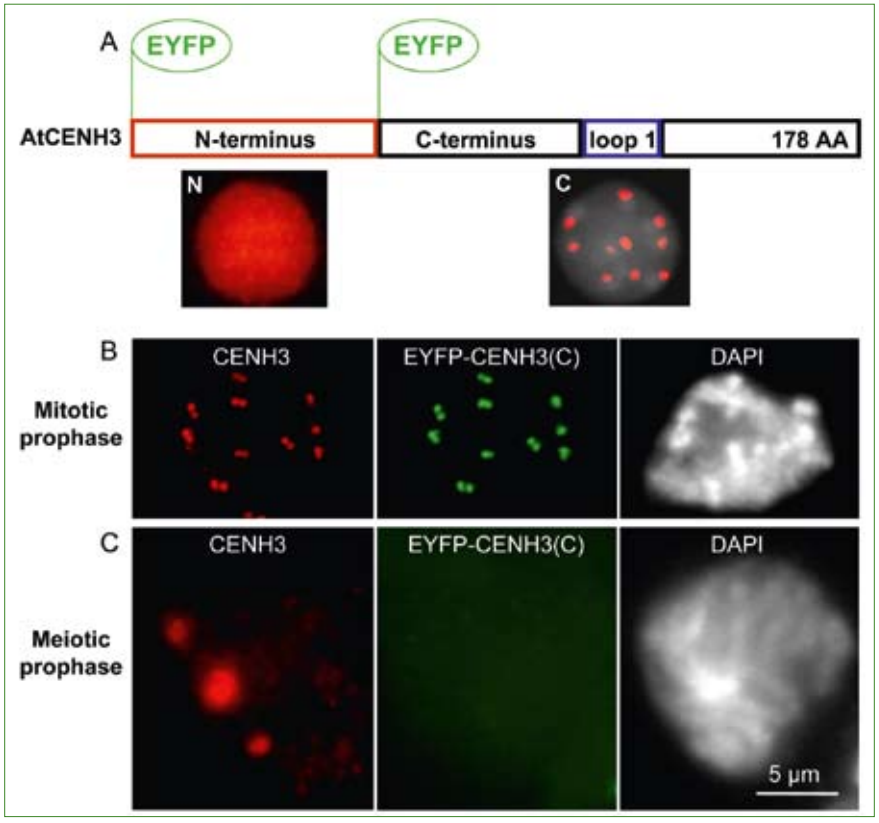


Abb. 23
Der C-terminale Teil der zentromerischen Histon-Variante CENH3 ist notwendig und hinreichend für die Aufnahme zentromerischer Nukleosomen während der G2-Phase des mitotischen Zyklus: der N-terminale Teil ist zusätzlich notwendig zur Ablagerung der meiotischen Nuclei an die Zentromere. A) Schema der Zusammensetzung der C- und N-terminalen Teile von CENH3 mithilfe von EYFP-Kennzeichnung. Der N-terminale Teil führt zu diffusen Signalen wohingegen der C-terminale Teil sich um Zentromere in somatischen transgenen *Arabidopsis thaliana*-Nuclei nachweisen lässt. B) Mitotischer Vorphasennucleus mit doppelten Signalen aufgrund von Schwesterkinetochoren. C) Meiotische Vorphasenkern mit Immunosignalen für CENH3 nur im Bereich der geclusterten Zentromere aber ohne EYFP-Signale für den C-terminalen Teil (I. Lermontova).

Fig. 23
The C-terminal part of the centromeric histone H3 variant CENH3 is necessary and sufficient for loading of centromeric nucleosomes during G2 of the mitotic cycle; the N-terminal part is required for deposition at centromeres of meiotic nuclei. A) Scheme of constructs of N- and C-terminal parts of CENH3 each labelled by EYFP. The N-terminal part results in diffuse signals whereas the C-terminal part targets centromeres in somatic transgenic *A. thaliana* nuclei. B) Mitotic prophase nucleus with double signals representing sister kinetochores. C) Meiotic prophase nucleus with immunosignals only for CENH3 at clustered centromeres, but without EYFP signals for the C-terminal part (I. Lermontova).

Erzeugung haploider Pflanzen durch uniparentale Chromosomeneliminierung

Der Verlust eines elterlichen Genoms nach interspezifischer Befruchtung ist oft eine Folge zwischenartlicher Kreuzungen. Im Ergebnis entstehen haploide Embryonen, die nur die Hälfte des normalen Chromosomenbestandes aufweisen. Obwohl die Eliminierung der Chromosomen eines Elters nach interspezifischer Kreuzung seit ca. 40 Jahren zur Erzeugung von Haploiden für Kartierungs- und Züchtungszwecke genutzt wird, sind die dafür verantwortlichen zellulären Mechanismen noch wenig verstanden. Die Gruppe Chromosomenstruktur und -funktion entdeckte, dass der uniparentalen Chromosomeneliminierung in Gerste-Hybriden ein Verlust der zentromerischen Histonvariante CENH3 in den betroffenen Chromosomen vorausgeht (s. Abb. 21, S. 54). Auch in chromosomal stabilen Artkombinationen werden nicht alle elterlichen CENH3-Varianten in die Zentromere eingebaut, obwohl alle entsprechenden Transkripte nachweisbar sind. Diese Befunde werden zur Etablierung effizienter Methoden der Haploidenerzeugung beitragen. (M. Sanei, R. Pickering, K. Kumke, S. Nasuda, A. Houben; Proc. Natl. Acad. Sci. U.S.A., highlighted in Faculty of 1000, Biology 2011).

Instant generation of haploid plants via chromosome elimination

Chromosome elimination - the removal of one parental genome after an egg is fertilised by sperm from another species - is one consequence of an interspecific hybridisation event. This process results in the formation of haploid embryos, which have half the normal number of chromosomes. Chromosome elimination has been exploited in barley and other species to produce doubled haploids for breeding and mapping purposes. Although this process was first described already 40 years ago, the actual cellular mechanism involved in the process of uniparental chromosome elimination remains poorly understood. The research group Chromosome Structure and Function revealed that uniparental chromosome elimination in interspecific barley hybrids is preceded by the loss of CENH3 from centromeres. In stable species combinations not all parental CENH3 variants are incorporated into centromeres despite the presence of *CENH3* transcripts from both parents (see Fig. 21, p. 54). These findings will help to establish more efficient methods for generating haploids (M. Sanei, R. Pickering, K. Kumke, S. Nasuda, A. Houben; Proc. Natl. Acad. Sci. U.S.A., highlighted in Faculty of 1000, Biology 2011).

Neue Funktionen der Histonvariante CENH3 bei der Aufrechterhaltung von Zentromeren

Das Zentromer ist die Chromosomenposition, an der bei allen Eukaryoten das Kinetochore, ein Multiproteinkomplex für die korrekte Segregation von Chromosomen während der Mitose und der Meiose, ausgebildet wird. Die Mechanismen für die Bestimmung der Zentromeridentität, den Aufbau und die Aufrechterhaltung der Kinetochore sind noch weitgehend unverstanden. Der zentromerischen Histon H3-Variante, CENH3, kommt eine wichtige Rolle bei der Assemblierung und Aufrechterhaltung von Kinetochoren zu. Nach dem Beweis, dass die Beladung zentromerischer Nukleosomen bei Pflanzen während der späten G2-Phase des Zellzyklus erfolgt (Lermontova et al. 2006, 2007, 2011a), konnte in Zusammenarbeit mehrerer Gruppen gezeigt werden, dass RNAi-bedingte CENH3-Verminderung in *Arabidopsis thaliana* zu Zwergwuchs durch reduzierte Mitosezahlen (die verbleibenden Mitosen verlaufen fehlerfrei) sowie zu verminderter Fertilität führt. Während der C-terminale Teil von CENH3 notwendig und ausreichend für die mitotische Teilung ist, ist der N-terminale Teil für den Einbau von CENH3 in die Zentromere meiotischer Kerne unverzichtbar. Die Expression von N-terminal verkürztem CENH3 kann die Menge von endogenem CENH3 verringern und so einen RNAi-Effekt simulieren. Die Folge von vermindertem endogenem CENH3 ist verringerte Fertilität aufgrund unzureichender Beladung der Zentromere mit CENH3 und nachfolgendem ‚Chromosomen-lagging' und Kleinkernbildung (I. Lermontova; O. Koroleva, John Innes Centre, Norwich, UK; T. Rutten, Abt. Physiologie und Zellbiologie; J. Fuchs; V. Schubert; I. Moraes; D. Koszegi, Abt. Molekulare Genetik; I. Schubert; Plant J. 2011) (s. Abb. 23, S. 58).

Evolution eines parasitären überzähligen B-Chromosoms

B-Chromosomen sind für Wachstum und Entwicklung eines Organismus nicht erforderlich. Dennoch werden sie in allen eukaryotischen Stämmen gefunden. Sie repräsentieren eine besondere Form des Vorkommens parasitärer DNA. In Zusammenarbeit zwischen den Gruppen Chromosomenstruktur und -funktion, Bioinformatik und Informationstechnologie, Karyotypevolution, Experimentelle Taxonomie und Genomdiversität (die letzten beiden Abteilung Genbank) wurden unerwartet viele von Genen abgeleitete Sequenzen auf dem B-Chromosom des Roggens gefunden, die es erlaubten, ihre ursprüngliche Position auf den A-Chromosomen zurückzuverfolgen. Verglichen mit den A-Chromosomen akkumuliert das B-Chromosom hohe Zahlen spezifischer Repeats und Insertionen von Organellen-DNA. Die Entstehung des Roggen-B-Chromosoms konnte auf 1,1 - 1,3 Mio. Jahre zurück datiert werden, d. h., etwa in die Zeit der Radiation der Gattung *Secale* vor 1,7 Mio. Jahren (s. Abb. 27, S. 67).

New roles of the histone variant CENH3 for centromere maintenance

The centromere is the chromosomal position where the kinetochore, a complex multiprotein structure, required for the proper segregation of chromosomes during mitosis and meiosis in all eukaryotes, is located. The mechanism(s) that determine centromere identity, assembly and maintenance of kinetochores are poorly understood. An important role in kinetochore assembly and function plays the centromeric histone H3 variant CENH3.

After proving that CENH3 loading onto centromeric nucleosomes occurs during late G2 in plants (Lermontova et al. 2006, 2007, 2011a), we showed that RNAi-mediated CENH3 knockdown in *Arabidopsis thaliana* caused dwarfism by a reduced number of mitoses (the remaining mitoses seemed to be error-free) as well as reduced fertility.

Whereas the C-terminal part of CENH3 is essential and sufficient for correct mitotic divisions, the N-terminal part is required for CENH3 deposition at centromeres of meiotic nuclei (see Fig. 23, p. 58). Expression of N-terminally truncated CENH3 can reduce the amount of endogenous CENH3, mimicking the effect of RNAi. The consequences of reduced endogenous CENH3 and of lack of meiotic incorporation of N-terminally truncated CENH3 are reduced fertility due to insufficient CENH3 loading to the centromeres of meiotic chromosomes, subsequent lagging of chromosomes and formation of micronuclei (I. Lermontova, O. Koroleva, John Innes Centre, Norwich, UK; T. Rutten, Dept. of Physiology and Cell Biology; J. Fuchs, V. Schubert, I. Moraes, D. Koszegi, Dept. of Molecular Genetics; I. Schubert; Plant J. 2011).

Evolution of a selfish supernumerary chromosome revealed

B chromosomes are not required for the normal growth and development of organisms, yet they are found in all eukaryotic phyla and are assumed to represent a specific type of selfish DNA. In close collaboration between the groups Chromosome Structure and Function, Bioinformatics and Information Technology, Karyotype Evolution, Experimental Taxonomy and Genome Diversity (the two latter Department of Genebank) we found that the B chromosomes of rye are unexpectedly rich in gene-derived sequences, which allowed to trace their origin to fragments of several A chromosomes. Compared to A chromosomes (As), the B chromosomes (Bs) were found to accumulate large numbers of specific repeats and insertions of organellar DNA. The origin of rye Bs was estimated at approximately 1.1 to 1.3 million years ago, during radiation of the genus *Secale* (1.7 million years ago) (see Fig. 27, p. 67).

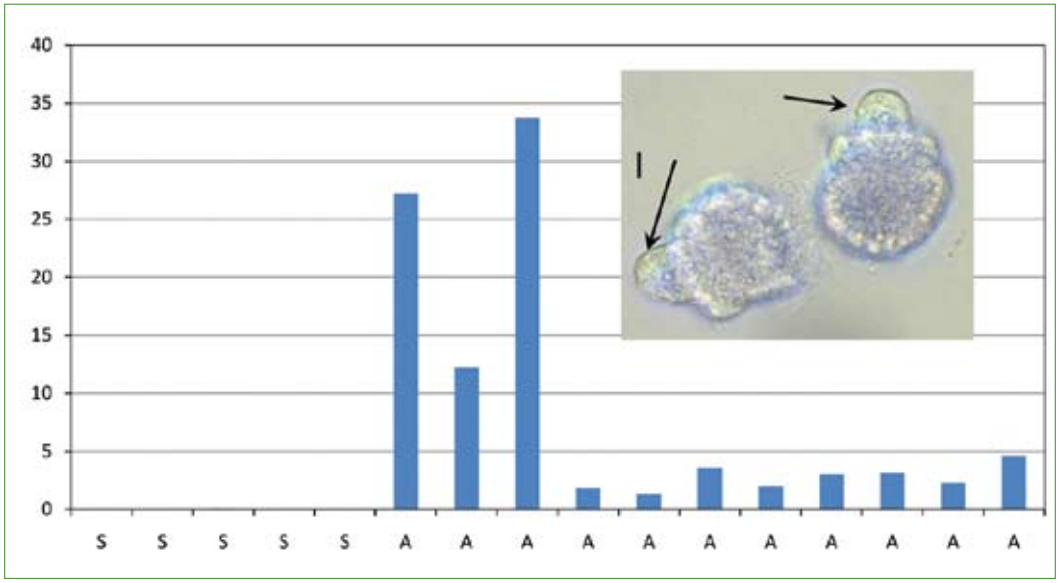


Abb. 24
Das Expressionsniveau der für Apomixis verantwortlichen Kandidatenallele in mikrodissektierten lebenden Eizellen (Pfeile deuten auf Megasporen-Mutterzellen) aus 5 diploiden sich geschlechtlich fortpflanzenden (S) und 8 diploiden apomiktischen (A) *Boechera*-Genotypen. Das Niveau wurde mithilfe von qRT-PCR im Vergleich zum Ubiquitin-Gen gemessen (J. Corral).
Fig. 24
Expression level of apomixis candidate allele, using qRT-PCR relative to the UBQ housekeeping gene, in microdissected live ovules (arrows show megaspore mother cells) from 5 diploid sexual (S) and 8 diploid apomictic (A) *Boechera* genotypes (J. Corral).

Ein Apomixis-spezifisches Allel wird ausschließlich in Ovulen apomiktischer Boechera-Pflanzen exprimiert

Ein durchflusszytometrischer Hochdurchsatz-Samen-Screen für >24.000 Einzelsamen von 110 *Boechera*-Akzessionen ergab genotypspezifische quantitative Unterschiede für die drei Apomixis-Komponenten Apomeiose, Parthenogenese und Pseudogamie. Außer unreduzierten Eizellen (Apomeiose) produziert *Boechera* häufig auch unreduzierte Pollen. Möglicherweise werden beide Phänomene durch ähnliche Mechanismen kontrolliert. Aus Sequenzen normalisierter blütenspezifischer cDNA-Bibliotheken wurden ‚high-density microarrays' erstellt und zum Vergleich der Expressionsprofile aus lebendem, mikrodissektiertem gametophytischem Gewebe sexueller und apomiktischer Akzessionen eingesetzt. Diese Analysen führten zur Identifizierung je eines Gens für die Bildung von unreduzierten Eizellen bzw. Pollen. Das Kandidatengen für Apomeiose zeigte einen spezifischen Polymorphismus in 12 apomiktischen Akzessionen unterschiedlicher geografischer Herkunft, der in keiner der getesteten sexuellen Akzessionen auftrat. Dieser Polymorphismus scheint im Laufe der Evolution der Gattung *Boechera* Rekombination erfahren zu haben, kommt jedoch in allen Apomikten, unabhängig vom genetischen, geografischen oder Ploidie-Hintergrund, vor. Die ausschließliche Expression des weiblichen ‚Apomixis-Allels' in apomiktischen Ovulen wurde durch qRT-PCR bestätigt (Abb. 24).

An apomeiosis-specific allele is exclusively expressed in apomictic Boechera ovules

Using high-throughput seed screening, we analysed >24,000 single seeds in 110 *Boechera* accessions, and have shown genotype-specific quantitative variation for the three apomixis components apomeiosis, parthenogenesis and pseudogamy. Besides unreduced egg cells (apomeiosis), *Boechera* also produces frequently unreduced pollen. Possibly, similar mechanisms control both processes. A pipeline has been established to compare expression profiles of microdissected live gametophytic tissue between sexual and apomictic *Boechera*. High-density microarrays were built using sequences generated from flower-specific normalised cDNA libraries. These analyses eventually led to the identification of a single gene each underlying unreduced egg (J. Corral) and pollen (M. Mau) formation. The candidate apomeiosis gene has led to the identification of a single "apomixis polymorphism" in 12 geographically distant apomictic accessions, but not in any tested sexual accession. This polymorphism appears to have undergone recombination during the evolution of *Boechera*, but is shared by all apomicts, regardless of genetic, ploidy or geographic backgrounds. The female "apomixis allele" has been verified by qRT-PCR showing exclusive expression in apomictic ovules (Fig. 24).

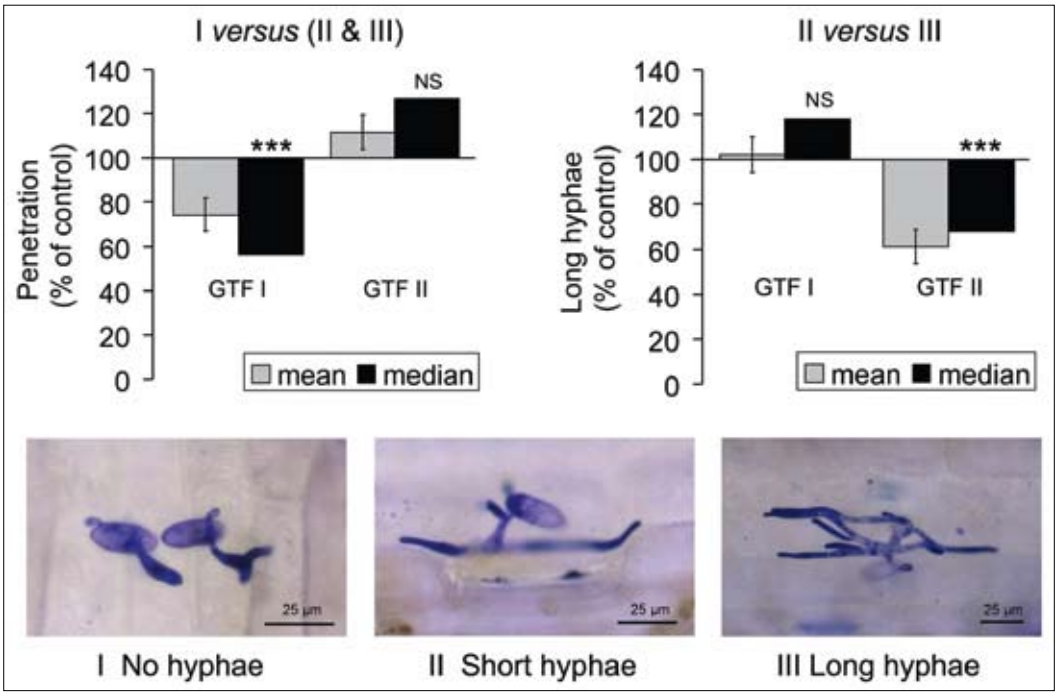


Abb. 25
Die reduzierte pilzliche Ausbreitung und Hyphenwachstum von *Blumeria graminis* f.sp. *tritici* auf Weizenpflanzen, die das Virus-induzierte Gen Silencing von *BgGTF1* und *BgGTFII* zeigen. ***, Signifikante Unterschiede im Vergleich zur leeren Vektorkontolle (BSMV:00) mit $p < 0{,}0001$. Die Durchschnitts- und Medianwerte aus 2-3 unabhängigen Experimenten mit insgesamt 77-102 Pflanzen (D. Nowara).

Fig. 25
Reduced fungal penetration and hyphal growth of *Blumeria graminis* f.sp. *tritici* on wheat plants exhibiting virus-induced gene silencing of *BgGTF1* and *BgGTFII*, respectively. ***, significantly different from empty-vector control (BSMV:00) with $p < 0.0001$. Mean and median values from 2-3 independent experiments comprising in total 77-102 plants are shown (D. Nowara).

Wirts-induziertes ‚Gen-Silencing' in phytopathogenen Pilzen

Phytopathogene Pilze sind die wichtigste Gruppe von Pflanzenparasiten und verursachen weltweit ernorme Schäden an Kulturpflanzen hinsichtlich Ertrag und Qualität. Pflanzen wehren sich gegen phytopathogene Pilze durch Zellwandverstärkung, antimikrobielle Verbindungen und programmierten Zelltod. Wir entdeckten, dass Akkumulation transgener doppelsträngiger RNA mit Homologie zu pilzlicher Boten-RNA Gerste und Weizen gegen Attacken durch den Mehltaupilz *Blumeria graminis* schützt und nannten dieses Phänomen Wirts-induziertes Gen-Silencing **(HIGS)**. Transiente Expression verschiedener Haarnadel-RNAi-Konstrukte in Gerste-Epidermis verhinderte das Eindringen der Pilz-Haustorien in die Pflanze. Die Aufnahme der RNA durch das Pathogen erfolgt offenbar wenige Stunden nach Inokulation, wenn der Pilz gerade im Begriff ist, die Epidermis zu penetrieren. Ähnlich wie transgene Gerste, die ein RNAi-Konstrukt gegen pilzliche Glucanosyltransferase I *(BgGTFI)* trägt, war mit dem ‚barley stripe mosaic virus' behandelter Weizen durch Virus-induziertes ‚Gen-Silencing' der Enzyme *BgGTFI* oder *BgGTFII* signifikant widerstandsfähiger gegen *B. graminis* als unbehandelte Pflanzen (Abb. 25). GTF-Proteine sind erforderlich für die pilzliche Zellwandbildung. Laufende Arbeiten weisen darauf hin, dass HIGS auch gegen *Fusarium*-Befall von Gerste und Weizen einsetzbar ist. Falls HIGS auch natürlicherweise vorkommt, wäre das gegenwärtige Paradigma der Wirts-Pathogen-Wechselbeziehung entsprechend zu modifizieren (D. Nowara, A. Gay, C. Lacomme, J. Shaw, C. Ridout, D. Douchkov, G. Hensel, J. Kumlehn, P. Schweizer; Plant Cell 2010).

Ingo Schubert, November 2011

Host-induced gene silencing in phytopathogenic fungi

Phytopathogenic fungi represent the most important group of plant parasitic organisms and cause enormous damage to crop yield and quality worldwide. Plants defend themselves against invading phytopathogenic fungi by cell-wall fortification, the accumulation of antimicrobial low-molecular-weight compounds, antimicrobial proteins and programmed cell death. We discovered that barley and wheat can also be protected from attack by the powdery mildew fungus *Blumeria graminis* via the accumulation of transgenic, double-stranded RNA targeting fungal mRNA sequences and named this phenomenon "host-induced gene silencing" **(HIGS)**. A number of RNAi hairpin constructs expressed transiently in barley epidermal cells stopped the fungus as early as the formation of the first haustorium suggesting that uptake of the silencing RNA molecules takes place within few hours after inoculation, when the fungus is just about to penetrate the epidermal cell wall. Similar to transgenic barley carrying an RNAi construct against fungal *glucanosyl transferase I* (*BgGTFI*), BSMV-treated wheat plants exhibiting virus-induced gene silencing of *BgGTFI or BgGTFII* were significantly more resistant to *B. graminis* (see Fig. 25). GTF proteins are required for fungal cell-wall formation and elongation. Work in progress indicates that HIGS can also be applied to the *Fusarium* head blight disease of wheat and barley. It remains to be examined whether HIGS is also a naturally occurring phenomenon modifying the current paradigm of plant-fungus communication (D. Nowara, A. Gay, C. Lacomme, J. Shaw, C. Ridout, D. Douchkov, G. Hensel, J. Kumlehn, P. Schweizer; Plant Cell 2010).

Ingo Schubert, November 2011

PROGRAMME: CYTOGENETICS
Research Group: Karyotype Evolution

Head: Prof. Ingo Schubert

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Fuchs, Jörg, Dr.
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Lermontova, Inna, Dr. (DFG, since 17.01.2011)
Sulzbacher, Sabine, Dr. (BMBF, 01.01.-31.07.2011)
Watanabe, Koichi, Dr. (BMBF, till 31.12.2010)

Visiting Scientists/Scholars
Cincu, Emilia (self-financed, 31.05.-04.06.2010)
Duc Trung, Tran (MOET-Vietnam, since 17.09.2011)
Endo, Takashi R., Prof. (IPK, 20.11.-25.11.2010)
Schroeder, Insa, Dr. (Martin Luther University Halle-Wittenberg, 01.01.-30.06.2011)
Seeliger, Katharina (self-financed, 11.04.-17.04.2010)
Temel, Aslihan (Fellowship University of Istanbul, 04.01.-30.09.2010)
Vu, Thi Ha Giang, Dr. (self-financed, 25.05.-03.06.2011; since 30.09.2011)
Wobus, Anna M., Prof. (self-financed, since 01.01.2011)

Goals

Elucidation of structure, plasticity, evolution and epigenetic modifications of plant genomes and functional chromosome domains.

Research Report

Centromere research. RNAi-mediated **knock-down of** the centromeric histone H3 variant **CENH3** of *Arabidopsis thaliana* **caused dwarfism** by a reduced number of mitoses. The remaining mitoses seemed to be error-free. CENH3 RNAi transformants revealed **reduced fertility** because of frequently disturbed meiotic chromosome segregation. **N-terminally truncated EYFP-CENH3** is deposited to and functional within centromeres of mitotic *A. thaliana* chromosomes but **cannot be loaded to centromeres of meiotic nuclei**. Thus, the N-terminal part is required for CENH3 loading during meiosis. N-terminally truncated EYFP-CENH3 expression can reduce the amount of endogenous CENH3, mimicking the effect of RNAi. The consequences of reduced endogenous CENH3 and of lack of meiotic incorporation of N-terminally truncated EYFP-CENH3 are reduced fertility caused by insufficient CENH3 loading to the centromeres of meiotic chromosomes, subsequent lagging of chromosomes and formation of micronuclei (I. Lermontova; O. Koroleva, John Innes Centre, Norwich, UK; T. Rutten, Dept. Physiology and Cell Biology (PCB); J. Fuchs; V. Schubert; I. Moraes; D. Koszegi, Dept. Molecular Genetics (MOG), I. Schubert; Plant J. 2011) (Fig. 23, p. 38).

Studies on the regulation of CENH3 transcription in *A. thaliana* revealed within the CENH3 promoter two binding motifs for E2F transcription factors which contribute in a concerted manner to the cell cycle-specific CENH3 expression (S. Heckmann; I. Lermontova; B. Bergmans, L. de Veylder, Ghent University, Belgium; H. Bäumlein, MOG; I. Schubert; Plant J. 2011).

Chromatin modifications. Studies on the nuclear distribution of histone methylation marks in dioecious *Rumex* species revealed that (i) methylation of H3K4me1,2,3 and H3K9me3 is restricted to euchromatin and excluded from the Y chromosome-derived heterochromatin; (ii) H3K9me1,2 and H3K27me1 label the Y chromatin similarily as the autosomal hetero- and euchromatin and (iii) H3K27me2 and H3K27me3 are enriched in Y chromatin of *Rumex* species with the XX/XY_1Y_2 sex determination system (Saxony-Anhalt Excellence Cluster, J. Fuchs, G. Jovtchev, B. Borisova-Todorova).

Interphase chromatin organisation. Chromosome territory (CT) arrangement, chromatin domain positions, and sister chromatid cohesion were studied in relation to the endopolyploidisation degree in *A. thaliana*. Whereas distinct CTs are mainly maintained, an increasing **dispersion of sister chromatids** (starting from mid arm positions toward telomeres and centromeres) **accompanies** increasing **endopolyploidy** levels (V. Schubert, A. Berr, A. Meister, Plant Physiol. 2012). Furthermore, a similar chromatin organisation was shown for A and B chromosomes of rye (V. Schubert, A. Meister, H. Tsujimoto, T.R. Endo, A. Houben; Chromosome Res. 2011).

Biological consequences of DNA double-strand breaks (DSB). 'Break-induced replication' (BIR), mimicking non-reciprocal recombination of regions distal to a DSB, was – based on genetic data – claimed to be a mechanism responsible for repair of >50 % of DSBs in budding yeast. BIR was also postulated for mammals without experimental evidence. After DSB-induction by bleomycin during S and G2 phase and simultaneous labelling of chromosomes by incorporation of the base analogue ethynyldeoxyuridine, we found **no** indication for the occurrence of **BIR in a higher plant** (*Vicia faba*). However, interstitial asymmetric labelling of sister chromatids indicated **DSB repair by gene conversion spanning hundreds of Kb** (Fig. 26). The apparent loss of heterozygosity after DSB repair in yeast and mammals can be interpreted by unbalanced segregation of reciprocally translocated chromosomes rather than by the hypothetical BIR (I. Schubert, V. Schubert, J. Fuchs; Frontiers in Plant Sci. 2011).

Chromosome engineering. A joint "Pakt für Forschung und Innovation" project (A. Houben, M.F. Mette, J. Kumlehn, I. Schubert) is aimed to generate **barley minichromosomes** as potential vehicles for gene transfer. Via transformation with telomere repeat containing constructs, it was possible to generate truncated chromosomes, which are **transmissible to the next generation**, in tetraploid *A. thaliana* as well as in tetraploid barley plants (C.H. Teo, L. Ma, E. Kapusi, G. Hensel, J. Kumlehn (PCB); I. Schubert; A. Houben; M.F. Mette; Plant J. 2011) (E. Kapusi, L. Ma, C.H. Teo, G. Hensel, A. Himmelbach, Dept. of Genebank (GB); I. Schubert, M.F. Mette, J. Kumlehn, A. Houben, Chromosoma 2011) (Fig. 21, p. 54).

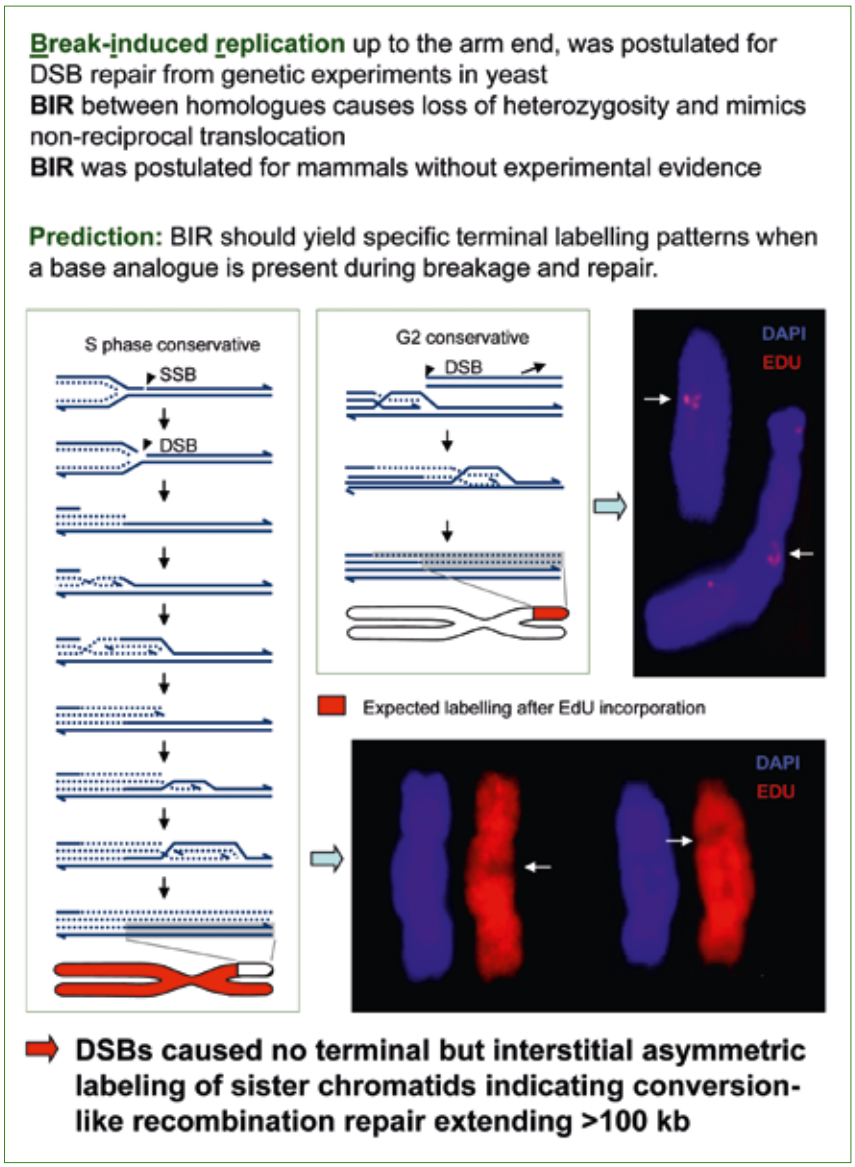

Fig. 26
Models for 'break-induced replication' were not confirmed by labelling of *Vicia faba* chromosomes with the base analogue ethynyldeoxyuridine in S and G2 after DSB induction; instead, extended conversion-like recombination repair was detected (I. Schubert, V. Schubert, J. Fuchs).

Genome Size Evolution. To elucidate the mechanisms which resulted in rapid shrinkage or expansion of the genomes of the carnivorous species *Genlisea pygmaea* (86 Mb) and *G. hispidula* (>1500 Mb), respectively, *de novo* sequencing of genomes and of transcriptomes of both species has been performed and assembly and annotation efforts have been started in collaboration with G. Vu and A. Pecinka, MPIPZ, Köln (J. Fuchs, H.X. Cao, GP, G. Jovtchev, I. Schubert, U. Scholz, T. Schmutzer, F. Bull, research group Bioinformatics and Information Technology (BIT).

Publications

Peer Reviewed Papers

2010

Banaei Moghaddam, A.M., J. Fuchs, T. Czauderna, A. Houben & M.F. Mette: Intraspecific hybrids of *Arabidopsis thaliana* revealed no gross alterations in endopolyploidy, DNA methylation, histone modifications and transcript levels. Theor. Appl. Genet. 120 (2010) 215-226.

Berr, A., E.J. McCallum, R. Menard, D. Meyer, J. Fuchs, A.W. Dong & W.H. Shen: *Arabidopsis* SET DOMAIN GROUP2 is required for H3K4 trimethylation and is crucial for both sporophyte and gametophyte development. Plant Cell 22 (2010) 3232-3248.

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Kinoshita, N., A. Berr, C. Belin, R. Chappuis, N.K. Nishizawa & L. Lopez-Molina: Identification of *growth insensitive to ABA3* (*gia3*), a recessive mutation affecting ABA signaling for the control of early post-germination growth in *Arabidopsis thaliana*. Plant Cell Physiol. 51 (2010) 239-251.

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Ma, L., G.T. Vu, V. Schubert, K. Watanabe, N. Stein, A. Houben & I. Schubert: Synteny between *Brachypodium distachyon* and *Hordeum vulgare* as revealed by FISH. Chromosome Res. 18 (2010) 841-850.

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Moraes, I.C., I. Lermontova & I. Schubert: Recognition of *A. thaliana* centromeres by heterologous CENH3 requires high similarity to the endogenous protein. Plant Mol. Biol. 75 (2011) 253-261.

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Sędzielewska, K.A., J. Fuchs, E.M. Temsch, K. Baronian, R. Watzke & G. Kunze: Estimation of the *Glomus intraradices* nuclear DNA content. New Phytol. 192 (2011) 794-797.

Teo, C.H., L. Ma, E. Kapusi, G. Hensel, J. Kumlehn, I. Schubert, A. Houben & M.F. Mette: Induction of telomere-mediated chromosomal truncation and stability of truncated chromosomes in *Arabidopsis thaliana*. Plant J. 68 (2011) 28-39.

Wiese, C., T. Nikolova, I. Zahanich, S. Sulzbacher, J. Fuchs, S. Yamanaka, E. Graf, U. Ravens, K.R. Boheler & A.M. Wobus: Differentiation induction of mouse embryonic stem cells into sinus node-like cells by suramin. Int. J. Cardiol. 147 (2011) 95-111.

Zakrzewski, F., B. Weisshaar, J. Fuchs, E. Bannack, A.E. Minoche, J.C. Dohm, H. Himmelbauer & T. Schmidt: Epigenetic profiling of heterochromatic satellite DNA. Chromosoma 120 (2011) 409-422.

PhD and Diploma Theses

2010

Weissleder, A.: Selection and characterization of *Arabidopsis thaliana* cohesin and condensin T-DNA insertion mutants. (PhD Thesis) Martin-Luther-Universität Halle-Wittenberg, Naturwissenschaftliche Fakultät I, Institut für Biologie, Halle/S. (2010) 90 pp.

2011

Moraes, I.: Structural requirements for CENH3 targeting to centromeric chromatin. (PhD Thesis) Martin-Luther-Universität Halle-Wittenberg, Naturwissenschaftliche Fakultät I, Institut für Biologie, Bereich Pflanzenphysiologie, Halle/S. (2011) 82 pp.

Research Group: Chromosome Structure and Function

Head: Dr. Andreas Houben

Scientists

IPK financed
Heckmann, Stefan (0.50)
Karimi Ashtiyani, Raheleh (Pakt für Forschung und Innovation, 01.09.2010-31.01.2011)
Ma, Lu, Dr. (0.50 Pakt für Forschung und Innovation, till 31.10.2011; 0.50, 01.11.-31.12.2011)

Grant Positions
Banaei Moghaddam, Ali Mohammad (DFG)
Demidov, Dmitri, Dr. (DFG / SFB 648)
Karimi Ashtiyani, Raheleh (Saxony-Anhalt, till 31.08.2010; 0.50 Overhead, 11.04.-31.07.2011; BMBF, since 01.08.2011)
Klemme, Sonja (0.50 DFG, since 01.03.2010)
Sanei, Maryam (0.50 DFG, till 30.09.2010; 0.50 Overhead, 01.10.-31.12.2010)

Visiting Scientists/Scholars
Acevedo-Garcia, Johanna (self-financed, 31.07.-13.08.2011)
Agueci, Francesco (self-financed, 01.01.-30.06.2010)
Caillieux, Erwann (DAAD, 10.10.-28.10.2011)
Cuacos, Maria (University of Madrid/Ministry of Education in Spain, 01.06.-31.08.2011)
Evtushenko, Elena, Dr. (DFG, 01.09.-29.11.2010)
Gonzalez Garcia, Miriam (University of Madrid/Ministry of Education in Spain, 02.05.-02.08.2010)
Ishii, Takayoshi (self-financed, 17.10.-30.10.2011)
Kaur, Gurmeet (DAAD, 17.10.-01.12.2010)
Sanei, Maryam (self-financed, 01.07.-01.10.2011)
Sousa, Aretuza (Ludwig Maximilians University Munich, 28.02.-11.03.2011)

Goals

Analysis and manipulation of structure and regulation of plant chromosomes.

Research Report

Supernumerary B chromosomes occur in all eukaryotic phyla and are assumed to represent a specific type of selfish DNA. Little is known about their origin and molecular composition. In cooperation with several cooperation partners we determined the sequence composition of rye B chromosomes. Based on a comparative sequence analysis of the A and B chromosomes of rye, we propose the **first comprehensive model of B chromosome evolution** (see Fig. 27, p. 67). This model includes the identification of the origin of B chromosomes by the recombination of A chromosome segments. This process was followed by capturing of additional A-derived and organellar sequences, and the amplification of repeats, which are important for the specific drive for B chromosome maintenance. The most unexpected result of our analysis is the discovery that **B chromosomes are rich in gene fragments** that represent copies of A chromosome genes (A. Banaei-Moghaddam, S. Klemme, in cooperation with the research groups Experimental Taxonomy, Bioinformatics and Information Technology, Genome Diversity and external cooperation partners).

Engineered minichromosomes offer an enormous opportunity to plant biotechnology as they have the potential to simultaneously transfer and stably express multiple genes. Following a top-down approach, we **truncated endogenous chromosomes in barley (*Hordeum vulgare*) and in *Arabidopsis*** by *Agrobacterium*-mediated transfer of T-DNA constructs containing telomere sequences. Truncated chromosomes were transmissible in sexual reproduction, but were inherited at rates lower than expected according to Mendelian rules (L. Ma, in cooperation with the research groups Structural Cell Biology; Karyotype Evolution and Plant Reproductive Biology – Department of Physiology and Cell Biology).

Precise segregation of chromosomes during cell divisions is essential for genetic stability. We demonstrated that **Aurora kinases of plants are involved in the regulation of the spindle assembly checkpoint** (SAC) pathway. The SAC proteins **AtMad2 and AtBub1-R1 interact with AtAurora1** *in vivo* and **serve as kinase substrates** for AtAurora1 *in vitro*. **Deregulation of SAC** expression **yields poly- and/or aneuploids** (D. Demidov, in cooperation with the research group Karyotype Evolution and external cooperation partners).
The cell cycle-specific phosphorylation of **histone H3 at threonine 3** is highly conserved, but the significance of **Haspin kinase** driven H3 phosphorylation for plant development is unclear. In *Arabidopsis*, AtHaspin contributes to embryonic patterning and altered expression of AtHaspin induced pleiotropic phenotypes. Further, a **cross-talk exists between phosphorylation of H3T3 by AtHaspin** and **other post-translational modifications**. The level of H3T3 phosphorylation activity of recombinant AtHaspin is reduced by methylation or acetylation of H3K4 and by phosphorylation at H3T6. Modifications at H3K9, H3S10 and H3T11 had no influence on the activity of AtHaspin (R. Karimi Ashtiyani).

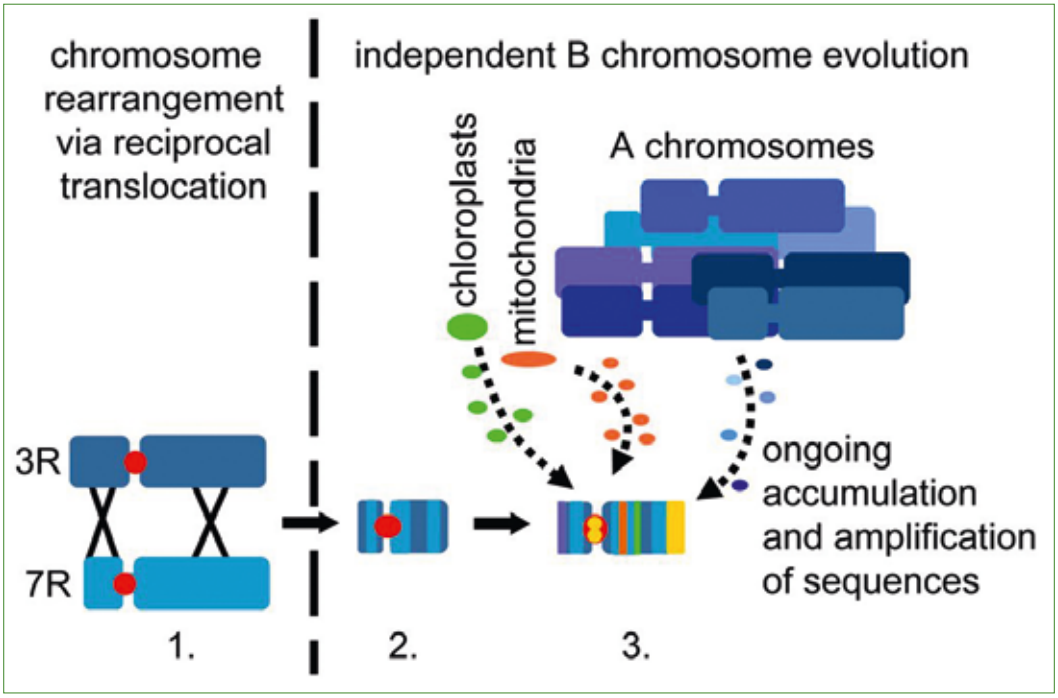

Fig. 27
Model on the stepwise evolution of the rye B chromosome. (1) Reciprocal translocation between 3R and 7R and subsequent imbalanced segregation of the small translocation product results in duplication of fragments of A chromosomes 3R and 7R (2) which do not pair to the homologous A chromosome regions and represent a proto-B. (3) Accumulation of organellar and A chromosome-derived DNA fragments, amplification of B-specific repeats, erosion and inactivation of A-derived genes (Muller's ratchet) as well as gain of a 'chromosome drive' result in a B chromosome (M. Martis, S. Klemme, A.M. Banaei Moghaddam, F. R. Blattner, J. Macas, T. Schmutzer, U. Scholz, H. Gundlach, T. Wicker, H. Šimková, P. Novák, P. Neumann, M. Kubaláková, E. Bauer, G. Haseneyer, J. Fuchs, J. Doležel, N. Stein, K.F.X. Mayer and A. Houben).

The chromatin features of generative and vegetative nuclei after **first and second pollen mitosis in rye** (*Secale cereale*) were analysed. The condensed chromatin of generative nuclei is earmarked by an enhanced level of histone H3K4 and/or K9 dimethylation and H3K9 acetylation. The less condensed vegetative nuclei are RNA polymerase II-positive. In rye, unlike in *Arabidopsis*, CENH3 is not excluded from the chromatin of the vegetative nucleus and the condensation degree of centromeric and subtelomeric regions did not differ between generative and vegetative nuclei. Differences between rye and *Arabidopsis* suggest that the **chromatin organisation** in mature nuclei of pollen grains **is not universal across angiosperms** (A. Houben, in cooperation with external cooperation partners).

The **structure of holocentric chromosomes** was analysed in mitotic cells of *Luzula elegans*. Our studies challenged the notion of a 'diffuse' centromere organisation along holocentric chromosomes. Instead, our observations provided evidence for a longitudinal CENH3-postive, centromere-like groove along each sister chromatid. We have first evidence that a holocentric centromere organisation exists throughout all stages of meiosis in *L. elegans*. From a cytological point of view, in *Luzula* the sequence of meiotic events seems to be inverted. Apparently, the **first division is equational whereas the second division is reductional** (S. Heckmann, in cooperation with external cooperation partners).

Publications

Peer Reviewed Papers

2010

Banaei Moghaddam, A.M., J. Fuchs, T. Czauderna, A. Houben & M.F. Mette: Intraspecific hybrids of *Arabidopsis thaliana* revealed no gross alterations in endopolyploidy, DNA methylation, histone modifications and transcript levels. Theor. Appl. Genet. 120 (2010) 215-226.

Kaczmarczyk, A., A. Houben, E.R.J. Keller & M.F. Mette: Influence of cryopreservation on the epigenetic state of potato. CryoLetters 31 (2010) 380-391.

Kotseruba, V., K. Pistrick, F.R. Blattner, K. Kumke, O. Weiss, T. Rutten, J. Fuchs, T. Endo, S. Nasuda, A. Ghukasyan & A. Houben: The evolution of the hexaploid grass *Zingeria kochii* (Mez) Tzvel. (2n=12) was accompanied by complex hybridization and uniparental loss of ribosomal DNA. Mol. Phylogenet. Evol. 56 (2010) 146-155.

Lolas, I.B., K. Himanen, J.T. Grønlund, C. Lynggaard, A. Houben, M. Melzer, M. Van Lijsebettens & K.D. Grasser: The transcript elongation factor FACT affects *Arabidopsis* vegetative and reproductive development and genetically interacts with HUB1/2. Plant J. 61 (2010) 686-697.

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Nelissen, H., S. De Groeve, D. Fleury, P. Neyt, L. Bruno, M.B. Bitonti, F. Vandenbussche, D. Van Der Straeten, T. Yamaguchi, H. Tsukaya, E. Witters, G. De Jaeger, A. Houben & M. Van Lijsebettens: Plant elongator regulates auxin-related genes during RNA polymerase II transcription elongation. Proc. Natl. Acad. Sci. U.S.A. 107 (2010) 1678-1683.

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2011

Arefian, E., J. Kiani, M. Soleimani, S.A. Shariati, S.H. Aghaee-Bakhtiari, A. Atashi, Y. Gheisari, N. Ahmadbeigi, A.M. Banaei-Moghaddam, M. Naderi, N. Namvarasl, L. Good & O.R. Faridani: Analysis of microRNA signatures using size-coded ligation-mediated PCR. Nucleic Acids Res. 39 (2011) e80.

Banaei Moghaddam, A.M., F. Roudier, M. Seifert, C. Berard, M.L. Magniette, R. Karimi Ashtiyani, A. Houben, V. Colot & M.F. Mette: Additive inheritance of histone modifications in *Arabidopsis thaliana* intra-specific hybrids. Plant J. 67 (2011) 691-700.

Bandopadhyay, R., S. Rustgi, R.K. Chaudhuri, P. Khurana, J.P. Khurana, A.K. Tyagi, H.S. Balyan, A. Houben & P.K. Gupta: Use of methylation filtration and C(0)t fractionation for analysis of genome composition and comparative genomics in bread wheat. J. Genet. Genomics 38 (2011) 315-325.

Heckmann, S., I. Lermontova, B. Berckmans, L. De Veylder, H. Bäumlein & I. Schubert: The E2F transcription factor family regulates *CENH3* expression in *Arabidopsis thaliana*. Plant J. 68 (2011) 646-656.

Heckmann, S., E. Schroeder-Reiter, K. Kumke, L. Ma, K. Nagaki, M. Murata, G. Wanner & A. Houben: Holocentric chromosomes of *Luzula elegans* are characterized by a longitudinal centromere groove, chromosome bending, and a terminal nucleolus organizer region. Cytogenet. Genome Res. 134 (2011) 220-8.

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Okada, T., K. Ito, S.D. Johnson, K. Oelkers, G. Suzuki, A. Houben, Y. Mukai & A.M. Koltunow: Chromosomes carrying meiotic avoidance loci in three apomictic eudicot *Hieracium* subgenus *Pilosella* species share structural features with two monocot apomicts. Plant Physiol. 157 (2011) 1327-1341.

Pedersen, D.S., F. Coppens, L. Ma, M. Antosch, B. Marktl, T. Merkle, G.T. Beemster, A. Houben & K.D. Grasser: The plant-specific family of DNA-binding proteins containing three HMG-box domains interacts with mitotic and meiotic chromosomes. New Phytol. 192 (2011) 577-589.

Sanei, M., R. Pickering, K. Kumke, S. Nasuda & A. Houben: Loss of centromeric histone H3 (CENH3) from centromeres precedes uniparental chromosome elimination in interspecific barley hybrids. (This article has been selected and evaluated by Jiming Jiang, a Member of the Faculty of 1000 (F1000), which places this work in that library of the top 2 % of published articles in biology and medicine). Proc. Natl. Acad. Sci. U.S.A. 108 (2011) E498-E505.

Schubert, V., A. Meister, H. Tsujimoto, T.R. Endo & A. Houben: Similar rye A and B chromosome organization in meristematic and differentiated interphase nuclei. Chromosome Res. 19 (2011) 645-655.

Teo, C.H., L. Ma, E. Kapusi, G. Hensel, J. Kumlehn, I. Schubert, A. Houben & M.F. Mette: Induction of telomere-mediated chromosomal truncation and stability of truncated chromosomes in *Arabidopsis thaliana*. Plant J. 68 (2011) 28-39.

van Damme, D., B. de Rybel, G. Gudesblat, D. Demidov, W. Grunewald, T. de Smet, A. Houben, T. Beeckman & E. Russinova: *Arabidopsis* α Aurora kinases function in formative cell division plane orientation. Plant Cell 23 (2011) 4013-4024.

PhD and Diploma Theses

2010

Agueci, F.: Characterization of NIMA-like kinases in *Arabidopsis thaliana*. (PhD Thesis) Martin-Luther-Universität Halle-Wittenberg, Naturwissenschaftliche Fakultät III, Halle/S. (2010) 129 pp.

Banaei Moghaddam, A.M.: Dynamics of chromatin modifications and other nuclear features in response to intraspecific hybridization in *Arabidopsis thaliana*. (PhD Thesis) Martin-Luther-Universität Halle-Wittenberg, Naturwissenschaftliche Fakultät I, Halle/S. (2010) 143 pp.

Houben, A.: Funktion und Evolution pflanzlicher B-Chromosomen. (Habilitation) Martin-Luther-Universität Halle-Wittenberg, Halle/S. (2010) 57 pp.

2011

Sanei, M.: Analysis of uniparental chromosome elimination in wide crosses. (PhD Thesis) Martin-Luther-Universität Halle-Wittenberg, Halle/S. (2011) 134 pp.

Additional Publications 2009

Karimi Ashtiyani, R.: AtHaspin, a putative histone H3-specific kinase in *Arabidopsis thaliana*? (PhD Thesis) Martin-Luther-Universität Halle-Wittenberg, Naturwissenschaftliche Fakultät I, Halle/S. (2009) 113 pp.

Research Group: Apomixis

Head: Dr. Timothy F. Sharbel

Scientists

IPK financed
Corral García, José María, Dr. (Pakt für Forschung und Innovation, till 28.02.2010; 0.75 / 1.00, 01.03.2010-31.12.2011)
Mau, Martin (0.50)

Grant Positions
Aliyu, Olawale Mashood, Dr. (DFG, since 01.04.2010)
Otto, Lars-Gernot, Dr. (0.50 BMBF, 15.02.-14.08.2011)
Pellino, Marco (0.50 DFG, since 11.01.2010)
Puente Molins, Marta, Dr. (DFG, till 14.04.2011; 0.50 Overhead, 15.04.-14.06.2011)

Visiting Scientists/Scholars
Amiteye, Samuel (International Max Planck Research School grant)
Dobes, Christoph, Dr. (FWF, 01.08.-08.08.2010)
Eradasappa, E. (Fellowship World Bank, since 14.10.2011)
Galla,Giulio(self-financed,08.03.-12.04.2010and05.08.-26.08.2011)
Geetha, K. A. (Fellowship World Bank, 02.05.-31.07.2011)
Hojsgaard, Diego, Dr. (FWF, 17.10.-23.10.2010; 23.03.-31.05.2011)
Jordon-Thadeus, Ingrid (DFG, 28.02.-06.03.2010)
Koperdakova, Jana (EU COST Action, 01.09.-19.09.2011)
Lovell, John Thomsen (DFG Fellowship, 25.09.-05.12.2011)
Majeský, Lúbos (University of Olomouc, 12.09.-12.12.2011)
Morillas, Javier (University of Granada, 21.02.-18.04.2011)
Otto, Lars-Gernot, Dr. (self-financed, till 31.07.2010; 1.08.2010-14.02.2011; since 15.08.2011)
Piwczynski, Marcin (Nicolaus Copernicus University, Poland, 30.08.-27.09.2010)
Puente Molins, Marta, Dr. (self-financed, since 15.06.2011)
Rois, Ana Sofia (Instituto Superior de Agronomia, 24.01.-04.02.2011)
Scheffknecht, Susanne (FWF, 01.08.-14.08.2010)
Scheriau, Charlotte (DFG, 28.02.-06.03.2010)
Thiel, Thomas (International Max Planck Research School grant)
Valverde, Francisco (University of Granada, 21.02.-18.04.2011)
Weber, Anna (EU COST Action, 14.08.-10.09.2011)

Goals

Genomic and transcriptomic analyses to identify candidate apomixis factors in wild monocot and dicot species.

Research Report

***Hypericum perforatum*:** We have chosen 650 accessions, representing different ploidies and worldwide geographic origins, for which data from 30 microsatellite markers have been analysed. A flow cytometric analysis of 96 seeds per each accession demonstrates genotype-specific quantitative variation for sexual and apomictic seed production. These data demonstrate (1) that *H. perforatum* colonised North America from three distinct European genetic lineages over the last 160 years, and (2) that invasiveness of this species has been characterised by an increased frequency of apomictic seed production in North America. We have **sequenced the complete flower transcriptomes (normalised cDNA) of two sexual and two apomictic accessions using 454 FLX technology** (at the IPK). These data are being mined for SNPs to test hypotheses of sexual and asexual genome evolution (G. Galla).

The *Boechera holboellii* complex: Using our high-throughput seed screening method, **we have analysed over 24,000 single seeds in 76 *Boechera* accessions, and have shown genotype-specific quantitative variation for apomeiosis, parthenogenesis and pseudogamy**. Besides the production of unreduced egg cells (apomeiosis), apomictic *Boechera* also produce high frequencies of unreduced pollen for balanced endosperm formation. Custom-made high-density microarrays were built using sequences generated from flower-specific normalised cDNA libraries which were sequenced using 454 technology, and our analyses have enabled us to design targeted experiments which have led to the identification of **a single gene each underlying unreduced egg (J. Corral) and pollen (M. Mau) formation.**

Our continuing work on the candidate apomeiosis gene has led to the identification of a **single apomixis-specific allele** shared by all apomicts, regardless of different genetic, ploidy or geographic backgrounds. Verification of this apomixis-specific allele has been performed using many hundreds of qRT-PCR analyses, which demonstrate that **the apomixis allele is exclusively expressed in apomictic ovules**.

We have designed a **3 x 750,000 feature custom (NimbleGen) comparative genome hybridisation (CGH) microarray** based upon the sequenced cDNA libraries, and have completed a copy number variation (CNV) experiment on 10 different genotypes each of sexual and apomictic *Boechera* genotypes. The data demonstrate (1) that **apomictic and sexual genomes are characterised by significant numbers of duplications and deletions respectively**, and (2) that **retroelements have accumulated in a clock-like pattern in apomictic genomes**, as would be expected by evolutionary theory (O. Aliyu, M. Seifert). We have furthermore cloned, sequenced and validated both **known and novel miRNAs from sexual and apomictic *Boechera***, and are presently examining their effect on differential gene regulation in microdissected ovules (see Fig. 28, p. 70; S. Amiteye).

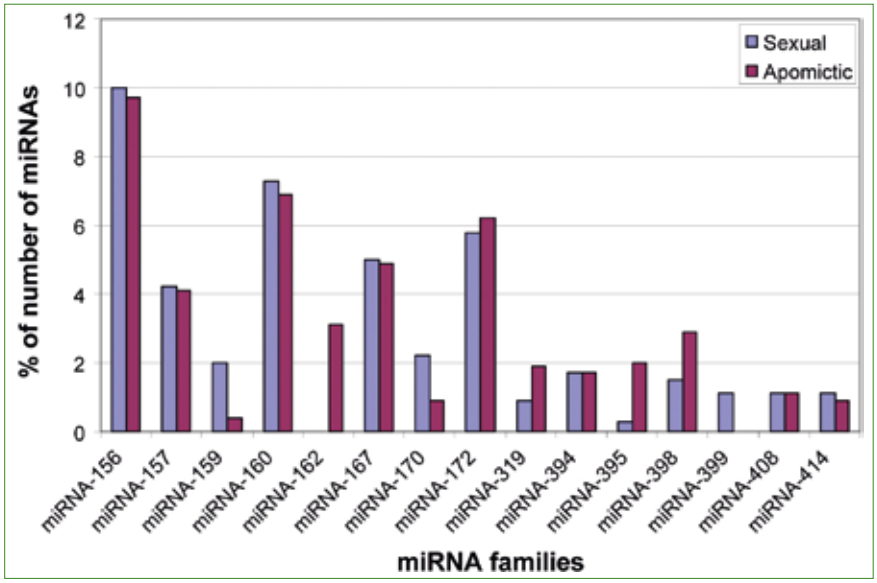

Fig. 28
Abundance (based on total number of transcripts) of previously-identified plant-miRNA families in sexual and apomictic *Boechera* (S. Amiteye).

The *Ranunculus auricomus* complex: Using Illumina technology, we have **sequenced the complete transcriptomes of two apomictic and three sexual *Ranunculus* genotypes**, and are using this data to design a **3 x 1.4 million feature custom (NimbleGen) expression microarray**. Live ovules from 4 developmental stages and 5 accessions each of sexual and apomictic *Ranunculus* have been microdissected for a comparative transcriptome profiling experiment. **Over 100,000 high quality SNPs have been mined from the sequence data**, and these are being analysed in order to test Muller's Ratchet, the hypothesised mutation accumulation that should occur in asexual genomes (M. Pellino, T. Schmutzer).

Publications

Peer Reviewed Papers

2010

Aliyu, O.M., M.E. Schranz & T.F. Sharbel: Quantitative variation for apomixis components in the genus *Boechera*. Am. J. Bot. 97 (2010) 1719-1731.

Ambrosi, D., G. Galla, M. Purelli, T. Barbi, A. Fabbri, S. Lucretti, T.F. Sharbel & G. Barcaccia: DNA Markers and FCSS analyses shed light on the genetic diversity and reproductive strategy of *Jatropha curcas* L. Diversity 2 (2010) 810-836.

Sharbel, T.F., M.L. Voigt, J.M. Corral, G. Galla, J. Kumlehn, C. Klukas, F. Schreiber, H. Vogel & B. Rotter: Apomictic and sexual ovules of *Boechera* display heterochronic global gene expression patterns (Hofmann, N.R.: Apomixis and gene expression in *Boechera*. Plant Cell 22 (2010) 539. Highlight of Sharbel et al. 2010 by Plant Cell scientific editor). Plant Cell 22 (2010) 655-671.

2011

Amiteye, S., J.M. Corral & T.F. Sharbel: Overview of the potential of microRNAs and their target gene detection for cassava (*Manihot esculenta*) improvement. Afr. J. Biotechnol. 10 (2011) 2562-2573.

Amiteye, S., J.M. Corral, H. Vogel & T.F. Sharbel: Analysis of conserved microRNAs in floral tissues of sexual and apomictic *Boechera* species. BMC Genomics 12 (2011) 500.

Bringezu, T.G.G., T.F. Sharbel & W.E. Weber: Grain development and endoreduplication in maize and the impact of heat stress. Euphytica 182 (2011) 363-376.

Corral, J.M., M.P. Molins, O.M. Aliyu & T.F. Sharbel: Isolation and characterization of microsatellite loci from apomictic *Hypericum perforatum* (Hypericaceae). Am. J. Bot. 98 (2011) e167-e169.

Galla, G., G. Barcaccia, A. Schallau, M. Puente Molins, H. Bäumlein & T.F. Sharbel: The cytohistological basis of apospory in *Hypericum perforatum* L. Sex. Plant Reprod. 24 (2011) 47-61.

Galla, G., S. Zenoi, G. Marconi, G. Marino, A. Botton, F. Pinosa, S. Citterio, S. Collani, B. Ruperti, K. Palme, E. Albertini, M. Pezzotti, H. de Jong, M. Mau, T.F. Sharbel, N. de Sorme, D. Geelen & G. Barcaccia: Sporophytic and gametophytic functions of the cell cycle-associated Mob1 gene in *Arabidopsis thaliana* L. Gene 484 (2011) 1-12.

Muñoz-Pajares, A.J., M.B. Herrador, M. Abdelaziz, F.X. Picó, T.F. Sharbel, J.M. Gómez & F. Perfectti: Characterization of microsatellite loci in *Erysimum mediohispanicum* (Brassicaceae) and cross-amplification in related species. Am. J. Bot. 98 (2011) e287-289.

Paule, J., T.F. Sharbel & C. Dobes: Apomictic and sexual lineages of the *Potentilla argentea* L. group (Rosaceae): Cytotype and molecular genetic differentiation. Taxon 60 (2011) 721-732.

Pellino, M., T.F. Sharbel, M. Mau, S. Amiteye & J.M. Corral: Selection of reference genes for quantitative real-time PCR expression studies of microdissected reproductive tissues in apomictic and sexual *Boechera*. BMC Res. Notes 4 (2011) 303.

Books and Book Chapters

2010

Albertini, E., G. Barcaccia, A. Mazzucato, T.F. Sharbel & M. Falcinelli: Apomixis in the era of biotechnology. In: Pua, E.-C. & M.R. Davey (Eds.): Plant Developmental Biology - Biotechnological Perspectives, Vol. 1, Springer, Berlin-Heidelberg (2010) 405-436.

Research Group: Genome Plasticity

Head: Dr. Renate Schmidt

Scientists

IPK financed
Le, Loan Thanh (0.50, since 05.01.2011)

Grant Positions
Boudichevskaia, Anastassia, Dr. (BMBF, till 30.09.2011; Saxony-Anhalt, 01.10.-31.10.2011; 0.50 Overhead, 01.11.-31.12.2011)
Cao, Hieu Xuan, Dr. (BMBF, since 28.06.2010)
Koppolu, Jahnavi (0.50 Saxony-Anhalt, since 01.05.2010)
Voigtländer, Susan (0.50 Saxony-Anhalt, till 31.08.2010)

Visiting Scientists/Scholars
Le, Phuong Dung (MOET/DAAD, since 24.09.2011)

Goals

Study and exploitation of naturally occurring genetic variation in Brassicaceae.

Research Report

Genetic analysis of seed and yield traits in *Arabidopsis thaliana*. We used digital image analysis to evaluate reciprocal recombinant inbred lines (RILs) with respect to seed length, width and area. Other traits related to seed yield were also assessed, such as 100-seed weight, seed weight per plant, silique length and number of seeds per silique. Transgression beyond the parental values was observed for all traits. Quantitative trait locus (QTL) mapping revealed genomic regions of importance for all characters of interest (A. Boudichevskaia, J. Koppolu, S. Voigtländer, in collaboration with T. Altmann, research group Heterosis) (Fig. 29). The same traits are also evaluated in a broad set of *Arabidopsis thaliana* natural accessions to serve as a basis for association analyses (J. Koppolu).
In order to find the genes underlying the seed traits, whole-genome expression profiles of seeds at one particular time point during seed development were established for >100 recombinant inbred lines. We are currently analysing which genes show expression QTL (eQTL) and whether some of these eQTL may colocalise with the QTL that were identified for the seed traits (A. Boudichevskaia).

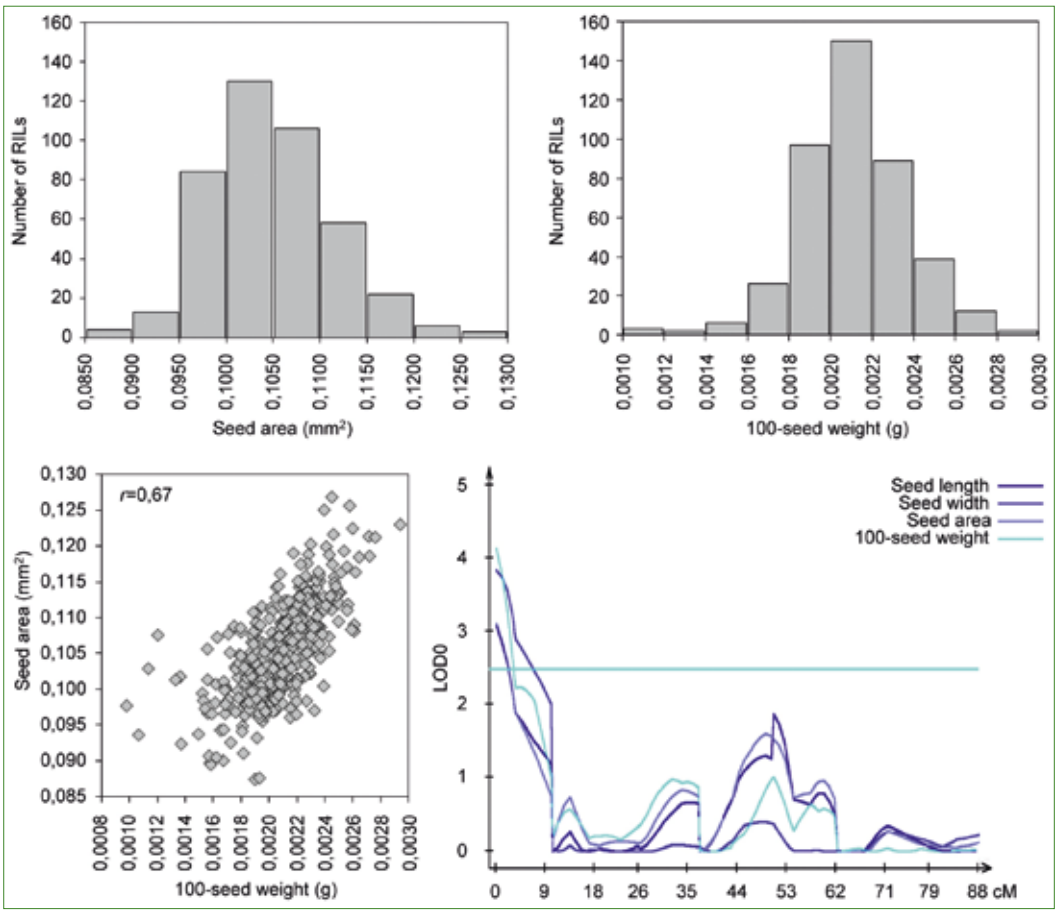

Fig. 29
The upper panel shows seed area and seed weight variation in reciprocal populations of recombinant inbred lines. The lower panel on the left presents correlations between seed area and seed weight in the different RILs. At the right the LOD scores for several seed traits are plotted along *Arabidopsis thaliana* chromosome 1 to reveal QTL (A. Boudichevskaia and J. Koppolu).

Natural variation of genes involved in post-transcriptional gene silencing (PTGS). The study of mutants with impaired PTGS led to the discovery of many genes that play important roles in this process. However, little is known about the genetic variability of these loci. To address this point we have selected genetically diverse *Arabidopsis thaliana* accessions and we are analysing genes involved in PTGS with respect to sequence variation. Alleles for functional tests are selected based on the results of the comparative sequence analysis.

Molecular genetic analysis of transgene expression in the *A. thaliana* accession Columbia-0 revealed that PTGS is triggered if the transcript level surpasses a gene-specific threshold. Importantly, the onset and/or the spread of silencing can be reliably monitored in populations of transgenic lines carrying multiple copies of a *GFP* transgene under the control of the CaMV 35S promoter. In order to study the functional relevance of selected sequence variants we are introgressing the alleles to be tested into the Columbia-0 lines carrying *GFP* transgenes. The onset and spread of silencing of the *GFP* genes will then be assessed in the different introgression lines and compared to the pattern observed in the Columbia-0 genetic background (L.T. Le, D.P. Le).

PCR-based screening platform for an oilseed rape BAC library. A *Brassica napus* BAC library consisting of more than 80,000 clones was used for this work. The 216 microtitre plates that contain all BAC clones of the library were conceptually arranged in a cube consisting of 36 layers, 48 columns, and 48 rows. The clones were pooled according to their position in the cube along the six distinct coordinate axes to yield a total of 276 clone pools. Using this scheme, each of the clones is represented only once in each of the six dimensions. Screening of the six-dimensional clone pools for a particular locus usually does not allow for the unambiguous deconvolution of all clone coordinates that may harbour this locus because the BAC library encompasses between 8 and 10 genome equivalents. In order to improve the deconvolution of the BAC coordinates, additional sets of clone pools were generated.

After confirming that the multidimensional screening platform was suitable for PCR-based screening it was evaluated whether screening in multiplex format is also feasible. Single nucleotide polymorphisms (SNPs) can be used in highly multiplexed fashion therefore gene-specific SNP assays were designed and used for the screening of all BAC clone pools with an Illumina Veracode® system. The results of the screening revealed that the multidimensional screening platform can be used successfully for multiplex PCR assays. The design of gene-specific SNP assays for the allopolyploid *Brassica napus* genome is hampered by high sequence identities between homoeologous genes. However, the high frequency of SNPs between homoeologous oilseed rape genes ("intergenomic SNPs") may represent an interesting alternative source for a BAC screening platform of this species. We are therefore particularly interested to study now whether intergenomic SNPs are suitable for identification and differentiation of homoeologous genes (H.X. Cao).

Publications

Books and Book Chapters

2011

Schmidt, R. & I. Bancroft: Perspectives on genetics and genomics of the Brassicaceae. In: Schmidt, R. & I. Bancroft (Eds.): Genetics and Genomics of the Brassicaceae. Plant Genetics and Genomics: Crops and Models, Vol. 9, Springer, New York-Dordrecht-Heidelberg-London (2011) 617-632.

Schmidt, R. & I. Bancroft (Eds.): Genetics and Genomics of the Brassicaceae. Plant Genetics and Genomics: Crops and Models, Vol. 9, Springer, New York-Dordrecht-Heidelberg-London (2011) 677 pp.

Town, C., R. Schmidt & I. Bancroft: Comparative genome analysis at the sequence level in the Brassicaceae. In: Schmidt, R. & I. Bancroft (Eds.): Genetics and Genomics of the Brassicaceae. Plant Genetics and Genomics: Crops and Models, Vol. 9, Springer, New York-Dordrecht-Heidelberg-London (2011) 171-194.

Research Group: Epigenetics

Head: Dr. Michael Florian Mette

Scientists

IPK financed
Finke, Andreas (0.50)
Teo, Chee How, Dr. (Pakt für Forschung und Innovation)

Grant Positions
Borisova-Todorova, Branimira, Dr. (0.50 Saxony-Anhalt, till 31.08.2010)
Bruchmüller, Astrid (0.50 Overhead, till 31.03.2010)
Jovtchev, Gabriele, Dr. (0.50 Saxony-Anhalt, 04.05.-31.08.2010)
Kuhlmann, Markus, Dr. (DFG / SFB 648)

Visiting Scientists/Scholars
Bruchmüller, Astrid (self-financed, 01.04.-30.09.2010)
Jachimoviciute, Simona (self-financed/IPK, 06.06.-18.06.2011)
Plochotnikova, Alexandra (self-financed / IPK, 06.06.-18.06.2011)

Goals

Analysis and utilisation of epigenetic control mechanisms acting at the chromatin level to warrant regulation and structural maintenance of plant genomes.

Research Report

In plants, short interfering (si) RNAs can act as a nucleotide sequence-specific signal for the induction of cytosine methylation in genomic DNA. If this **RNA-directed DNA methylation** (RdDM) is targeted to homologous promotor regions, it can result in **RNA-directed transcriptional gene silencing** (RdTGS).

The genetic dissection of RdTGS in *Arabidopsis thaliana* by several groups has identified a considerable number of factors required for this process. The majority of these proteins are involved in siRNA generation and metabolism, DNA methylation or chromatin remodeling. To identify the complete spectrum of factors essential for RdTGS, a screen for EMS-induced mutations showing a "suppressor of silencing" phenotype was performed using a transgene system with particularly efficient transcriptional silencing. Mutant lines with a stable release of reporter gene expression and reduced cytosine methylation in non-CG context indicative for a defect in RdDM were crossed to accession *L-er* to initiate rough mapping of the affected genes. Subsequent fine mapping and complementation tests have so far localised mutations in three genes known to be involved in RdDM, proving the functionality of the approach. The mapping of new mutations is ongoing (IPK funded, A. Finke, M. F. Mette).

Beside DNA methylation, histone modifications play a central role in the regulation of gene activity in plants. To check the role of histone methylation in RdDM in *A. thaliana*, DNA methylation and transcript formation at *AtSN1*, an endogenous target of RdDM, were tested in plants carrying mutations in two SET-domain histone methyltransferase genes. Indeed, DNA methylation was reduced and transcript accumulation enhanced, demonstrating an important cross-talk between histone marks and RdDM (DFG SFB 648, M. Kuhlmann, M.F. Mette).

In a collaborative approach to harness **minichromosomes as shuttles for recombinant gene expression** in cereals, chromosome truncation via transgene-induced telomer seeding has been established. For this, T-DNA constructs containing blocks of *A. thaliana* telomeric repeats were assembled and transferred into the genomes of *A. thaliana* and barley via *Agrobacterium*-mediated transformation. In both plant species, formation of transgene-associated telomeres correlated with the truncation of chromosomes was readily observed. The truncated chromosomes were somatically stable and seed-transmissible, although at a lower rate than to be expected from Mendelian segregation (Pakt für Forschung und Innovation, C.H. Teo, M. F. Mette, in collaboration with Karyotype Evolution, Chromosome Structure and Function and Plant Reproductive Biology, Dept. of Physiology and Cell Biology).

The way how chromosomes are arranged in interphase nuclei is considered to affect DNA replication, transcription, and repair. Thus, the **architecture of interphase nuclei** in *A. thaliana* has been approached by fluorescence *in situ* hybridisation (FISH) or chromatin tagging using lacI-GFP fusion proteins and transgenic *lacO* tandem repeats. However, FISH can be performed only on fixed material and presence of transgenic *lacO* tandem repeats potentially alters the chromosome arrangement in interphase nuclei (G. Jovtchev, B.E. Borisova, M. Kuhlmann, J. Fuchs, K. Watanabe, I. Schubert and M.F. Mette 2011). As alternative, transcription activator–like effector (TALE)-based engineered DNA binding proteins are being tested for their ability to target endogenous sequences in live plant nuclei. Initial results (see Fig. 30, p. 74) indicate successful targeting of 45S rDNA by GFP-fusion proteins specifically binding to a conserved sequence in region coding for 5.8S rRNA. The approach will be extended to further repetitive sequences (DFG proposal submitted, C.H. Teo, M. F. Mette, in collaboration with research group Chromosome Structure and Function and J. Boch, MLU Halle-Wittenberg).

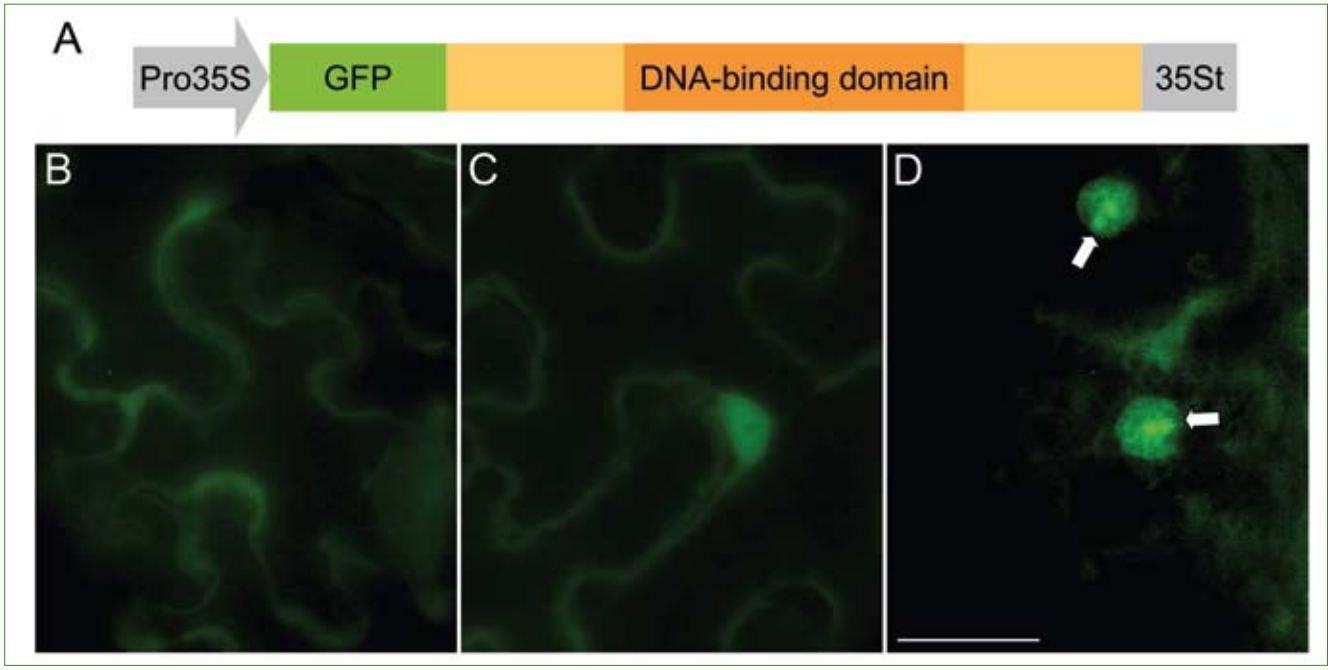

Fig. 30
Targeting of endogenous repetitive sequences by TALE-derived DNA-binding domain-GFP fusion proteins. A) Sketch of T-DNA cassette for protein expression. B - D) Microscopic GFP-fluorescence *in vivo* images of lower epidermal cells of *Agrobacterium*-infiltrated spots in *Nicotiana benthamiana* leaves. B) *Agrobacterium* without T-DNA construct. C) T-DNA construct without specific TALE-derived DNA-binding domain. D) T-DNA construct with TALE-derived DNA-binding domain targeting the 5.8S rDNA of *N. benthamiana*. Arrows indicate GFP-labeled nucleoli. The scale bar indicates 10 µm (C.H. Teo).

Publications

Peer Reviewed Papers

2010

Banaei Moghaddam, A.M., J. Fuchs, T. Czauderna, A. Houben & M.F. Mette: Intraspecific hybrids of *Arabidopsis thaliana* revealed no gross alterations in endopolyploidy, DNA methylation, histone modifications and transcript levels. Theor. Appl. Genet. 120 (2010) 215-226.

Kaczmarczyk, A., A. Houben, E.R.J. Keller & M.F. Mette: Influence of cryopreservation on the epigenetic state of potato. CryoLetters 31 (2010) 380-391.

2011

Banaei Moghaddam, A.M., F. Roudier, M. Seifert, C. Berard, M.L. Magniette, R. Karimi Ashtiyani, A. Houben, V. Colot & M.F. Mette: Additive inheritance of histone modifications in *Arabidopsis thaliana* intra-specific hybrids. Plant J. 67 (2011) 691-700.

Jovtchev, G., B.E. Borisova, M. Kuhlmann, J. Fuchs, K. Watanabe, I. Schubert & M.F. Mette: Pairing of *lacO* tandem repeats in *Arabidopsis thaliana* nuclei requires the presence of hypermethylated, large arrays at two chromosomal positions, but does not depend on H3-lysine-9-dimethylation. Chromosoma 120 (2011) 609-619.

Teo, C.H., L. Ma, E. Kapusi, G. Hensel, J. Kumlehn, I. Schubert, A. Houben & M.F. Mette: Induction of telomere-mediated chromosomal truncation and stability of truncated chromosomes in *Arabidopsis thaliana*. Plant J. 68 (2011) 28-39.

PhD and Diploma Theses

2010

Banaei Moghaddam, A.M.: Dynamics of chromatin modifications and other nuclear features in response to intraspecific hybridization in *Arabidopsis thaliana*. (PhD Thesis) Martin-Luther-Universität Halle-Wittenberg, Naturwissenschaftliche Fakultät I, Halle/S. (2010) 143 pp.

Research Group: *In vitro* Differentiation (till 31 December 2010)

Head: Prof. Anna M. Wobus

Scientists

Grant Positions
Sulzbacher, Sabine, Dr. (BMBF, till 31.12.2010)

Visiting Scientists/Scholars
Schroeder, Insa, Dr. (Martin Luther University Halle-Wittenberg, till 31.12.2010)
Daniel-Wojcik, Anna (self-financed, 01.03.-31.08.2010)
Sharif Panah, Elham, Dr. (self-financed, 22.02.-25.02.2010)

Goals

Research of the "*In vitro* Differentiation" group was dedicated to the analysis of regulatory mechanisms during *in vitro* differentiation of mouse embryonic stem (ES) cells into the endoderm and pancreatic as well as cardiogenic lineages. In parallel, dedifferentiation and reprogramming strategies have been applied to human cord blood-derived cells to enhance their developmental potential.

Research Report

The following results have been achieved during the reporting period (2010-2011):

Endoderm differentiation, selection and characterisation of Sox17-expressing ES cells:
The pancreatic differentiation potential of ES cells was investigated by transcriptional profiling and cell biological analysis. Specifically, Sox17-DsRed-puro^r expressing ES cells were differentiated with and without activin A induction. The number of Sox17-DsRed-positive cells was measured by flow cytometry (FACS), which allowed the determination of the transcriptional profile and the developmental potential of Sox17+ cells. Differentiating ES cells revealed the capacity to develop into mesendoderm (Brachyury+)-, definitive endoderm (Cxcr4+, Foxa2+, Sox17+)-, primitive gut (Hnf4+)- and posterior foregut (Pdx1+)-positive cells. The pancreatic precursor cells had the potential to develop into the three pancreatic lineages of ductal (CK19+), exocrine (Hes1+) and endocrine (Nkx6.1+, Nkx2.2+, Ngn3+) cells. In contrast, activin A induction decreased the differentiation into ectoderm (Pax6+, NeuroD6+) and primitive endoderm (Sdf1+, Sox7+, Afp+) cells (Schroeder et al., CTO in press; collaboration with I. Schroeder, MLU Halle, M. Solimena, R. Meisterfeld, TU Dresden). The experiments are ongoing at the University of Halle.

Dedifferentiation and reprogramming of cord blood (CB)-derived cells: Dedifferentiation and epigenetic modification (i.e. by TSA, 5-azaC) of CB-derived CD14+ cells showed only limited efficiency of reprogramming to pluripotency. Repeated (4 times) transfections of adult mouse and human cells with viral vectors expressing the three pluripotency-associated transcription factors (Oct4, Sox2, Klf4) were necessary to partially reprogram CB-derived mesenchymal stem cells (MSCs) into an ES-like state and to up-regulate transcript levels of pluripotency markers (dissertation by A. Daniel-Wojcik; collaboration with A. Finkensieper, M. Wartenberg). The work has been continued by using further reprogramming strategies at the University of Halle.

Cardiac differentiation of ES cells and selective induction of pacemaker cells: Based on previous studies of the "*In vitro*-Differentiation" group (Wiese et al. 2011) showing the selective differentiation of sinus node-like cells by Suramin, the collaboration with Dr. Alexander Kleger and Dr. Stefan Liebau at the University of Ulm resulted in the identification of a new mechanism for the generation of cardiac and pacemaker-like cells by the activation of Ca^{2+}-activated potassium channels (Kleger et al. 2010; Liebau et al., in press).

Comparative analysis of human ES cell research in Germany and worldwide:
Working as guest scientist in the Department of Cytogenetics in 2011, studies of A.M. Wobus on human (h) ES cell research resulted in reviews on the present state and future perspectives of pluripotent stem cells in toxicology (Wobus and Löser 2011) and on the performance of hES cell research in Germany in international comparison (Löser et al. 2011; Löser et al. 2011; Wobus and Löser, in press; collaboration with Dr. P. Löser, RKI Berlin).

Publications

Peer Reviewed Papers

2010

Kleger, A., T. Seufferlein, D. Malan, M. Tischendorf, A. Storch, A. Wolheim, S. Latz, S. Protze, M. Porzner, C. Proepper, C. Brunner, S.F. Katz, G. Varma Pusapati, L. Bullinger, W.M. Franz, R. Koehntop, K. Giehl, A. Spyrantis, O. Wittekindt, Q. Lin, M. Zenke, B.K. Fleischmann, M. Wartenberg, A.M. Wobus, T.M. Boeckers & S. Liebau: Modulation of calcium-activated potassium channels induces cardiogenesis of pluripotent stem cells and enrichment of pacemaker-like cells. Circulation 122 (2010) 1823-1836.

Löser, P., J. Schirm, A. Guhr, A.M. Wobus & A. Kurtz: Human embryonic stem cell lines and their use in International Research. Stem Cells 28 (2010) 240-246.

Rolletschek, A., I.S. Schroeder, H. Schulz, O. Hummel, N. Huebner & A.M. Wobus: Characterization of mouse embryonic stem cell differentiation into the pancreatic lineage *in vitro* by transcriptional profiling, quantitative RT-PCR and immunocytochemistry. Int. J. Dev. Biol. 54 (2010) 41-54.

Seufert, G., G. Päth, P. Feilen, C. Krautz, I. Schröder, A.M. Wobus, E. Lammert & M. Solimena: Mechanismen und Methoden der Regeneration und des Ersatzes von Insulin produzierenden Beta-Zellen des endokrinen Pankreas bei *Diabetes mellitus*. Med. Welt 61 (2010) 87-93.

Wobus, A.M.: The Janus face of pluripotent stem cells: Connection between pluripotency and tumourigenicity. Bioessays 32 (2010) 993-1002.

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Wiese, C., T. Nikolova, I. Zahanich, S. Sulzbacher, J. Fuchs, S. Yamanaka, E. Graf, U. Ravens, K.R. Boheler & A.M. Wobus: Differentiation induction of mouse embryonic stem cells into sinus node-like cells by suramin. Int. J. Cardiol. 147 (2011) 95-111.

Wobus, A.M. & P. Löser: Present state and future perspectives of using pluripotent stem cells in toxicology research. Arch. Toxicol. 85 (2011) 79-117.

Books and Book Chapters

2010

Wobus, A.M., U. Wobus & B. Parthier (Eds.): Der Begriff der Natur – Wandlungen unseres Naturverständnisses und seine Folgen. Gaterslebener Begegnung 2009. Nova Acta Leopoldina, Bd. 109, Heft 376, Wissenschaftliche Verlagsgesellschaft, Stuttgart (2010) 266 pp.

Wobus, A.M. & U. Wobus: Gaterslebener Begegnung 2009. Der Begriff der Natur – Wandlungen unseres Naturverständnisses und seine Folgen. In: Jahrbuch 2009 der Deutschen Akademie der Naturforscher Leopoldina Halle/S. LEOPOLDINA (R. 3), 55 (2010) 419-420.

Other Papers

2011

Löser, P., B. Hanke & A.M. Wobus: Humane pluripotente Stammzellen – Perspektiven ihrer Nutzung und die Forschungssituation in Deutschland. Naturwiss. Rundschau 64 (2011) 453-465.

PhD and Diploma Theses

2011

Daniel-Wojcik, A.: Differentiation, dedifferentiation and reprogramming experiments using embryonic stem and cord blood-derived cells. (PhD Thesis) Martin-Luther-Universität Halle-Wittenberg, Naturwissenschaftliche Fakultät I, Institut für Biologie, Halle/S. (2011) 153 pp.

Additional Publication 2009

Beier, H.M., B. Fehse, B. Friedrich, M. Götz, I. Hansmann, F. Hucho, K. Köchy, B. Müller-Röber, H.-J. Rheinberger, J. Reich, H.-H. Ropers, H.R. Schöler, B. Schöne-Seifert, K. Sperling, K. Tanner, J. Taupitz & A.M. Wobus (Eds.): Neue Wege in der Stammzellforschung - Reprogrammierung von differenzierten Körperzellen. Berlin-Brandenburgische Akademie der Wissenschaften, Berlin (2009) 28 pp.

PROGRAMME: GENOME ANALYSIS
Research Group: Transcriptome Analysis

Head: Dr. Patrick Schweizer

Scientists

IPK financed
Himmelbach, Axel, Dr. (Pakt für Forschung und Innovation, 01.05.2010-31.10.2011)
Liu, Luo (0.50, 01.07.-31.12.2010)

Grant Positions
Chen, Wanxin, Dr. (BMBF, till 31.03.2010; 0.50 Overhead, 01.04.-30.04.2010; BMBF, since 01.05.2010)
Douchkov, Dimitar, Dr. (BMBF, till 30.04.2011; 0.75 Overhead, 01.05.-30.06.2011; BMBF, since 01.07.2011)
Hasan, Mainul (0.50 BMBF, since 01.11.2011)
Himmelbach, Axel, Dr. (0.75 BMBF, till 30.04.2010)
Nowara, Daniela, Dr. (Industry, since 15.04.2010)
Rajaraman, Jeyaraman (0.50 DFG)
Stengel, Doreen (0.50 BMBF, till 30.04.2010)

Visiting Scientists/Scholars
Baum, Tobias (BMBF, 09.03.-30.06.2011)
Ihlow, Alexander, Dr. (TH Ilmenau, till 30.11.2011)
Liu, Luo (self-financed, till 30.06.2010)
Marzin, Stephan (self-financed, till 31.01.2010)
Metzner, Ernst (self-financed, till 31.07.2010)
Pliego Prieto, Clara, Dr. (self-financed, 20.09.-20.10.2010)
Siegwart, Gerald (self-financed, 20.09.-16.10.2010)

Goals

Gene regulation and -function in pathogen-attacked and drought-stressed cereals.

Research Report

Phenomics and genes in pathogen-attacked barley:
According to current models, both nonhost- as well as race-nonspecific host resistance are manifestations of pathogen-associated molecular pattern (PAMP)-triggered plant immunity and should be analysed in an integrative approach. Therefore, the projects **detailed functional analysis and application potential of barley genes for nonhost resistance** and **identifying barley genes for race-nonspecific host resistance or -susceptibility** are closely interconnected within the group, partly sharing the same candidate genes.

Genes for nonhost resistance: The genes of interest were derived from a TIGS (Transient Induced Gene Silencing) screening in barley epidermal cells attacked by the wheat powdery mildew (Bgt). Out of 10 identified *RNR* (*Required for Nonhost Resistance*) genes we examined three, ***RNR5*** encoding a partial duplicate of an **U-box ARM-repeat E3 ligase**, ***RNR6*** encoding a **cellulose synthase-like protein** of the D clade (*CSLD2*) and ***RNR8*** encoding an **LRR-containing receptor-like kinase** (RLK) in greater detail. For RNR5 encoding the "sticky" protein-protein interaction ARM domain of the ancient U-box E3 ligase, we have identified 6 strongly interacting plant proteins in a yeast 2-hybrid screening using a prey library from barley powdery mildew (Bgh)-attacked barley leaves, in collaboration with TU München. These 6 potential *in vivo* interactors are now analysed with respect to transcript regulation, TIGS phenotype, and *in vivo* interaction with RNR5 by split YFP assay. Transgenic T1 populations of events exhibiting strong *RNR5* silencing were identified and will be characterised for Bgh and Bgt resistance. New transcripts with a clear differential regulation between host- and nonhost responses in barley and wheat are being identified in a large-scale transcript profiling approach using 44K Agilent arrays of barley and wheat hybridised with RNA samples from inoculated, peeled epidermis in order to obtain a comprehensive picture of nonhost-related regulation events in Triticeae cereals (J. Rajaraman). For RNR6, evidence for an important role in race-nonspecific host as well as nonhost resistance has been obtained using transgenic RNAi lines. The transgenic super-susceptible phenotype of these lines could be rescued by transient expression of a synthetic *RNR6* gene, which is immune to RNAi due to silent point mutations, a few hours prior to Bgt inoculation. Obviously, the *HvCSLD2* gene is involved in a dynamic local response to pathogen challenge representing a novel mechanism independent of lignification (see Fig. 31, p. 78). Although the enzymatic activity of the encoded CSL protein is still unknown, ongoing cell-wall analysis in collaboration with Adelaide University indicates a role in cellulose cristallinity and cell-wall thickness (D. Douchkov). For RNR8, the phenomenon of transgenomic complementation in wheat of nonhost-like resistance against Bgt could be confirmed using 55 additional receptor-like kinases of barley that are associated with upregulated transcripts in Bgh-attacked leaves. Approximately 13 additional RLKs were identified that induced resistance in wheat to Bgt. These are now subcloned for further analyses (A. Himmelbach).

Genes for race-nonspecific (basal) host resistance: In order to identify genes that mediate race-nonspecific resistance of barley to Bgh we combined a functional-genomics approach based on transcript profiling and automated TIGS (~1,400 genes up-regulated by pathogen attack, belonging to defence-related multigene families or mapping to a QTL confidence interval) with association-genetic (re-sequencing) and meta-QTL mapping approaches. This guided us to a shortlist of approximately 40 candidates with evidence for an important role in race-nonspecific resistance of barley. Candidates of special interest encode proteins involved in cell-death regulation such as HvLsd1a or HvWRKY2 and in cell-wall re-shaping such as the germin-like protein HvGER4 or cellulose-synthase like proteins D2 and H1. Some of these candidates will be validated by stable transgenics as well as allele introgression by backcrossing (D. Douchkov, A. Johrde, A. Himmelbach).

Host-induced gene silencing (HIGS):
The novel phenomenon of HIGS in fungal pathogens was further examined in barley and wheat attacked by powdery mildew and *Fusarium* head blight (FHB) fungi. In the barley/Bgh HIGS system main emphasis lies on the identification of double-transgenic lines carrying RNAi constructs against both glucanosyltransferase GFT1 and GFT2 genes of the fungus. This should address the question of functional redundancy of the two proteins and optimise HIGS efficiency for plant protection (see Fig. 25, p. 61). In the barley and wheat/FHB systems we are characterising single and triple transgenic events targeting either highly conserved fungal housekeeping genes or excellent virulence-related candidates. New functional HIGS targets in FHB were identified in a transient-assay system of adult wheat plants recently established in the lab that is based on virus-induced gene silencing by the barley-stripe mosaic virus (D. Nowara, W. Chen).

Phenomics of drought tolerance:
The aim of this project is to identify new candidate genes for osmotic stress (drought) tolerance in barley using a recently developed, high-throughput transient-induced gene silencing assay (TIGS_drought). In this assay, stress tolerance is reflected by the number of cells accumulating native dsRed reporter protein during a stress period of four days. In a collaboration with the lab of Luigi Cattivelli (CRA Fiorenzuola d'Arda, Italy) we addressed the role of a RING-type E3 ubiquitin ligase and its *in vitro* as well as *in vivo* interaction partners in desiccation tolerance of barley. As a result, TIGS of the E3 ligase enhanced desiccation sensitivity of transformed leaf epidermal cells whereas transient over-expression rendered the cells more robust against the stress, compared to the empty-vector controls (S. Marzin).

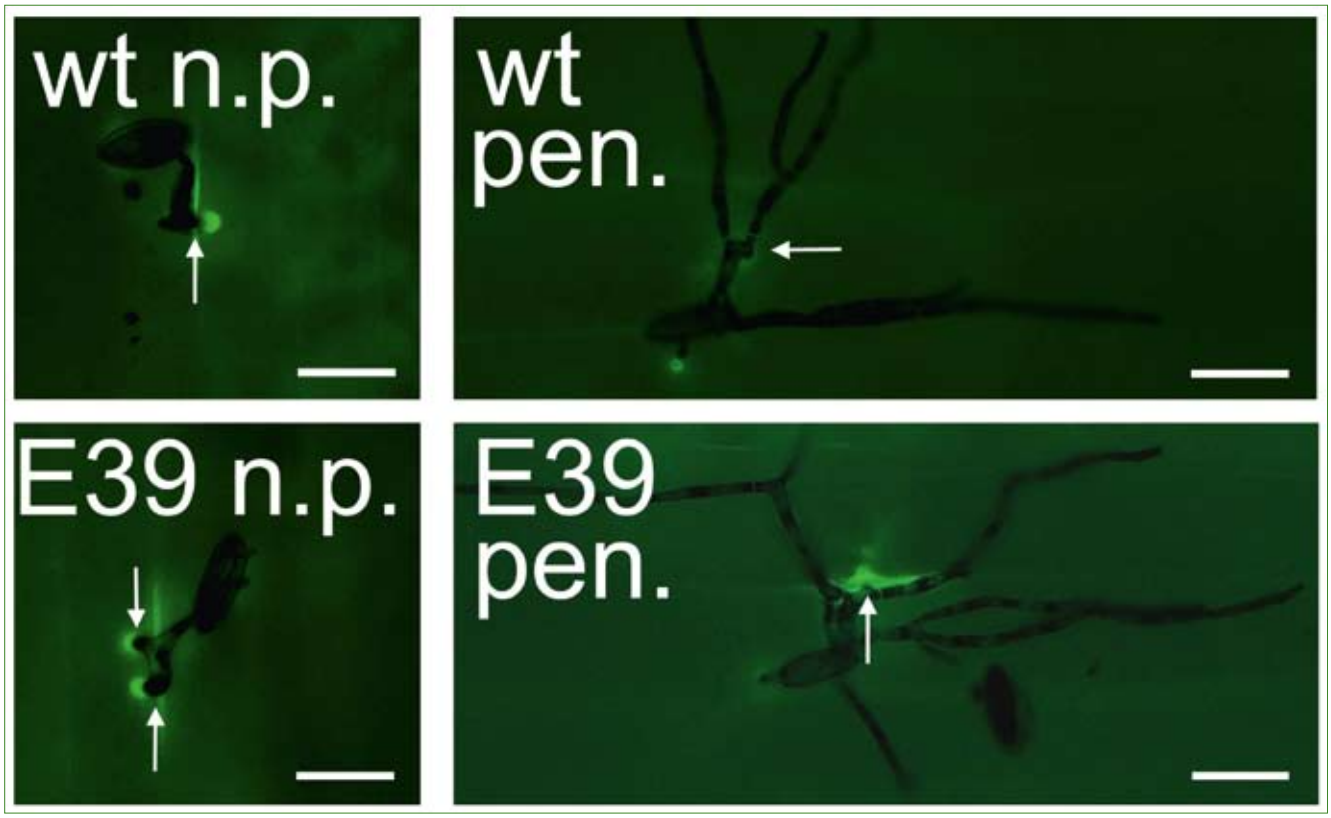

Fig. 31
A high proportion of penetrated papillae of *HvCSLD2*-silenced barley plants are strongly autofluorescing. Examples of non-penetrated (n.p.) and penetrated (pen.) papillae of wildtype (wt) and transgenic plants (line E39), 48 h after inoculation with *Blumeria graminis* f. sp. *tritici* (Bgt). Arrows point at sites of attempted penetration (D. Douchkov). Bar = 25 µm.

Publications

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Aghnoum, R., T.C. Marcel, A. Johrde, N. Pecchioni, P. Schweizer & R.E. Niks: Basal host resistance of barley to powdery mildew: connecting quantitative trait loci and candidate genes. Mol. Plant Microbe Interact. 23 (2010) 91-102.

Eichmann, R., M. Bischof, C. Weis, J. Shaw, C. Lacomme, P. Schweizer, D. Douchkov, G. Hensel, J. Kumlehn & R. Hückelhoven: BAX INHIBITOR-1 is required for full susceptibility of barley to powdery mildew. Mol. Plant Microbe Interact. 23 (2010) 1217-1227.

Himmelbach, A., L. Liu, U. Zierold, L. Altschmied, H. Maucher, F. Beier, D. Müller, G. Hensel, A. Heise, A. Schützendübel, J. Kumlehn & P. Schweizer: Promoters of the barley germin-Like *GER4* gene cluster enable strong transgene expression in response to pathogen attack. Plant Cell 22 (2010) 937-952.

Kocsy, G., B. Athmer, D. Perovic, A. Himmelbach, A. Szücs, I. Vashegyi, P. Schweizer, G. Galiba & N. Stein: Regulation of gene expression by chromosome 5A during cold hardening in wheat. Mol. Genet. Genomics 283 (2010) 351-363.

Nowara, D., A. Gay, C. Lacomme, J. Shaw, C. Ridout, D. Douchkov, G. Hensel, J. Kumlehn & P. Schweizer: HIGS: host-induced gene silencing in the obligate biotrophic fungal pathogen *Blumeria graminis*. Plant Cell 22 (2010) 3130-3141.

Sečenji, M., Á. Lendvai, P. Miskolczi, G. Kocsy, Á. Gallé, A. Szucs, B. Hoffmann, É. Sárvári, P. Schweizer, N. Stein, D. Dudits & J. Györgyey: Differences in root functions during long-term drought adaptation: comparison of active gene sets of two wheat genotypes. Plant Biol. 12 (2010) 871-882.

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Baum, T., A. Navarro-Quezada, W. Knogge, D. Douchkov, P. Schweizer & U. Seiffert: HyphArea – Automated analysis of spatiotemporal fungal patterns. J. Plant Physiol. 168 (2011) 72-78.

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Hückelhoven, R. & P. Schweizer: Quantitative disease resistance and fungal pathogenicity in *Triticeae*. J. Plant Physiol. 168 (2011) 1-2.

Schweizer, P. & N. Stein: Large-scale data integration reveals co-localization of gene functional groups with meta-QTL for multiple disease resistance in barley. Mol. Plant Microbe Interact. 24 (2011) 1492-1501.

Other Papers

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PhD and Diploma Theses

2010

Johrde, A.: Assoziationsstudie zur Resistenz gegen den echten Gerstenmehltau (*Blumeria graminis* f.sp. *hordei)* in einer genetisch diversen Gerstenpopulation (*Hordeum vulgare* L.). (PhD Thesis) Martin-Luther-Universität Halle-Wittenberg, Naturwissenschaftliche Fakultät III, Halle/S. (2010) 165 pp.

Marzin, S.: Entwicklung einer RNAi basierten Screeningmethode zur Charakterisierung der Trockenstressantwort bei Gerste (*Hordeum vulgare* L.). (PhD Thesis) Martin-Luther-Universität Halle-Wittenberg, Naturwissenschaftliche Fakultät I, Halle/S. (2010) 150 pp.

Research Group: Gene and Genome Mapping

Head: Dr. Marion Röder

Scientists

IPK financed
Hanemann, Anja, Dr. (0.75 Pakt für Forschung und Innovation, till 12.06.2010; 0.25/1.00, till 31.12.2010)
Kollers, Sonja, Dr. (0.75, 01.07.-30.09.2011)
Marzin, Stephan, Dr. (0.50/0.75 Pakt für Forschung und Innovation, 01.02.-31.12.2010; 0.25/1.00, 01.05.2010-14.02.2011)
Paliwal, Rajneesh (0.50 Pakt für Forschung und Innovation, 01.07.-31.12.2010)
Sharma, Shailendra, Dr. (Pakt für Forschung und Innovation, till 31.03.2010)
Weichert, Nicola, Dr. (Pakt für Forschung und Innovation, 01.01.-31.12.2010)
Worch, Sebastian, Dr. (Pakt für Forschung und Innovation, 01.10.-31.12.2010)

Grant Positions
Kollers, Sonja, Dr. (BMBF, till 30.06.2011; 0.25 Overhead, 01.07.-30.09.2011)
Marzin, Stephan, Dr. (DFG, since 15.02.2011)
Matthies, Inge, Dr. (BMBF, till 28.02.2011)
Worch, Sebastian, Dr. (BMBF, till 30.09.2010)

Visiting Scientists/Scholars
Absattarova, Aiman (IAOE Fellowship, 11.01.-19.03.2010)
Castellanos, Thelma, Dr. (BMBF, 28.07.-29.09.2010)
Diaz de Leon Alvarez, José Luis, Dr. (BMBF, 28.07.-29.09.2010 and 04.09.-04.10.2011)
Ilyas, Mehmoona (Research Fellowship of Higher Education Commission, since 18.08.2011)
Kifetew Haile, Jemanesh (DAAD)
Kumar, Uttam, Dr. (BMBF, since 01.06.2011)
Leonova, Irina, Dr. (DFG, 10.10.-09.12.2010)
Mora, Merit (BMBF, 03.08.-29.09.2010)
Paliwal, Rajneesh (DAAD Fellowship, till 30.06.2010)
Salina, Elena, Dr. (BMELV, 04.10.-23.10.2010)

Goals

Exploitation of the natural genetic diversity in plants for identification, genetic mapping and cloning of genes for agronomically important traits in cereals.

Research Report

A **map-based cloning effort for the barley scald resistance gene *Rrs2*** has resulted in a family of expressed pectin esterase inhibitor genes (*PEI1-PEI4*) as possible candidates (S. Sharma). A virus-induced gene silencing (VIGS)-based assay was developed and improved to achieve functional screening of candidate genes in *Rhynchosporium*-infected barley plants. First results indicate that silencing of the *PEI2* target gene in barley stripe mosaic virus (BSMV)-mediated transient transformation assays increased susceptibility and hence facilitated fungal growth (see Fig. 32, p. 81) (S. Marzin).
Additionally, stably transformed plants were generated in collaboration with the research group Plant Reproductive Biology (J. Kumlehn, G. Hensel), in which the *PEI2* gene is over-expressed in the background of the susceptible cultivar 'Golden Promise'.

The **fine mapping of a QTL for grain size** on wheat chromosome 7D was continued in collaboration with J. Doležel and H. Simkova (Institute of Experimental Botany, Olomouc, Czech Republic). A number of 7D-specific wheat BACs from the QTL containing region were obtained and 454-sequenced in collaboration with the research group Genome Diversity (N. Stein, A. Himmelbach). The BAC sequences were annotated and used for further marker enrichment in the region of interest (N. Weichert, M. Röder).

The **potential use of historic data** was tested in a genome-wide association study of European barley cultivars using diversity arrays technology (DArT) markers. In collaboration with F. v. Eeuwijk and M. Malosetti (Biometris, University Wageningen, The Netherlands) a model based on best linear unbiased estimations (BLUEs) was applied for association analysis of an unbalanced phenotypic dataset based on historic data for malting and kernel quality with varying varieties over years (I. Matthies).

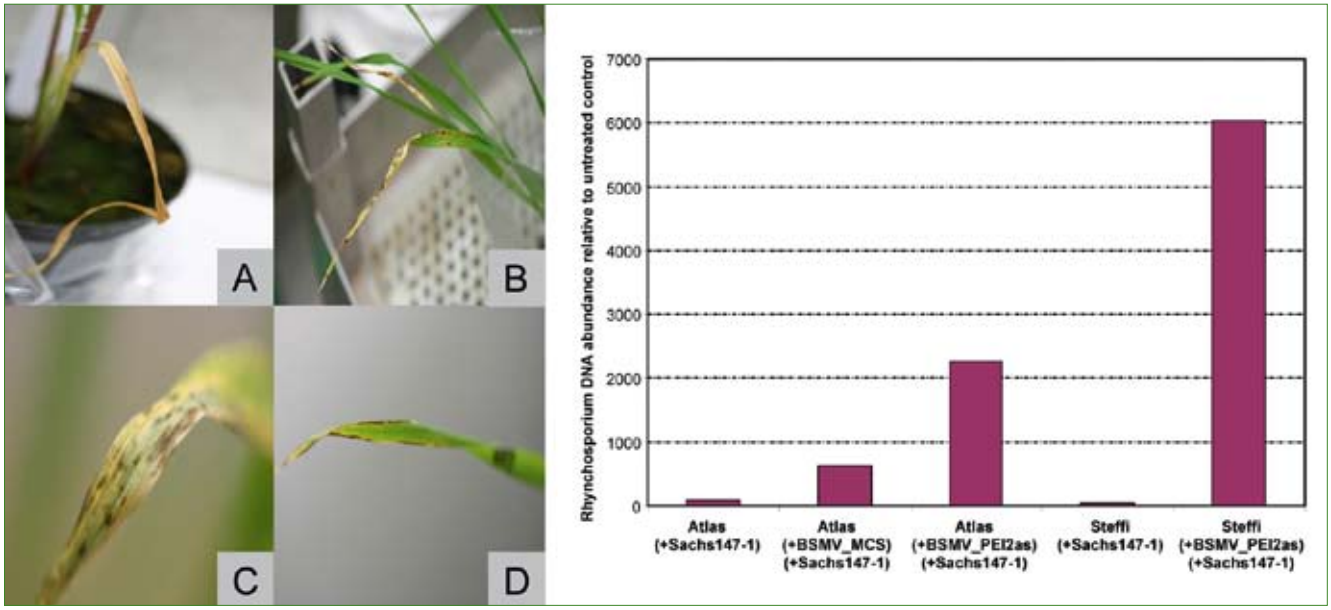

Fig. 32
Rhynchosporium infection on barley seedlings and preliminary results of qRT-PCR analysis.
Left: Pictures A-D show typical symptoms of *Rhynchosporium* infection on the susceptible cv. Steffi (A, C) plants and the resistant cv. Atlas (B, D), 17 days after inoculation with isolate Sachs147-1. Right: DNA-abundance of *Rhynchosporium*-DNA in infected plants 13 days after inoculation determined by qRT-PCR. BSMV-mediated transient transformation was used for silencing of the candidate gene *PEI2* and caused an increase of fungal DNA in comparison to the untreated control in both cultivars, indicating the importance of *PEI2* as a scald resistance gene. (Sachs147-1 = *Rhynchosporium* isolate; BSMV = Barley stripe mosaic virus; MCS = empty multiple cloning site; *PEI2* = Pectinesterase inhibitor gene 2) (S. Marzin).

A comprehensive set of phenotypic and genotypic data was generated for **358 European winter wheat varieties. Genome-wide association analysis** was performed for agronomic and baking quality traits, as well as for resistance to the fungal pathogens *Fusarium culmorum* and *Fusarium graminearum, Septoria tritici* and *Drechslera tritici-repentis* in collaboration with B. Rodemann (Julius Kühn Institute, Braunschweig) (S. Kollers).

The **impact of drought stress on the regulatory networks of barley seed development** was investigated in an introgression line population in collaboration with N. Sreenivasulu (research group Stress Genomics). Morphological and biochemical QTL for kernel traits were discovered and the expressions of candidate genes were monitored using a quantitative Real Time PCR approach (S. Worch).

The mapping of quantitative resistance against the **stem rust pathovar UG99** was performed in a *Triticum durum* wheat population and markers linked to stem rust resistance were applied on a set of *T. durum* cultivars and landraces (J.K. Haile)

Publications

Peer Reviewed Papers

2010

Achtar, S., M.Y. Moualla, A. Kalhout, M.S. Röder & N. Mirali: Assessment of genetic diversity among Syrian durum (*Triticum turgidum* ssp. *durum*) and bread wheat (*Triticum aestivum* L.) using SSR markers. Russ. J. Genet. 46 (2010) 1320-1326.

Castillo, A., H. Budak, C. Martín, G. Dorado, A. Börner, M. Röder & P. Hernandez: Interspecies and intergenus transferability of barley and wheat D-genome microsatellite markers. Ann. Appl. Biol. 156 (2010) 347-356.

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De León, J.L.D., R. Escoppinichi, R. Zavala-Fonseca, T. Castellanos, M.S. Röder & A. Mujeeb-Kazi: Phenotypic and genotypic characterization of salt-tolerant wheat genotypes. Cereal Res. Commun. 38 (2010) 15-22.

Garcia-Suarez, J.V., J.L.D. De León & M.S. Röder: Identification of QTLs and associated molecular markers related to starch degradation in wheat seedlings (*Triticum aestivum* L.) under saline stress. Cereal Res. Commun. 38 (2010) 163-174.

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Kerfal, S., P. Giraldo, M. Rodríguez-Quijano, J.F. Vázquez, K. Adams, O.M. Lukow, M.S. Röder, D.J. Somers & J.M. Carrillo: Mapping quantitative trait loci (QTLs) associated with dough quality in a soft × hard bread wheat progeny. J. Cereal Sci. 52 (2010) 46-52.

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Khlestkina, E.K., M.S. Röder & A. Börner: Mapping genes controlling anthocyanin pigmentation on the glume and pericarp in tetraploid wheat (*Triticum durum* L.). Euphytica 171 (2010) 65-69.

Khlestkina, E.K., M.S. Röder, T.A. Pshenichnikova & A. Börner: Functional diversity at the *Rc* (red coleoptile) gene in bread wheat. Mol. Breed. 25 (2010) 125-132.

Kumar, U., A.K. Joshi, S. Kumar, R. Chand & M.S. Röder: Quantitative trait loci for resistance to spot blotch caused by *Bipolaris sorokiniana* in wheat (*T. aestivum* L.) lines 'Ning 8201' and 'Chirya 3'. Mol. Breed. 26 (2010) 477-491.

Kumar, U., A.K. Joshi, M. Kumari, R. Paliwal, S. Kumar & M.S. Röder: Identification of QTLs for stay green trait in wheat (*Triticum aestivum* L.) in the 'Chirya 3' × Sonalika' population. Euphytica 174 (2010) 437-445.

Leonova, L.N., E.B. Budashkina, K. Flath, A. Weidner, A. Börner & M. Röder: Microsatellite mapping of a leaf rust resistance gene transferred to common wheat from *Triticum timopheevii*. Cereal Res. Commun. 38 (2010) 211-219.

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Research Group: Bioinformatics and Information Technology

Head: Dr. Uwe Scholz

Scientists

IPK financed
Lange, Matthias, Dr.
Steuernagel, Burkhard (Pakt für Forschung und Innovation, since 01.01.2011)

Grant Positions
Mascher, Martin (0.50/1.00 BMBF, since 01.02.2011)
Schmutzer, Thomas (0.50/1.00 BMBF, since 01.01.2010)
Steuernagel, Burkhard (BMBF, till 31.12.2010)
Weise, Stephan, Dr. (BMBF, till 31.12.2010; Industry, since 01.01.2011)

Visiting Scientists/Scholars
Czernicka, Malgorzata, Dr. (DAAD, 28.02.2010-31.12.2011)
Munoz Amatriain, Maria (University of Minnesota, 06.06.-17.07.2011)
Schlüter, Urte, Dr. (self-financed, 06.06.-10.06.2011)

Goals

Development of information systems, data integration pipelines, life science search engines, and usage/adaptation of bioinformatics tools for sequence analysis/assembly. Moreover, the research group is responsible for the IT infrastructure of the whole institute as well as for the establishment and the operation of a laboratory information management system (LIMS).

Research Report

The rapid progress in high-throughput experiments is directly coupled with a strong growth of primary research data: To overcome the disadvantages of local storage of such data within the research groups (e.g. missing long-term data access, problems in reusability and no citation possibilities fulfilling the German Research Council guidelines "Rules of good scientific practice") the IPK is now a data centre in the international DataCite consortium (http://www.datacite.org). In the frame of this membership, an infrastructure for registering DOI citations was developed. Furthermore, systems like **LIMS-Light** and **eDAL** are supporting the publication pipeline for primary research data (M. Lange, C. Colmsee, F. Flemming, B. Röhl, D. Arend, J. Benz).

With the **LAILAPS** search engine (http://lailaps.ipk-gatersleben.de) we built a system with the aim to find relevant data in non-integrated life science databases. The core of LAILAPS is a probabilistic model for relevance prediction based on neural networks. To consider the fact that data relevance is highly subjective to the user of an information retrieval system, we support specific neural networks. The system is available for IPK databases as well as for external databases such as UniProt or the DAWIS data warehouse developed at Bielefeld University. Currently, an EU-scaled application is implemented in the frame of the EU-FP7 project "**transPLANT**" (M. Lange, J. Chen).

Within the **BARLEX** project we provided the data storage and assembly of 454 sequenced barcoded BAC pools. In total, assemblies for 3,500 BACs have been calculated. Additionally pipelines for whole-genome shotgun sequencing using Illumina platform were developed and implemented. Using these pipelines, those large datasets can now be *de novo* assembled, or mined for SNPs (B. Steuernagel and collaboration with the research group Genome Diversity).

In the frame of the "Pakt für Forschung und Innovation" project "**Sequencing of the Barley Chromosome 3H**" the pipeline for assembling BACs has been applied for further sequencing. More than 2,000 BACs have been assembled. New strategies for sequencing pooled paired-end libraries of BACs have been evaluated and pilot-experiments have been analysed (B. Steuernagel and collaboration with the research groups Genome Diversity and Plant Bioinformatics).

In the RYE-EXPRESS project we assembled over 2.5 million RNA-seq reads into contigs representing a **comprehensive genomics resource for rye**. From sequence comparisons 5,234 single nucleotide polymorphisms (SNPs) were identified to develop the Rye5K high-throughput SNP genotyping array. The process has been integrated into a pipeline for detection of single nucleotide polymorphism (T. Schmutzer and collaboration with the research group Genome Diversity).

Within the **CORNFED** project we designed a yield related NimbleGen Sequence Capture array. Over 4.5 k genes have been selected so far that led to first experimental studies with 454 reads from captured B73 lines. A new strategy and its prototype pipeline has been developed for the workflow to study the diversity in maize lines (T. Schmutzer and collaboration with the research group Heterosis).

In the GENOBAR project we were in charge of the management of primary data. Moreover, we developed the **GENOBAR-WAREHOUSE**, providing information for genome-wide association studies in barley based on phenotypic data as well as molecular markers (SNP, SSR, DArT and Illumina). We continued our work in the frame of this project (until 08/2010) and finished the development of the data warehouse (S. Weise and collaboration with the research groups Genome Diversity, Gene and Genome Mapping).

In close collaboration with the research groups Plant Bioinformatics and Systems Biology we continued to improve the **MetaCrop** information system managing manually curated data about crop plant metabolism. The web-based user interface was reworked and the SBML exporter has been enhanced. Furthermore, MetaCrop data is now indexed by the life science search engine LAILAPS (S. Weise, M. Lange, J. Chen).

In cooperation with the Satellite Collections North of the IPK Genebank we are reengineering the Diversity Studies Toolkit (DiSTo) software. **DiSTo2** provides a convenient Java-Swing-based user interface for studying the genetic diversity of *Lolium* accessions, but is also applicable to other crop species. The software enables researchers to perform comparative as well as multivariate analyses using phenotypic, genotypic and passport data (S. Weise).

The BMBF-funded BioEnergy 2021 project OPTIMAS (since 2009) explores diverse biological processes with the aim of increasing yield and biomass production in maize. We established a database as an extension of the CropHouse system and developed an Oracle Application Express (APEX)-based web interface for data retrieval and presentation. In 2010 we extended our database to allow the storage of data from different data domains. In 2011 we developed an APEX-based web platform, **OPTIMAS-EDP,** which allows to browse and filter all experimental data and additionally to download the data for further analysis. Following a correlation network-based approach we developed a high-throughput analysis pipeline that integrates transcriptome, metabolite and phenotypic data to identify key metabolites and candidate genes for yield and biomass production. In cooperation with the Plant Bioinformatics group, we established methods for comfortably visualising network data, exchanging analysis results as well as incorporating feedback from our experimentalist partners which will facilitate the validation of *in silico* predicted regulators (C. Colmsee, M. Mascher).

In addition, the research group works on the establishment of an IPK-wide laboratory information management system (**LIMS**). The results of a study performed by the research group led to the decision to establish the commercial system **LIMSOPHY**. Currently, use cases are implemented for several research groups (M. Lange, D. Schüler).

Publications

Peer Reviewed Papers

2010

Breuillin, F., J. Schramm, M. Hajirezaei, A. Ahkami, P. Favre, U. Druege, B. Hause, M. Bucher, T. Kretzschmar, E. Bossolini, C. Kuhlemeier, E. Martinoia, P. Franken, U. Scholz & D. Reinhardt: Phosphate systemically inhibits development of arbuscular mycorrhiza in *Petunia hybrida* and represses genes involved in mycorrhizal functioning. Plant J. 64 (2010) 1002-1017.

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Hippe, K., C. Colmsee, T. Czauderna, E. Grafahrend-Belau, B.H. Junker, C. Klukas, U. Scholz, F. Schreiber & S. Weise: Novel developments of the MetaCrop information system for facilitating systems biological approaches. J. Integr. Bioinform. 7 (2010) e125.

Lange, M., K. Spies, J. Bargsten, G. Haberhauer, M. Klapperstück, M. Leps, C. Weinel, R. Wunschiers, M. Weissbach, J. Stein & U. Scholz: The LAILAPS search engine: relevance ranking in life science databases. J. Integr. Bioinform. 7 (2010) 110.

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PhD and Diploma Theses

2011

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Friedrich, C.: Entwurf und Implementierung einer JAVA-API zum Zugriff und zur DBMS-unabhängigen Persistierung von Bild- und Metadaten aus einer Pflanzenphänotypisierungsanlage. (Diploma Thesis) Hochschule Harz, Fachbereich Automatisierung und Informatik, Wernigerode (2011) 147 pp.

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Abteilung Molekulare Genetik/
Department of Molecular Genetics

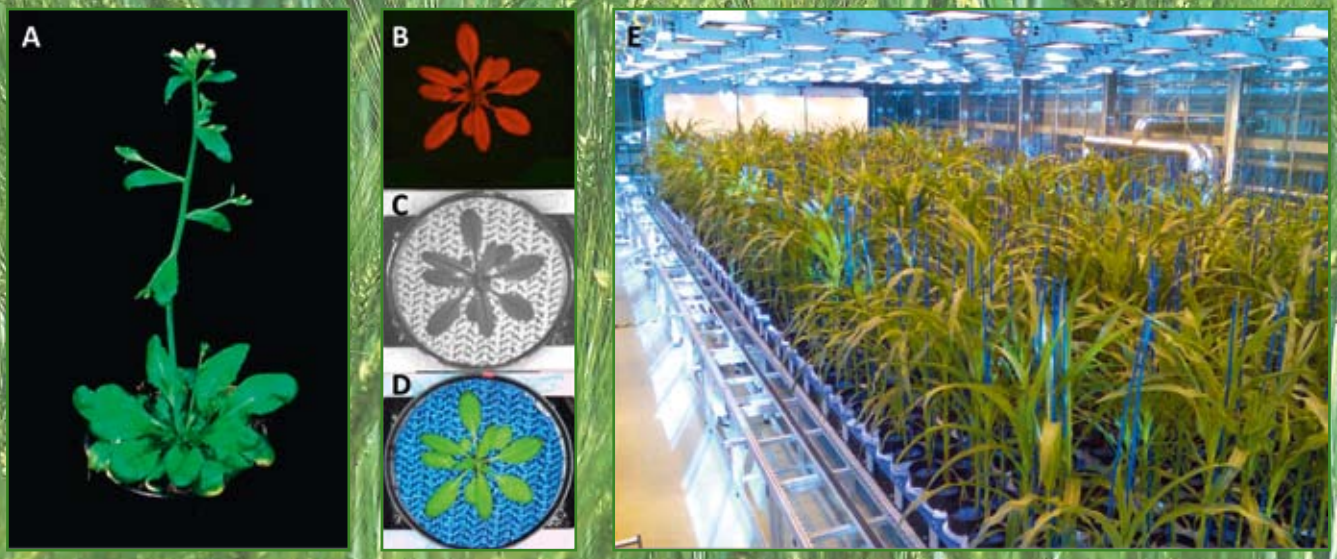

Abb. 33
Erfassung sichtbarer Merkmale in automatisierten Phänotypisierungseinrichtungen bei Arabidopsis (A-D) und Mais (E). (A) *Arabidopsis thaliana*-Pflanze in früher generativer Entwicklungsphase (Blühstadium). (B-D) *Arabidopsis thaliana*-Pflanze in vegetativer Entwicklungsphase (Rosettenstadium); (B) Fluoreszenzbild (Anregung 400-500 nm, Emission: 520-750 nm; hauptsächlich Erfassung der roten Chlorophyllfluoreszenz), (C) Nahinfrarotbild (1450-1550 nm; hauptsächlich Erfassung des Wassergehaltes als dunkle Signale), (D) Farbbild im sichtbaren Bereich (390-750 nm). (E) Population genetisch diverser Maispflanzen in automatisierter Phänotypisierungsanlage (integriertes Kultivierungs-, Transport- und Aufnahmesystem).

Fig. 33
Monitoring visible plant characteristics of Arabidopsis (A-D) and maize (E) in automated phenotyping systems. (A) *Arabidopsis thaliana* plant in early generative development phase (flowering stage). (B-D) *Arabidopsis thaliana* plant in vegetative development phase (rosette stage); (B) Fluorescence image (Excitation 400-500 nm, Emission: 520-750 nm; mainly detection of red chlorophyll fluorescence), (C) near infrared image (1450-1550 nm; mainly detection of water content as dark signals), (D) color image in the visible range (390-750 nm). (E) Population of genetically diverse maize plants in automated phenotyping installation (integrated cultivation, transport, and imaging system).

Abteilung Molekulare Genetik

Leiter: Prof. Dr. Thomas Altmann

Allgemeine Forschungsziele

Das übergeordnete Thema der Forschungsarbeiten in der Abteilung Molekulare Genetik ist die Analyse und die Modulation der Leistungsfähigkeit von Pflanzen, wobei ertragsbezogene physiologische Prozesse im Kontext bestimmter Entwicklungsprozesse adressiert werden. Die Arbeiten gliedern sich damit überwiegend in den IPK-Forschungsschwerpunkt „Integrative Biologie pflanzlicher Leistungen" ein, wobei Aspekte der Erforschung genetischer Diversität von Pflanzen steigende Berücksichtigung finden. Sowohl vegetatives Wachstum/Biomasseproduktion und Heterosis (gesteigerte Leistung von Kreuzungsnachkommen gegenüber ihren Eltern) als auch generative Prozesse, wie Keimzellbildung, Samenentwicklung und -physiologie und Samenertrag, werden intensiv erforscht. Ein wesentliches Ziel der Arbeiten ist die Aufklärung der Regulation zentraler Entwicklungs- und Stoffwechselprozesse, wobei besonders die Rolle von Transkriptionsfaktoren und Metaboliten, von Phytohormonen und von neuartigen/komplexen Signalen untersucht wird. Das Forschungsprogramm ist geprägt durch die Integration von Arbeiten zur Aufklärung grundlegender biologischer Prozesse und Phänomene, der Entwicklung und Anwendung neuartiger Methoden und Forschungsansätze und der biotechnologischen, anwendungsorientierten Forschung.

Die wesentlichen Forschungsfelder der Abteilung umfassen

- Grundlagenforschung im Bereich der Molekularbiologie und Stoffwechselphysiologie pflanzlicher Entwicklungsprozesse:
  Aufklärung molekularer Kontrollmechanismen der Gametenentwicklung, der frühen Embryogenese und der Apomixis (Identifizierung und Charakterisierung von (transkriptionellen) Regulatoren);
  Analyse genetischer Ursachen und molekularer Mechanismen der Variation von Stoffwechselleistungen unter günstigen und ungünstigen Umweltbedingungen (vegetatives Wachstum und Biomasseakkumulation, Heterosis; Samenentwicklung und Speicherstoffakkumulation);
- biotechnologische, anwendungsorientierte Forschung: „Phyto-F(Ph)arming" (Produktion neuartiger pflanzlicher Inhaltsstoffe für pharmazeutische und industrielle Anwendungen); Entwicklung von Hybridtechnologien (Verfahren zur effizienten Erzeugung von Hybridsaatgut); Ertrag, Ertragsstabilität und Qualität von Samen und deren Inhaltsstoffen;
- Entwicklung und Anwendung bioinformatischer Verfahren:
  Integrative Bioinformatik und Netzwerkanalyse (Datenrepräsentation und –integration, Visualisierung und Exploration, Analyse und Simulation);
  Identifizierung von DNA-Motiven, Analyse von RNA- und Proteinexpressionsdaten;
  Bildanalyse für automatisierte Phänotypisierung;

Department of Molecular Genetics

Head: Prof. Thomas Altmann

Research Goals

The greater topic of the research performed in the Department of Molecular Genetics is the analysis and modulation of plant performance addressing yield-related physiological processes in the context of certain developmental processes. The work is thus predominantly assigned to the IPK research topic "Integrative biology of plant performance" with aspects of investigating plant genetic diversity receiving increasing attention. Both, vegetative growth/biomass production and heterosis (enhanced performance of crossbreds over their parental inbreds) and generative processes such as germ cell formation, seed development and physiology, and seed yield are studied in detail. A major goal of the work is the elucidation of the regulation of central developmental and metabolic processes addressing in particular the roles of transcription factors and metabolites, of phytohormones, and of novel/complex signals. The research programme is characterised by integration of work directed towards the elucidation of basic biological processes and phenomena, the development and application of novel methods and approaches, and biotechnological, application-oriented research.

The major areas of research in the department are:

- Basic research on molecular biology and metabolic physiology of plant developmental processes:
  Elucidation of molecular control mechanisms of gamete development, early embryogenesis, and apomixis (identification and characterisation of (transcriptional) regulators);
  Analysis of genetic causes and molecular mechanisms of metabolic performance variation under optimal and suboptimal environmental conditions (vegetative growth and biomass accumulation, heterosis; seed development and storage compound accumulation);
- Biotechnological, application-oriented research:
  „Phyto-F(Ph)arming" (production of novel products for pharmaceutical or industrial applications in plants);
  Development of hybrid technologies (procedures for efficient production of hybrid seeds);
  Yield, yield stability and quality of seeds and their constituents;
- Development and application of bioinformatic procedures:
  Integrative bioinformatics and network analysis (data representation and integration, visualisation and exploration, analysis and simulation);
  DNA motif identification, RNA and protein expression data analysis; image analysis for automated phenotyping;
  and
- Experimental resource-, technology-, and method development (e.g. microsampling and analysis, NMR-based localisation and quantification of content substances, GC-MS- and LC-MS-based metabolite analytics, microsensorics,

und
– Entwicklung experimenteller Ressourcen, Technologien und Methoden (u.a. Mikroprobennahme und -analyse, NMR-basierte Inhaltsstofflokalisierung und -quantifizierung, GC-MS- und LC-MS-basierte Metabolitanalytik, Mikrosensorik, immunologische Verfahren, Nukleinsäureanalytik und -sequenzierung neuester Generation, automatisierte nicht-invasive Phänotypisierung).

Zentrales Ziel der Forschung ist es, durch integrative und systemorientierte Analysen ein tieferes Verständnis der Kontrolle und Regulation pflanzlicher Wachstums- und Entwicklungsprozesse in Bezug auf vegetative und generative Leistungen von Pflanzen zu erlangen und Grundlagenerkenntnisse in anwendungsorientierte Untersuchungen einzubringen.

Entwicklung im Berichtszeitraum

Im Berichtszeitraum wurden die Arbeitsgruppen „Bildanalyse" (zum 1. Mai 2010; Leiter Dr. C. Klukas) und Stress-Genomik (zum 1. November 2010; Leiter Dr. N. Sreenivasulu) neu eingerichtet. In beiden Fällen handelt es sich um Nachwuchswissenschaftlergruppen. Die Arbeitsgruppe Stress-Genomik ist Teil des Interdisziplinären Zentrums für Nutzpflanzenforschung (IZN) der Martin-Luther-Universität Halle-Wittenberg und kooperierender außeruniversitärer Einrichtungen. Es wechselte die Leitung der Arbeitsgruppe Dateninspektion (seit 1. Februar 2010; Dr. S. Friedel) und es wurde die Arbeitsgruppe „Expressionskartierung" (Leiter Dr. L. Altschmied bis 30. September 2011) aufgelöst und als Infrastruktureinheit Nukleinsäureanalytik in die Arbeitsgruppe „Heterosis" integriert. Innerhalb dieser Arbeitsgruppe werden die Projektbereiche „Natürliche Variation und Heterosis von Pflanzenwachstum und -stoffwechsel" sowie „Lipidstoffwechsel und Ölspeicherung" von Dr. R. Meyer und Prof. Dr. T. Altmann bzw. von Dr. L. Borisjuk geleitet.

Sehr wesentliche Investitionen flossen in den Berichtsjahren in den Aufbau automatisierter Phänotypisierungsanlagen (LemnaTec-Systeme für kleine Pflanzen, z.B. *Arabidopsis*, *Boechera*, und für große Pflanzen, z.B. Mais, Hirse), in denen mehrere hundert bis tausend Pflanzen unter kontrollierten Umweltbedingungen kultiviert werden können und ihre Eigenschaften regelmäßig mittels verschiedener elektronischer Kamerasysteme (für unterschiedliche Spektralbereiche) erfasst werden können. Außerdem wurde eine neue Hochdurchsatz-Sequenziereinrichtung installiert, die es ermöglicht, bis zu 6 Mrd. Sequenzabschnitte von ca. 100 nt Länge pro Gerätelauf zu sequenzieren.

Im Folgenden werden, wie in vergangenen Berichten, einige wesentliche im Berichtszeitraum erzielte Forschungsergebnisse aufgeführt. Sie sind hier nach den oben genannten Forschungsfeldern gegliedert dargestellt. Detaillierte Erläuterungen der Ergebnisse mit Publikationshinweisen finden sich in den einzelnen Berichten der zehn Arbeitsgruppen der Abteilung, die während des Berichtszeitraumes bestanden.

immunological techniques, nucleic acids analytics and next generation sequencing, automated non-invasive phenotyping).

Central goal of the research is to gain a deeper understanding of the control and the regulation of plant growth and development with respect to vegetative and generative performance by using an integrative and systems-oriented approach and to transfer results of basic research into application-oriented investigations.

Developments in 2010 and 2011

In the reporting period, the research groups Image Analysis (since 1 May 2010; head Dr. C. Klukas) and Stress Genomics (since 1 November 2010; head Dr. N. Sreenivasulu) have been newly established. Both are junior research groups, the Stress Genomics group is part of the Interdisciplinary Center of Crop Plant Research (IZN) of the Martin Luther University Halle-Wittenberg and co-operating non-university institutions. The head of the Data Inspection research group changed (since 1 February 2010; head Dr. S. Friedel) and the research group Expression Mapping (head Dr. L. Altschmied till 30 September 2011) has been dissolved and has been integrated as the infrastructure unit Nucleic Acids Analytics into the research group Heterosis. Within this group, the project areas "Natural Variation and Heterosis of Plant Growth and Metabolism" and "Lipid Metabolism and Oil Storage" are headed by Dr. R. Meyer and Prof. T. Altmann as well as Dr. L. Borisjuk, respectively.

During the reporting period, very substantial investments were made into the setup of automated phenotyping installations (LemnaTec systems for small plants, e. g. *Arabidopsis*, *Boechera*, and for large plants such as maize or sorghum), in which several hundred to thousand plants can be cultivated under controlled environmental conditions and their features can be monitored regularly using different digital camera systems (for different spectral ranges). Furthermore, a new high-throughput sequencer has been installed that allows the generation of up to 6 billion sequence reads of approx. 100 nt length per machine run.

In the following, as it has been the case in previous reports, a selection of major results achieved in the reporting period are briefly summarised. They are presented in order of the aforementioned research areas. More detailed documentation of results along with references can be found in the individual reports of the ten research groups of the department, that were active during the reporting period.

Molecular biology and metabolic physiology of plant developmental processes

– Elucidation of genetic and epigenetic mechanisms of gamete development, early embryogenesis, and apomixis: Important advances were made with respect to the identification and characterisation of the apospory locus *HAPPY* (a genomic region conditioning embryo formation from unfertilised cells) in *Hypericum perforatum* (St. John´s

Molekularbiologie und Stoffwechselphysiologie pflanzlicher Entwicklungsprozesse

– Aufklärung genetischer und epigenetischer Mechanismen der Gametenentwicklung, der frühen Embryogenese und der Apomixis:
  Entscheidende Fortschritte gelangen in der Identifizierung und Charakterisierung des Aposporie-Locus *HAPPY* (einer genomischen Region, die Embryobildung aus unbefruchteten Zellen verursacht) von *Hypericum perforatum* (Echtes Johanniskraut). Dabei wurden sowohl sexuelle als auch apospore Allele isoliert und es wurde gezeigt, dass das apospore Allel eine komplexe Zusammensetzung mit mehrfachen z.T. zerstörten Genkopien und inserierten Transposons aufweist. Die weitere Untersuchung von Genen mit Eizell-spezifischer Expression in Weizen und *Arabidopsis* führte zu dem Nachweis, dass Missexpression von Mitgliedern der RKD-Familie pflanzlicher Transkriptionsfaktoren in sporophytischen Zellen zu deren Reprogrammierung und der Annahme von Aspekten der Eizellidentität führt. Mit Hilfe der ChIP-Chip-Methodik und der Transkriptomanalyse wurden Zielgene von zentralen Regulatoren der Genexpression während der Embryogenese (LEC1, ABI3) identifiziert. Diese Daten lieferten Hinweise auf neue Phytohormon-vermittelte Funktionen von LEC1 und auf das durch 98 Gene repräsentierte ABI3-Regulon. Ein weiterer Themenkomplex betrifft die Charakterisierung des pflanzlichen RETINOBLASTOMA-Homologs (RBR), das als Schlüsselkomponente in die Regulation von DNA- und Histon-Methylierung bei der Kontrolle des Zellschicksals von Gameten mitwirkt.
– Analyse genetischer Ursachen und molekularer Mechanismen der Variation von Stoffwechselleistungen unter günstigen und ungünstigen Umweltbedingungen:
  Vegetatives Wachstum und Biomasseakkumulation, Heterosis: Mit Hilfe der Analyse von Rekombinanten Inzuchtlinien (RILs) und Introgressionslinien (ILs) von *Arabidopsis thaliana* sowie deren Testkreuzungsnachkommen gelang die Identifizierung von 10 QTL-Regionen für Biomasse-Heterosis. Mit der Feinkartierung eines dieser QTL und dessen Eingrenzung auf ca. 45 kb gelangen entscheidende Schritte zur Aufklärung der für Heterosis ursächlichen Erbgutvariation und der zur Heterosis-Ausprägung führenden molekularen Mechanismen. Weiterhin wurden Kandidatengene für Metabolit-QTL identifiziert, darunter ein Gen für eine zweite Fumarase in *Arabidopsis thaliana* (FUM2), dessen Allele erhebliche Expressionsunterschiede aufweisen. Wichtige Informationen über die Beziehungen von Enzymaktiviäten, Metabolitgehalten und Wachstum sowie über genomweite DNA-Variation und deren Zusammenhang mit Wachstums- und Stoffwechseleigenschaften wurden durch Untersuchungen der in vielfältigen Wildformen von *Arabidopsis thaliana* (Akzessionen) repräsentierten natürlichen Diversität erlangt. Sehr umfangreiche genetische, phänotypische und molekulare/biochemische Charakterisierung von Maisdiversitätskollektionen lieferten klare Hinweise auf die Vorhersagekraft von genetischen und metabolischen Markern für die Eigenleistung, Hybridleistung und das Ausmaß der Heterosis, wie zuvor bei *Arabidopsis* beobachtet. Diese

wort). This involved the isolation of sexual and asexual alleles and it was shown that the aposporic allele has a complex composition with multiple und in part disrupted gene copies and inserted transposable elements. Further analysis of genes that exhibit egg cell-specific expression in wheat and *Arabidopsis* resulted in the demonstration that misexpression of members of the RKD family of plant transcription factors in sporophytic cells results in their re-programming and their adoption of aspects of egg cell identity. Using the ChIP-Chip method and transcriptome analyses, target genes of central regulators of gene expression during embryogenesis (LEC1, ABI3) were identified. These data gave indications of novel phytohormone-mediated functions of LEC1 and of the ABI3-regulon represented by 98 genes. A further addressed topic concerns the characterisation of the plant RETINOBLASTOMA homolog (RBR) that is involved in gamete cell fate control as a key component in the regulation of DNA and histone methylation.

– Analysis of genetic causes and molecular mechanisms of metabolic performance variation under optimal and suboptimal environmental conditions:
  Vegetative growth and biomass accumulation, heterosis: Through analysis of recombinant inbred lines (RILs) and introgression lines (ILs) of *Arabidopsis thaliana* and their test crosses, the identification of 10 QTL regions for biomass heterosis was achieved. With fine mapping of one of these QTL and its delineation to approx. 45 kb, major steps were made towards elucidation of the genome variation causing heterosis and the molecular mechanisms resulting in heterosis expression. Furthermore, candidate genes of metabolite QTL were identified, including a gene encoding a second fumarase in *Arabidopsis thaliana* (FUM2) the alleles of which exhibit very substantial differences in expression. Important information on the relations of enzyme activities, metabolite contents, and growth as well as genome-wide DNA variation and its connection with growth and metabolism features were achieved by investigation of the natural diversity represented by the various wild isolates of *Arabidopsis* (accessions). Very extensive genetic, phenotypic, and molecular/biochemical characterisation of maize diversity collections resulted in clear indications of the predictive power of genetic and metabolic markers on inbred and hybrid performance and the degree of heterosis as shown before for *Arabidopsis*. These findings point to a strong potential for future applications in maize breeding.
  Seed development and storage compound accumulation: The analysis of barley mutants affected in starch accumulation and in the regulation of the contents of the phytohormone abscisic acid (ABA) gave hints on overlaps of metabolic and hormonal regulation during seed development and filling. Results of comparative analyses using transgenic pea plants confirmed the importance of ABA content and sensitivity variation for the regulation of developmental phase transitions and of storage metabolism in seeds. More in-depth information on signalling cascades and regulatory interactions between different tissues were gained via detailed metabolite and transcript analyses of isolated

Erkenntnisse deuten auf ein wertvolles Potenzial für zukünftige Anwendungen in der Maiszüchtung hin.

Samenentwicklung und Speicherstoffakkumulation: Die Analyse von Gerstenmutanten mit Störungen in der Stärkeakkumulation und in der Regulation des Gehaltes des Phytohormons Abscisinsäure (ABA) lieferten Hinweise auf Überlagerung metabolischer und hormoneller Regulation während der Samenentwicklung und -füllung. Vergleichende Analysen unter Verwendung transgener Erbsenpflanzen bestätigten die Bedeutung der Variation von ABA-Gehalten und -Sensitivität für die Regulation des Übergangs von Entwicklungsphasen und des Speicherstoffwechsels in Samen. Vertiefende Informationen über Signalkaskaden und regulatorische Wechselwirkungen zwischen verschiedenen Geweben wurden durch eingehende Metabolit- und Transkriptuntersuchungen isolierter Gewebeproben aus Samen verschiedener Entwicklungsstadien gewonnen. Als weitere putative Faktoren mit wichtigen Funktionen bei zellulären Abbauprozessen, die im Zusammenwirken zwischen maternalen und filialen Geweben und der Versorgung von Speichergeweben eine wichtige Rolle spielen, wurden neben dem zuvor charakterisierten Cystein-reichen JEKYLL-Protein der Gerste vakuoläre Prozessierungsenzyme (VPEs) in Gerste und kleine Cystein-reiche Proteine in Erbse identifiziert. Schließlich wurde nachgewiesen, dass die in transgenen Weizenpflanzen erzielte gesteigerte Saccharoseaufnahmekapazität zu einer Stimulierung der Speicherproteinsynthese führt und eine Erhöhung des Korngewichtes bewirkt. Mit Hilfe der Analyse einer Population von Gerstenintrogressionslinien, die Wildgerstengenomsegmente enthalten, wurden insgesamt 28 Haupt-QTL für agronomische Leistungsparameter unter terminalen Trockenstressbedingungen identifiziert. Die durch detaillierte Analyse kontrastierender Linien belegte Bedeutung von Abscisinsäure (ABA) für die Ertragsstabilität unter terminalen Trockenstressbedingungen wurde durch eingehende Untersuchungen von ABA-Synthese, -Abbau und -Signalübertragung in verschiedenen Organen vertieft und deutliche Unterschiede in ABA-Homöostase und -Reaktionen zwischen toleranten und sensitiven Linien nachgewiesen. Diese Ergebnisse wurden durch Analysen transgener Pflanzen mit gezielter Veränderung von ABA-Akkumulation und -Sensitivität bestätigt. Mit Hilfe weiterentwickelter (NMR-basierter) bildgebender Verfahren für die dreidimensionale Topologie von Samen und Sameninhaltsstoffen sowie Methoden der Mikroprobennahme und -analytik wurden entscheidende neue Erkenntnisse über die räumlichen und zeitlichen Verläufe von Import, Verteilung und Konversion von Metaboliten und die Akkumulation von Speichersubstanzen in Samen gewonnen. Neuartige Sensoren für O_2 und NO wurden erfolgreich für die Analyse der Konzentrationen dieser Gase in verschiedenen pflanzlichen Geweben eingesetzt.

Biotechnologische, anwendungsorientierte Forschung

– „Phyto-F(Ph)arming“:
  Neben verschiedenen individuellen Spinnenseidenproteinen, die mit Hilfe besonders gestalteter Expressionsvektoren in

tissue samples from seeds of different developmental stages. In addition to the previously characterised cysteine-rich JEKYLL-protein in barley, vacuolar processing enzymes (VPEs) in barley and small cysteine-rich proteins in pea were identified as further putative factors with function in cellular disintegration processes, which play important roles in the interaction between maternal and filial tissues and the nutrient supply to storage tissues. Finally, it was confirmed that enhanced sucrose import capacity specifically achieved in transgenic wheat plants provokes a stimulation of storage protein synthesis and an increase in grain weight.

Analysis of a population of barley introgression lines carrying wild barley genome segments resulted in the identification of a total of 28 major QTL for agronomic performance parameters expressed under terminal drought stress conditions. The importance of ABA for yield stability under these conditions shown by investigations of contrasting lines and deepened through detailed analyses of ABA synthesis, degradation, and signal transduction in different organs and substantial differences in ABA-homeostasis and responses were verified for tolerant vs. sensitive lines. These results were confirmed through investigation of transgenic plants with targeted alterations of ABA accumulation or sensitivity.

Using further developed (NMR-based) imaging techniques for the 3-dimensional topology of seeds and seed contents as well as microsampling and analysis methods, crucial novel insights into spatial and temporal progression of import, allocation, and conversion of metabolites and the accumulation of storage compounds were gained. Novel O_2 and NO sensors were successfully applied to analyse the concentrations of these gases in different plant tissues.

Biotechnological, application-oriented research

– „Phyto-F(Ph)arming“:
  In addition to the production of various individual spider silk proteins in plants using specially designed expression vectors, the development and application of a novel concept for the production of multimeric spider silk proteins in plants was achieved. Isolated and purified multimers were characterised using electron microscopy. Furthermore, different antigens of the avian flue virus (H5N1) partly in form of fusions to ELP (elastin-like polypeptide) were produced in plants. The mITC technology was developed for improved purification of ELPylated proteins and was used to generate hemagglutinin and neuraminidase in increased quality. Produced hemagglutinin trimers and virus-like particles were successfully used for immunisation of mice. Finally novel specific antibodies against tumor necrosis factor alpha could be isolated.
– Development of hybrid technologies:
  As an alternative to chemical pollen inactivation, a highly effective system for the production of hybrid plant seeds that is based on a split-gene approach has been further developed. The two protein fragments produced in the female parental line from the two parts of the gene cause pollen ablation and thus male sterility. As always only one of the two partial genes is transmitted to the progeny

Pflanzen produziert wurden, gelang es, ein neuartiges Konzept für die Produktion multimerer Spinnenseidenproteine in Pflanzen zu entwickeln und einzusetzen. Isolierte und gereinigte Multimere wurden mittels Elektronenmikroskopie untersucht. Ferner wurden verschiedene Antigene des Vogelgrippevirus (H5N1) u.a. als Fusionen mit ELP (Elastin-ähnliches Polypeptid) in Pflanzen produziert. Für die verbesserte Reinigung ELPylierter Proteine wurde die mITC-Technologie entwickelt und für die Erzeugung von Hämagglutinin und Neuraminidase in erhöhter Qualität eingesetzt. Produzierte Hämagglutinin-Trimere und Virus-ähnliche Partikel wurden erfolgreich zur Immunisierung von Mäusen eingesetzt. Schließlich konnten neue spezifische Antikörper gegen Tumornekrosisfaktor alpha isoliert werden.

– Entwicklung von Hybridtechnologien:
  Als Alternative zu chemischer Pollenabtötung wurde ein hoch effizientes Verfahren zur Erzeugung von Hybridsaatgut bei Pflanzen weiterentwickelt, das auf einem „geteilten Gen" beruht. Die (Teil-)Proteine, die in den als mütterliche Elternlinie herangezogenen Pflanzen von den zwei Teilen dieses Gens produziert werden, führen zum Absterben der Pollen und damit zu männlicher Sterilität. An die durch Fremdbefruchtung erzeugten Nachkommen wird jedoch nur jeweils eines der zwei Teilgene vererbt, die für sich inaktiv sind. Daher sind die erzeugten Hybriden vollständig fruchtbar. Im Berichtszeitraum konnte die Expressionsstärke und damit die Penetranz der ausgelösten Sterilität entscheidend erhöht werden. Darüber hinaus wurden Verfahren zur Identifizierung guter Pollenspender und zur Erzeugung von Doppelhaploiden bei Weizen entwickelt.

Entwicklung und Anwendung bioinformatischer Verfahren

Als generische Verfahren gehören bioinformatische Methoden zum unverzichtbaren Repertoire moderner pflanzenbiologischer Forschung und finden abteilungsübergreifend Anwendung in vielfältigen Projekten. Wichtige Beiträge von Arbeitsgruppen der Abteilung Molekulare Genetik umfassen:

– Koordination der Bioinformatikarbeiten am IPK
  (Prof. Dr. F. Schreiber)
– Integrative Bioinformatik und Netzwerkanalyse:
  Das open source System VANTED für die Analyse experimenteller Daten im Kontext biologischer Netzwerke wurde weiterentwickelt (aktuell in Version 2.0 verfügbar) und um neue Algorithmen für die erleichterte Integration, Exploration und Analyse von Daten (u.a. zur Integration von metabolischen und regulatorischen Kenntnissen oder zur Erkennung überrepräsentierter exprimierter Gene bestimmter Stoffwechselwege) erweitert und in vielfältigen Projekten eingesetzt. Zudem wurden diverse add-ons (Hive, SBGN-ED, CentiLib, FluxMap) entwickelt, die neue Funktionalitäten bereitstellen. Ferner wurde die Weiterentwicklung des MetaCrop Informationssystems für Stoffwechselwege fortgeführt und die Version 2.0 freigegeben. Mit der Erweiterung der Inhalte von MetaCrop sind nun Informationen zu ca. 62 Stoffwechselwegen aus mehr als 1800 Publikationen verfügbar. Diese Daten stellen die Grundlage für diverse stoichiometrische Stoffwechselmodelle dar, die entwickelt und analysiert wurden. Das DBE2

produced through cross-pollination, which on its own is inactive, the produced hybrids are fully fertile. During the reporting period the expression level and thereby the penetrance of the induced sterility was vitally improved. In addition, procedures for the identification of good pollen donors and for the generation of doubled haploids in wheat were developed.

Development and application of bioinformatic procedures

Bioinformatics methods are indispensible components of the technological repertoire of modern plant biology research. According to their generic nature, the developed and implemented procedures are used across departments in numerous projects. Important contributions of groups of the Molecular Genetics department include:

– Co-ordination of bioinformatics research at IPK
  (Prof. F. Schreiber).
– Integrative bioinformatics and network analysis:
  The open source system VANTED for the analysis of experimental data in the context of biological networks has been further developed (currently available as version 2.0) and has been expanded through addition of novel algorithms for facilitated integration and analysis of data (e.g. for integration of metabolic or regulatory knowledge or for recognition of overrepresented expressed genes of certain pathways) and has been used in various projects. In addition, several add-ons (Hive, SBGN-ED, CentiLib, FluxMap) were developed which offer new functionalities. Furthermore, development of the MetaCrop information system for metabolic pathways has been continued and version 2.0 has been released. The extended contents of MetaCrop now cover information on approx. 62 metabolic pathways derived from more than 1800 publications. These data are the basis of various stoichiometric metabolic models that have been developed and analysed. The DBE2 information system for the management of biological experiment data and a system to display and handle biological networks based on an international convention (SBGN) were further developed. Finally, an established image analysis pipeline for the analysis of data produced by automated phenotyping facilities has been further developed and various novel algorithms for the structural network analysis and display as well as efficient algorithms using parallel architectures were developed, implemented, and used.
– Processing, visualisation, and interpretation of high-dimensional biological data:
  Applying machine learning techniques and Hidden Markov Models, array-CGH and ChIP-Chip data sets were used for comparative genome analysis and epigenetic chromatin modification investigation of diverse *Arabidopsis thaliana* accessions and hybrids thereof. They were expanded towards identification of newly inserted transposons through analysis of the DNA methylation status. A novel tool for *de novo* identification of DNA motifs (Dispom) has been developed for transcription factor binding site recognition and a new motif was found in auxin-regulated promotors. *Arabidopsis* gene regulation networks affected

Informationssystem für das Management biologischer Experimentdaten und ein auf internationalen Konventionen (SBGN) beruhendes System zur Darstellung und Handhabung biologischer Netzwerke wurden weiterentwickelt. Schließlich wurde eine erstellte Bildanalysepipeline für die Verarbeitung von Daten aus automatisierten Phänotypisierungsanlagen weiterentwickelt und diverse neue Algorithmen für die strukturelle Netzwerkanalyse und die Netzwerkdarstellung sowie effiziente Algorithmen unter Verwendung paralleler Architekturen entwickelt, implementiert und angewendet.

– Prozessierung, Visualisierung und Interpretation hoch-dimensionaler biologischer Daten:
  Mit Hilfe von Verfahren des maschinellen Lernens und unter Einsatz von Hidden Markov-Modellen wurden Array-CGH- und ChIP-Chip-Datensätze zur vergleichenden Genomanalyse einschließlich epigenetischer Chromatinmodifikationen verschiedener *Arabidopsis thaliana*-Akzessionen und deren Hybriden eingesetzt. Diese wurden für die Identifizierung neu inserierter Transposons unter Analyse des DNA-Methylierungsstatus erweitert. Ein neues Werkzeug für die *de-novo*-Identifizierung von DNA-Motiven (Dispom) wurde für die Erkennung von Transkriptionsfaktorbindestellen entwickelt und damit ein neues Motiv in Promotoren Auxin-regulierter Gene gefunden. Mittels reverse engineering wurden Genregulationsnetzwerke rekonstruiert, die bei *Arabidopsis* Veränderungen durch die Überexpression von AtHb1 erfahren. Schließlich wurden neue Verfahrensweisen unter Nutzung moderner probabilistischer Methoden für die Auswertung historischer Daten zu Genbank-Akzessionen entwickelt und für die Identifizierung von Akzessionen mit gesuchten Eigenschaften bzw. die Kennzeichnung kontrastierender Akzessionen eingesetzt.
– Entwicklung von Systemen für die Speicherung und Analyse von Hochdurchsatz-Bilddaten:
  Zur effektiven Handhabung und Analyse von Bilddaten, die von multiplen Kamerasystemem in automatisierten Phänotypisierungsanlagen geliefert werden, wurde ein Java-basiertes Informationssystem (IAP) eingerichtet, das Nutzern verschiedene Funktionalitäten bereitstellt: Analyse von Bilddaten und weiteren experimentellen Daten, Datentransfer für langfristige Archivierung, Herunterladen von Daten für eigene Analysen und Ausführen automatisierter Bildanalyseprozeduren für Experimentdaten. Innerhalb von IAP wurde eine Reihe von Bildverarbeitungs- und Analysefunktionen eingerichtet, die es nach Vorverarbeitung erlauben, Informationen über Pflanzeneigenschaften (u.a. Höhe, Breite, projizierte Fläche, geschätzte Biomasse etc.) zu extrahieren. Ergebnisse der Datenanalysen können in Form von Datentabellen und als automatisch erzeugte Berichtsdateien exportiert werden.

Die folgenden Berichte der Arbeitsgruppen geben detailliertere Einblicke in die Forschungsarbeiten und die erzielten Ergebnisse der einzelnen Arbeitsgruppen der Abteilung.

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by overexpression of AtHb1 were reconstructed through reverse engineering. Finally, novel procedures based on modern probabilistic models were used to evaluate historic data on Genebank accessions and supported the identification of accessions with desired features or the selection of contrasting accessions.

– Development of storage and analysis systems for high-throughput image data:
  A Java-based system (IAP) for efficient handling and analysis of image data generated by multiple camera systems of the automated phenotyping systems has been developed that offers various functionalities to users: Processing of images and further experimental data, data transfer for long-term archiving, download of data for individual analyses, and performance of automated image analysis for experimental data. Within IAP several image processing and analysis procedures were implemented that after preprocessing support the extraction of information on plant features (including height, width, projected area, estimated biomass, etc.). Results of data analyses can be exported as data tables or as automatically generated report files.

The following group reports provide more detailed insights into the research and the achieved results of the individual research groups of the department.

Thomas Altmann, November 2011

Research Group: Heterosis

Head: Prof. Thomas Altmann

Scientists

IPK financed
Altschmied, Lothar, Dr. (since 01.08.2011)
Borisjuk, Lioudmilla, Dr.
Meyer, Rhonda, Dr.
Radchuk, Ruslana, Dr. (0.50, 01.03.-31.07.2011; since 01.08.2011)
Riewe, David, Dr.
Schiebold, Silke (0.50, 01.08.-31.10.2010)

Grant Positions
Arana Ceballos, Fernando, Dr. (DFG, since 15.07.2010)
Ernst, Michaela, Dr. (BMBF, till 31.08.2010)
Fuchs, Johannes (0.50 Industry)
Gryczka, Corina, Dr. (BMBF, since 01.09.2010)
Heinzel, Nicolas, Dr. (Industry)
Jasik, Jan, Dr. (Industry, till 31.12.2010)
Kalladan, Rajesh (0.50 BMBF, till 30.09.2010)
Melkus, Gerd (BMBF, till 30.06.2010; Industry 01.07.-30.09.2010)
Müller, Margarete, Dr. (BMBF, till 30.04.2011)
Muraya, Moses Mahugu, Dr. (BMBF)
Radchuk, Ruslana, Dr. (0.50 Industry, 01.04.-31.07.2011)
Rolletschek, Hardy, Dr. (Industry)
Rosso, Mario, Dr. (BMBF)
Schiebold, Silke (0.50 Industry, till 31.07.2010; 01.11.2010-14.04.2011)
Seyfarth, Monique (0.50 Saxony-Anhalt)
Tschiersch, Henning, Dr. (0.50 Industry, till 31.07.2010; BMBF, since 01.08.2010)
Weigelt, Kathleen (BMBF, till 31.03.2011)

Visiting Scientists/Scholars
Ernst, Michaela, Dr. (self-financed, 01.09.2010-31.03.2011; since 25.11.2011)
Jeon, Hea-Jung (Korean government, since 27.09.2010)
Koohi-Dehkordi, Mehrana (Iranian Ministry of Science, Research and Technology, 10.01.-31.08.2010; 01.12.2010-30.09.2011)

Goals

With the major aim of identifying factors controlling plant performance characteristics, two complementary research areas are addressed within the group:

- Genetic/genomic approaches are followed to identify growth and metabolism controlling factors of vegetative development (addressing mainly *Arabidopsis* and maize). Major emphasis is given to the discovery of genetic and biological markers for the prediction of (vegetative) biomass accumulation and to the identification of loci contributing to heterosis

and

- Lipid metabolism and sucrose allocation in seeds (mainly rapeseed, oat, and barley) is investigated using topographical biophysical, biochemical, and molecular analysis procedures to uncover determinants and limiting factors of yield.

Research Report

Project area *Analysis of Growth and Metabolism during Vegetative Development*

Identification and fine mapping of QTL for biomass heterosis in *Arabidopsis thaliana* accessions Col-0 and C24

Analysis of previously established recombinant inbred line (RIL; Törjek et al. 2006) and introgression line (IL; Törjek et al. 2008) populations of the *Arabidopsis* accessions Col-0 and C24 jointly with their respective testcrosses (TCs) for dry matter yield and leaf area during early vegetative development resulted in the identification of genomic regions, that condition heterosis for vegetative growth/biomass accumulation (see Fig. 34, p. 96) (Meyer et al. 2010). Using data of RILs/RIL-TCs and ILs/IL-TCs, a total of ten genomic regions responsible for early stage biomass heterosis were identified that individually explained between 2.4 % and 15.7 % of the observed phenotypic variation. Individual heterotic QTL mostly exhibited overdominant gene action. Furthermore, the obtained results suggest that biomass heterosis in this *Arabidopsis* cross involves a combination of dominance, overdominance and epistasis. Three heterotic biomass (hb)QTL located on chromosomes 1, 3, and 4 were chosen for fine mapping and detailed molecular characterisation. Using genotype and phenotype information of approx. 600 individuals of IL families (ILFs) segregating for genomic segments spanning the hbQTL on chromosome 4, the QTL region was confined to a region of approx. 45 kb harbouring 14 annotated genes (R. Schmidt, R. Meyer, unpublished data). Analysis of corresponding subILs and their testcrosses confirmed heterosis to be caused by heterozygosity of the fine-mapped region (R. Schmidt, K. Weigelt, R. Meyer, unpublished data). Characterisation of T-DNA k.o. mutants of genes in the support interval and testcrosses thereof as well as generation of transgenic plants transformed with segments of this region derived from the opposite genotype is ongoing (R. Meyer, D. Riewe, B. Ebert, K. Weigelt, H.-J. Jeon, unpublished data). The hbQTL located on chromosomes 1 and 3 are fine-mapped via phenotyping and genotyping of RIL-derived segregating heterogeneous inbred families (HIFs) and ILFs (K. Weigelt, F. Arana-Ceballos, unpublished data). The same strategy is followed for fine mapping of another (non-heterotic) biomass QTL located on chromosome 3, suspected to be involved in cross-talk between metabolism and growth control (M. Seyfarth, unpublished data).

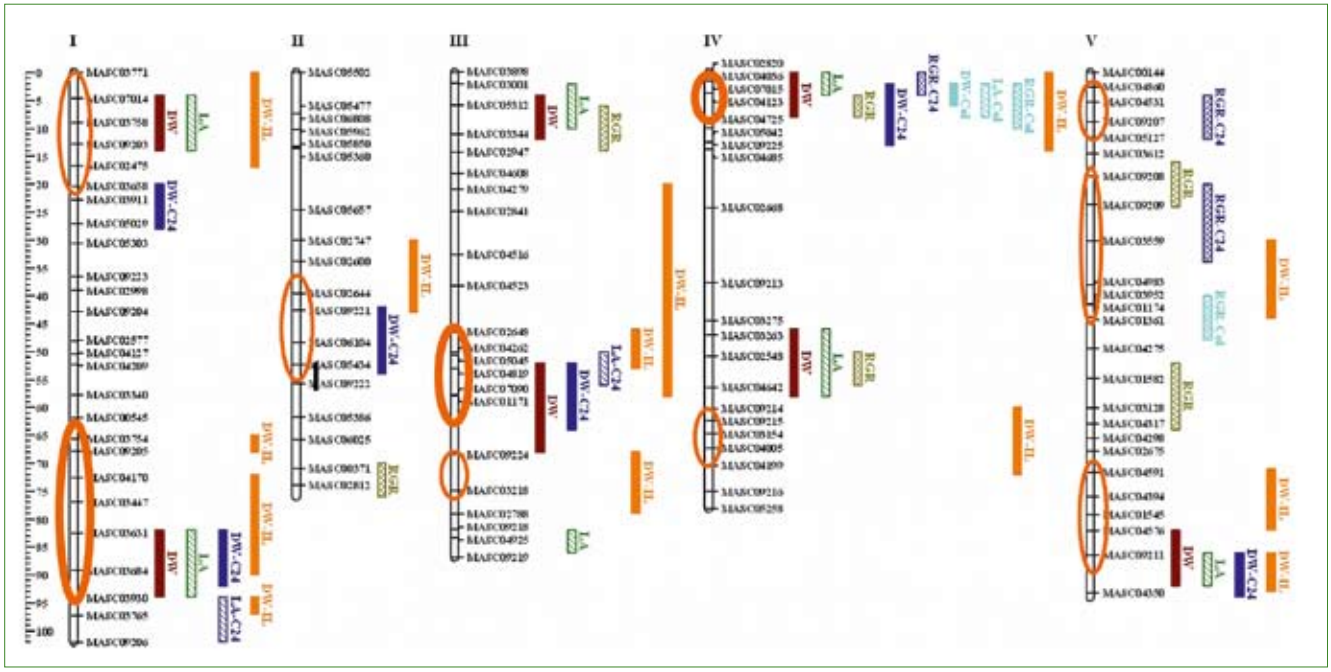

Fig. 34
Localisation of heterotic and *per se* QTL on Col-0/C24 genetic map. DW – dry matter yield, LA – leaf area, RGR – relative growth rate, -C24 – mid-parent-heterosis in cross C24 × RIL, -Col – mid-parent-heterosis in cross Col-0 × RIL, DW-IL – hbQTL detected in IL. (Meyer et al. 2010)

Characterisation of genes corresponding to metabolite QTL in *Arabidopsis thaliana* and further investigation of growth – metabolism relations

Based on previous data of metabolite (m)QTL identified through gas chromatography/mass spectrometry (GC/MS)-based metabolic profiling of the aforementioned RIL and IL populations (Lisec et al. 2008), 30 candidate genes were selected for an initial analysis according to their proposed enzymatic role related to 15 different metabolites affected by mQTL. Effects on abundance of the corresponding metabolite were observed by T-DNA k.o. mutations of 5 genes that were selected for further investigation using also TILLING mutants and dsRNAi lines subjected to GC/MS analyses (Brotman et al. 2011; D. Riewe, M. Koohi, M. Pfeiffer, unpublished data). One of the five genes (At5g50950) was thus shown to encode a second functional fumarase (FUM2) isoform in *Arabidopsis* (Brotman et al. 2011). The Col-0 and C24 alleles of this gene (corresponding to the fumarase mQTL alleles) were shown to differ approx. 16-fold in the level of their expression, which very likely causes a substantial difference in FUM2 activity and thus fumarate accumulation (Brotman et al. 2011).

Natural genetic variation of metabolism and growth in *Arabidopsis* was further studied in a collection of 129 accessions that were characterised for activities of 37 enzymes from central metabolism in addition to metabolite contents and accumulated biomass (Sulpice et al. 2010). While highly co-ordinated changes were observed for most enzymes and for certain subsets of metabolites, little correlation was found between enzyme activities and metabolites and only weak correlations between individual enzyme activities and biomass. However, the fraction of total protein allocated to enzymes was positively correlated with biomass and additive to the negative starch-biomass correlation (Sulpice et al. 2010). A subset of 54 of the accessions was furthermore subjected to deep genotypic characterisation through single feature polymorphism (SFP) analysis using tiling arrays of 3 million oligonucleotides (Childs et al. 2010). This resulted in the detection of more than 1 million SFPs. A total of 198 significant associations between SFPs of metabolic genes and 9 metabolic and growth-related traits were observed and five significant selective sweep regions were detected, one of which is significantly associated with a metabolic trait (Childs et al. 2010).

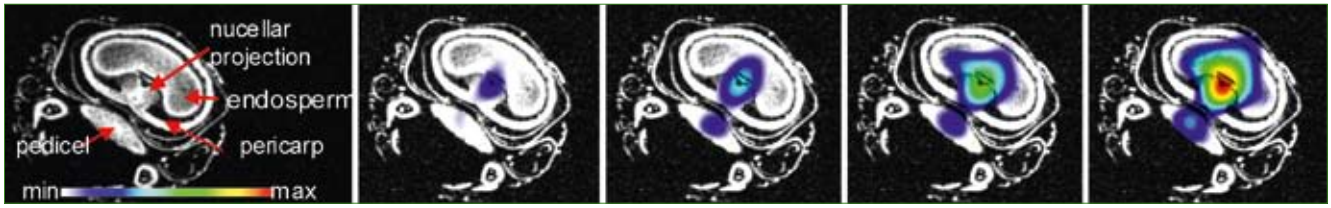

Fig. 35
Visualisation of 13C-sugar allocation within the caryopsis using double resonant 13C/1H NMR. A proton NMR reference image is shown at the left. Right are selected 2D colour coded maps demonstrating the distribution of 13C-sugar during 12 h long monitoring experiment (Melkus et al. 2011).

Characterisation of diverse maize inbred line collections

In the frame of the GABI-ENERGY and PLANT-KBBE CornFed co-operation projects (jointly with A. Melchinger, University of Hohenheim; L. Willmitzer and M. Stitt, MPI-MP, Golm; J. Selbig, Potsdam University; A. Charcosset, INRA Moulon; D. Brunel, CNG Evry; C. Schön, TU München; M. Ouzunova, KWS Einbeck; and their co-workers) detailed genetic and phenotypic characterisation of diverse collections of maize inbred lines (`flint´, ´dent´, and `tropical´ panels), DH lines and testcrosses thereof is being carried out. These joint efforts have led to the accumulation of genotype data based on the maize 50k SNP array for a total of more than 1,000 inbred lines and more than 2,200 DH lines (the latter are arranged in a nested association mapping (NAM) design). In addition to field characterisation of 289 dent inbreds and testcrosses with two testers for agronomic traits and metabolite profiles (Larhlimi et al. submitted; Riedelsheimer et al. submitted), a subset of 92 inbreds and testcrosses thereof (selected after initial analysis of the entire population) has been characterised for vegetative growth performance under controlled (greenhouse) conditions, for metabolite composition, and for transcript profiles (M. Ernst, C. Gryczka, S. Friedel, unpublished data). The collected data are being used for the demonstration of metabolite and SNP-based prediction of inbred and hybrid performance, as well as association mapping of QTL affecting growth and metabolism.

Project area *Lipid Metabolism in Oil-storing Seeds*

Modelling lipid metabolism using a systems biology approach

Lipid metabolism and seed filling of rape seed were analysed using histological methods, NMR-based modelling and the lipid imaging tool. The project is in progress and relies on extensive collaboration with partners from University Hannover, Brookhaven National Lab (USA) and Bayer CropScience (Belgium). A novel quantitative assay for evaluation of promoter activity was developed, which integrates laser-microdissection and an enzymatic assay (Jasik et al. 2011). We also developed tools for the analysis of metabolites and storage products in laser microdissected tissues, which are easily combined with gene expression analysis (Schiebold et al. 2011). The bioanalytical tools were also used in other collaborations (e.g. GABI-Grain; SysSeed) and resulted in several publications (Rolletschek et al. 2011; Cornelius et al. 2011; Hayden et al. 2011; Seiler et al. 2011).

***In vivo* analysis of storage and metabolite distribution in plants**

The NMR-based lipid mapping tool was applied for investigation of lipid metabolism in oat, and resulted in defining of the cofactome as a promising target for biotechnological improvements of seed. (Hayden et al. 2011). This work represents an ongoing cooperation with UC Davis/USA (Prof. K. Dehesh). To study the distribution and flow of metabolites non-invasively, we applied NMR-based approaches. Current methods have been developed based on 1H/13C-NMR (SysSeed and in collaboration with University of Würzburg/Prof. P. Jakob). This allowed for the first time to visualise the allocation of sucrose in living seeds (Fig. 35, Melkus et al. 2011). Application of this new technology to barley seeds as a model visualised the site of primary synthesis of alanine and revealed compartmentation of the starchy endosperm (Rolletschek et al. 2011). We aim to improve this method and widen its application, but this *in vivo* technology already represents a significant breakthrough in seed research with high biotechnological relevance.

Microsensor-based technology for the investigation of oxygen, carbon dioxide, and nitric oxide in plants

Planar oxygen sensors are developed, which allow to quantify oxygen and nitric oxide (NO) on the surface of tissues. Both oxygen and NO are important signalling molecules involved in dynamic adjustment of seed metabolism to environmental and developmental changes (Thiel et al. 2011). A planar sensor for oxygen was successfully applied on different plant species and tissues (Tschiersch et al. 2011). Sensor development is in progress in cooperation with PreSense GmBH (Regensburg/Germany).

Publications

(The publication with a "*" is based on work that has been carried out when N. Heinzel was at the Max Planck Institute for Chemical Ecology Jena).

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2010

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Books and Book Chapters

2011

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2010

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2010

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Research Group: Seed Development

Head: Dr. Winfriede Weschke

Scientists

IPK financed
Meitzel, Tobias (0.50, 01.04.-30.04.2010)
Radchuk, Ruslana, Dr. (0.50, till 30.06.2010)
Sreenivasulu, Nese, Dr. (01.07.-31.10.2010)
Thiel, Johannes, Dr. (16.02.-30.04.2011)
Weber, Hans, Dr.

Grant Positions
Andersch, Franka (0.50 DFG, since 01.05.2011)
Harshavardhan, Vokkaliga Thammegowda (0.50 BMBF, till 31.10.2010)
Kohl, Stefan (0.50 DFG)
Meitzel, Tobias (0.50 DFG, till 31.03.2010, since 01.05.2010)
Palakolanu, Sudhakar Reddy (0.50 BMBF, 08.03.-30.10.2010)
Radchuk, Ruslana, Dr. (0.50 BMBF, 01.07.2010-28.02.2011)
Radchuk, Volodymyr, Dr. (1.00/0.75 BMBF, till 28.02.2011; DFG, since 01.03.2011)
Seiler, Christiane, Dr. (BMBF, till 30.06.2010)
Sreenivasulu, Nese, Dr. (BMBF, till 30.06.2010)
Staroske, Nicole (0.50 BMBF, till 30.06.2010)
Thiel, Johannes, Dr. (DFG, till 15.02.2011; since 01.05.2011)
Weier, Diana, Dr. (DFG, till 30.04.2010)

Visiting Scientists/Scholars
Mora Ramirez, Maria Isabel (DAAD, since 01.10.2011)
Pirko, Yaroslav, Dr. (DFG, since 03.07.2011)
Prasad, Manoj, Dr. (DLR, 12.02.-28.02.2010)
Seiler, Christiane, Dr. (self-financed, 01.07.-31.10.2010)
Staroske, Nicole (self-financed, 01.04.-30.04.2011; 01.08.-31.12.2011)
Strickert, Marc, Dr. (self-financed, 01.02.-31.10.2010)
Tran Thi Thuy, Van (Ministry of Education and Training, Vietnam, since 21.08.2011)

Goals

The general goal of our scientific work is to understand and influence regulatory networks of differentiation and storage product accumulation in developing crop seeds. In more detail, our interest is focused on metabolic and hormonal regulation of these processes. Thereby, specific emphasis is laid on differentiation of barley endosperm transfer cells (ETCs). Scientific work is further focused on sink-source relationships and on cellular disintegration processes in developing seeds. Aim of our work is to improve yield and quality of crop seeds.

Research Report

(1) Metabolic regulation of seed development
In frame of the GABI-SysSEED project, developing grains of the **barley endosperm mutant *Risø 16*** that is deficient in the cytosolic small subunit of ADP-glucose pyrophosphorylase (AGPase) were analysed in detail. On the regulatory level, an overlap of metabolic and hormonal regulation is deduced which leads to parallel transcriptional down-regulation of endosperm-specific genes (storage proteins) and those involved in phytohormone (ABA)-induced storage product accumulation. Results indicate that decreasing carbon fluxes into starch of barley endosperm leads to re-partitioning of carbon, and affects the pathway of amino acid and subsequently, storage proteins biosynthesis (Faix et al., accepted by Plant J.). In cooperation with P. Geigenberger (University Munich) starch metabolism was analysed in developing wild type and *Risø 16* grains using a non-aqueous fractionation method. The results are accepted for publication (Thiessen et al., J. Exp. Bot.). In transgenic pea embryos, diminishing of trehalose-6 phosphate (T6P) levels leads to a wrinkled seed phenotype. Previous results suggest that starch biosynthesis is likely be influenced by **T6P-mediated activation of AGPase** (T. Meitzel, financed by DFG). In cooperation with W. Link (University Göttingen) **embryonic heterosis** was analysed in *V. faba* seeds. Hybrid embryos develop enhanced sink strength which is established during early seed development and probably mediated by auxin effects (Meitzel et al. 2011).

(2) Hormonal influences on seed development
In developing pea embryos and developing barley caryopses abscisic acid **(ABA) deficiency** was induced by immunomodulation (cooperation with Udo Conrad). In pea, immunomodulation attenuates developmental phase transition and storage metabolism (Radchuk et al. 2010). In barley, drastically elevated ABA amounts are related to altered metabolite and transcript levels preferentially during the transition phase of endosperm development. Evaluation of transcript profiling data hints to mechanisms reducing ABA sensitivity of transcriptional regulation. As a result, mature transgenic grains show only slight phenotypic variations (N. Staroske, PhD thesis, financed by BMBF). In the **barley mutant *seg8***, deregulation of ABA content causes abnormal development of ETCs. Feedback responses between ABA-producing maternal and filial grain tissues during the transition phase are suggested (Sreenivasulu et al. 2010). 454-transcriptome sequencing of microdissected developing ETC favours the two component system (TCS) as a major signalling cascade (J. Thiel, in preparation, financed by DFG). **Hormonal influences on the activity of TCS-associated histidine kinases** are supposed but not confirmed yet. Transcript and metabolite profiling of microdissected developing ETCs will probably gain additional insights into hormon signalling

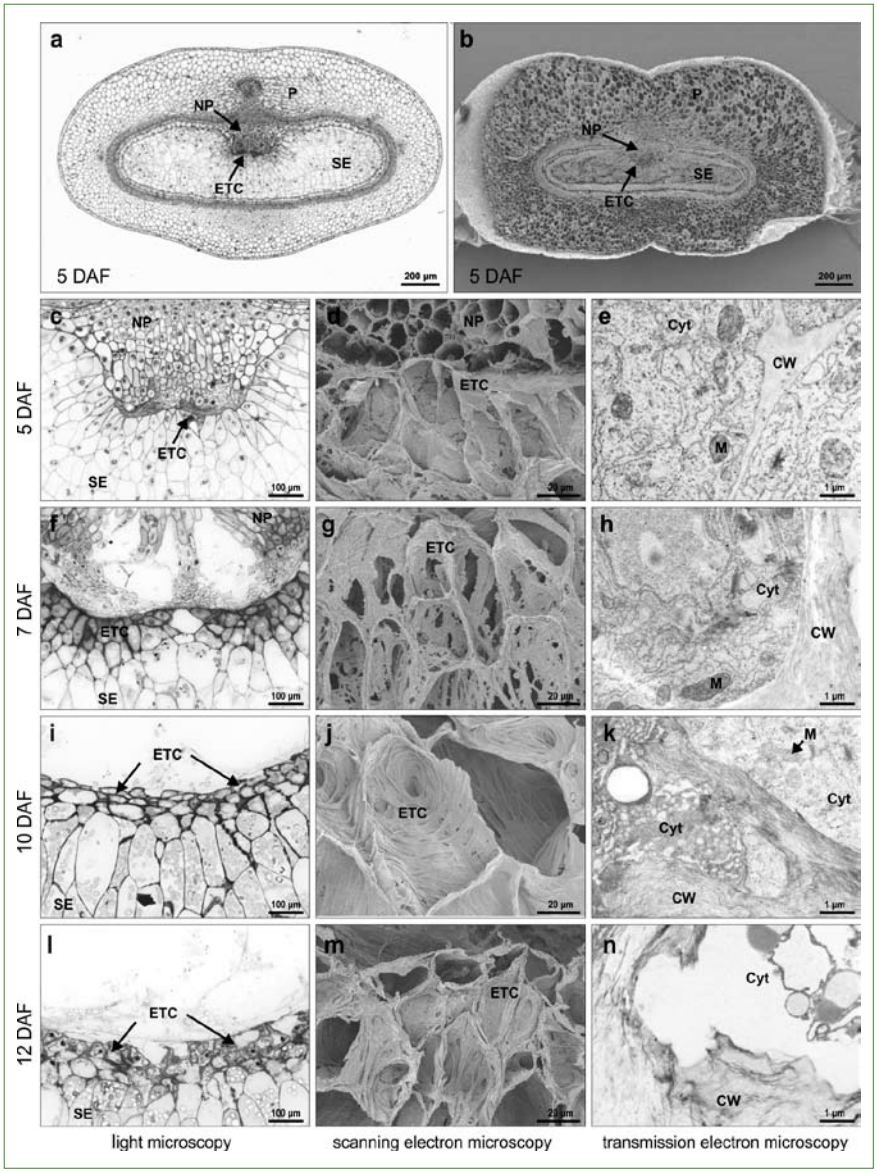

Fig. 36
Structural analysis of the cell architecture of the endosperm transfer cells in developing grains of *Hordeum vulgare*. Light microscopy (a, c, f, i, l) scanning electron microscopy (b, d, g, j, m) and transmission electron microscopy (e, h, k, n) of grains 5 DAF (a, b, c, d, e), 7 DAF (f - h), 10 DAF (i - k) and 12 DAF (l - n).
CW, cell wall; Cyt, cytoplasm; DAF, days after flowering; ETC, endosperm transfer cells; M, mitochondria; NP, nucellar projection; P, pericarp; SE, starchy endosperm (J. Thiel, T. Rutten, H. Weber and M. Melzer).

but also regulatory networks responsible for the establishment of a specific wall architecture (Fig. 36) typically found in transfer cells (J. Thiel, in preparation).

qRT-PCR analyses of ABA-biosynthesis and signalling genes in microdissected tissues of developing barley caryopses suggest that ABA synthesised in the maternal chlorenchyma might be responsible for the activity of ABA-signalling genes in the endosperm (J. Schmeichel, Diploma thesis, IPK-financed).

(3) Sink-source relationships
Sucrose uptake capacity increased by expression of a barley sucrose transporter in developing wheat grains (**transgenic model HOSUT**) stimulates storage protein synthesis and results in significant increase of thousand grain weight (Weichert et al. 2010). In cooperation with M. Röder, genetic and metabolic control of grain shape and weight is analysed in HOSUT grains and grains of a wheat introgression line (F. Andersch, financed by DFG). The HOSUT modulation has also a positive impact on vegetative development (I. Saalbach, I. Mora Ramirez, financed by DAAD). Transcript and metabolite profiling of remobilising flag leaves, glumes and developing grains suggest that the transient phase of grain development is registered also in ear-near vegetative tissues. A development-specific signal is supposed to mediate **sink-source communication during grain development** (S. Kohl, manuscript in preparation, financed by DFG).

(4) Cellular disintegration and crop seed development
In barley, development of maternal grain tissues is mediated by regulated cell expansion and cell disintegration and coordinated with endosperm growth. Cell disintegration is mediated by programmed cell death (PCD) events that might be coupled to the activity of **vacuolar processing enzymes** (VPEs) (Radchuk et al. 2011). RNAi suppression of members of the VPE gene family will probably show influence of VPE gene activity on barley grain development (V. Tran Thie Thyu). Cellular disintegration and PCD in the nucellar projection of developing grains are coupled to the activity of the small cystein-rich protein Jekyll (Radchuk et al. 2006). Jekyll activity has to undergo fine-tuned regulation. Transcriptional

regulation of Jekyll expression and protein composition of **the regulatory Jekyll complex** will be analysed in cooperation with U. Conrad (V. Radchuk, financed by DFG). Two members of a gene family encoding small cystein-rich proteins were identified in pea (T. Meitzel, R. Radchuk). The respective proteins might be responsible for cellular disintegration and nutrient release in the pea seed coat. Further work will verify this hypothesis.

Publications

Peer Reviewed Papers

2010

Kaspar, S., D. Weier, W. Weschke, H.P. Mock & A. Matros: Protein analysis of laser capture micro-dissected tissues revealed cell-type specific biological functions in developing barley grains. Anal. Bioanal. Chem. 398 (2010) 2883-2893.

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Radchuk, R., U. Conrad, I. Saalbach, M. Giersberg, R.J. Emery, H. Küster, A. Nunes-Nesi, A.R. Fernie, W. Weschke & H. Weber: Abscisic acid deficiency of developing pea embryos achieved by immunomodulation attenuates developmental phase transition and storage metabolism. Plant J. 64 (2010) 715-730.

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Riebeseel, E., R.E. Häusler, R. Radchuk, T. Meitzel, M.R. Hajirezaei, R.J. Neil Emery, H. Küster, A. Nunes-Nesi, A.R. Fernie, W. Weschke & H. Weber: The 2-oxoglutarate/malate translocator mediates amino acid and storage protein biosynthesis in pea embryos. Plant J. 61 (2010) 350-363.

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Sreenivasulu, N., V. Radchuk, A. Alawady, L. Borisjuk, D. Weier, N. Staroske, J. Fuchs, O. Miersch, M. Strickert, B. Usadel, U. Wobus, B. Grimm, H. Weber & W. Weschke: De-regulation of abscisic acid contents causes abnormal endosperm development in the barley mutant *seg8*. Plant J. 64 (2010) 589-603.

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Andriunas, F.A., H.M. Zhang, H. Weber, D.W. McCurdy, C.E. Offler & J.W. Patrick: Glucose and ethylene signalling pathways converge to regulate *trans*-differentiation of epidermal transfer cells in *Vicia narbonensis* cotyledons. Plant J. 68 (2011) 987-998.

Govind, G., C. Seiler, U. Wobus & N. Sreenivasulu: Importance of ABA homeostasis under terminal drought stress in regulating grain filling events. Plant Signal. Behav. 6 (2011) 1228-1231.

Meitzel, T., R. Radchuk, A. Nunes-Nesi, A.R. Fernie, W. Link, W. Weschke & H. Weber: Hybrid embryos of *Vicia faba* develop enhanced sink strength, which is established during early development. Plant J. 65 (2011) 517-531.

Melkus, G., H. Rolletschek, J. Fuchs, V. Radchuk, E. Grafahrend-Belau, N. Sreenivasulu, T. Rutten, D. Weier, N. Heinzel, F. Schreiber, T. Altmann, P.M. Jakob & L. Borisjuk: Dynamic (13) C/(1) H NMR imaging uncovers sugar allocation in the living seed. Plant Biotechnol. J. 9 (2011) 1022-1037.

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Worch, S., K. Rajesh, V.T. Harshavardhan, C. Pietsch, V. Korzun, L. Kuntze, A. Börner, U. Wobus, M.S. Röder & N. Sreenivasulu: Haplotyping, linkage mapping and expression analysis of barley genes regulated by terminal drought stress influencing seed quality. BMC Plant Biol. 11 (2011) 1.

Books and Book Chapters

2010

Sreenivasulu, N., R. Sunkar, U. Wobus & M. Strickert: Array platforms and bioinformatics tools for the analysis of plant transcriptome in response to abiotic stress. In: Sunkar, R. (Ed.): Plant Stress Tolerance – Methods and Protocols, Methods Mol. Biol., Vol. 639. Humana Press (2010) 71-93.

Weber, H., N. Sreenivasulu & W. Weschke: Molecular physiology of seed maturation and seed storage protein biosynthesis. In: Pua, E.-C. & M.R. Davey (Eds.): Plant Developmental Biology – Biotechnological Perspectives, Vol. 2. Springer, Berlin (2010) 83-104.

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Wobus, A.M. & U. Wobus: Gaterslebener Begegnung 2009. Der Begriff der Natur – Wandlungen unseres Naturverständnisses und seine Folgen. In: Jahrbuch 2009 der Deutschen Akademie der Naturforscher Leopoldina (Halle/S.) LEOPOLDINA (R.3), 55 (2010) 419-420.

2011

Thiel, J., D. Weier & W. Weschke: Laser capture microdissection of developing barley seeds and cDNA array analysis of selected tissues. In: Murray, G.I. (Ed.): Laser capture microdissection: methods and applications, 2nd Edition (Methods Mol. Biol. 755). Springer New York (2011) 461-475.

Other Papers

2010

Sreenivasulu, N., M.S. Röder & U. Wobus: Trockenstress – eine Suche nach den Ursachen und nach neuen Wegen zur Züchtung trockentoleranter Getreide. GenomXPress 4 (2010) 4-6.

PhD and Diploma Theses

2010

Andersch, F.: Seneszenz-assoziierter Stickstofftransport in Gerste. (Diploma Thesis) Friedrich-Schiller-Universität, Jena (2010) 104 pp.

Weigelt, K.: Transkriptionelle und biochemische Untersuchungen des veränderten Stickstoff- und Kohlenstoffmetabolismus in genetisch modifizierten Erbsensamen. (PhD Thesis) Martin-Luther-Universität Halle-Wittenberg, Institut für Biologie, Halle/S. (2010) 237 pp.

2011

Schmeichel, J.: Establishment of a development and tissue specific cDNA collection to monitor gene expression gradients of ABA biosynthesis enzymes in developing barley grains. (Diploma Thesis) Friedrich-Schiller-Universität, Jena (2011) 62 pp.

Stefani, D.: Protein-Protein-Interaktionsstudien an pflanzlichen Trehalose-6-Phosphatsynthasen und -Phosphatasen. (Diploma Thesis) Martin-Luther-Universität Halle-Wittenberg, Halle/S. (2011) 88 pp.

Research Group: Gene Regulation

Head: Dr. Helmut Bäumlein

Scientists

IPK financed
Kirioukhova, Olga, Dr. (since 01.07.2011)
Köszegi, David, Dr. (till 30.06.2011)
Lee Hong, Diep (0.50, 01.04.-30.09.2010)
Mildner, Maria (0.50 Pakt für Forschung und Innovation, till 28.02.2010; 0.50, 01.03.-31.03.2010)

Grant Positions
Gryczka, Corina, Dr. (BMBF, till 31.08.2010)
Johnston, Amal Joseph, Dr. (DFG, till 31.08.2010)
Kirioukhova, Olga, Dr. (DFG, 01.09.2010-30.06.2011)
Köszegi, David, Dr. (0.50 DFG, since 01.07.2011)
Rizzo, Paride (0.50 DFG, since 01.07.2011)
Schallau, Anna, Dr. (0.75/1.00 DFG, since 01.03.2011)

Visiting Scientists/Scholars
Johnston, Amal Joseph, Dr. (Humboldt fellowship, since 01.09.2010)
Lee Hong, Diep (Ministry of Education and Training Vietnam, till 31.03.2010; 01.10.2010-14.03.2011)
Mildner, Maria (self-financed, 01.10.-31.10.2010)
Sarahnova, Petra (DAAD, 28.10.2010-07.02.2011; since 04.10.2011)
Schallau, Anna, Dr. (self-financed/IPK, 11.08.2010-28.02.2011)

Goals

Analysis of gene networks during gametophyte development and embryogenesis.

Research Report

The group deals with the molecular dissection of genetic and epigenetic pathways that control sexual and asexual plant reproduction including zygotic, apomictic, somatic and androgenetic processes.

In *Hypericum,* we have identified and characterised *HAPPY*, a locus which co-segregates with **apospory**, an important component of **apomixis** (A. Schallau, A.J. Johnston, D. Köszegi; cooperation with G. Barcaccia, Italy). Apospory is inherited as a dominant simplex locus at the tetraploid level. An apospory-specific CAPS marker has been applied to isolate both sexual (150 kb) and aposporous alleles (400 kb) of the *HAPPY* locus. The apo-linked allele contains destroyed genes, is extended by the insertion of copia-like transposons and composed of three contributing sexual loci (collaboration with research groups Expression Mapping, Apomixis and Experimental Taxonomy).

Another approach concerns the identification of regulatory networks that control **gametophytic development**. Based on egg cell-specific genes of wheat (A. Czihal), we discovered a novel class of transcription factors in *Arabidopsis*, designated as RKD factors (D. Köszegi, A.J. Johnston, O. Kirioukhova). The plant-specific occurrence, egg cell-specific expression, the mis-expression phenotype and evolutionary conservation identify RKD factors as key regulators of female gamete identity (see Fig. 37). Ectopic expression of RKD genes causes the reprogramming of sporophytic cells to adopt aspects of egg cell identity (Köszegi et al. 2011). Currently, we aim to identify promoter regions responsible for egg cell-specific expression (A. Czihal, M. Mildner, D. Köszegi) and to isolate multiple mutants in *RKD* genes, also including the TALEN technology (O. Kirioukhova, D. Köszegi, A.J. Johnston; cooperation with J. Boch, Halle/S.).

Fig. 37
Egg cell-specific promoter activity of a RKD-controlled gene (D. Köszegi).

We concluded work on the regulation of gene expression during **late embryogenesis**. ChIP-chip experiments and transcriptome analysis has been applied to identify putative target genes of the transcription factors LEC1 and ABI3 (A. Junker, collaboration with research group Phytoantibodies and research group Expression Mapping). These approaches suggest novel phytohormone-mediated functions of LEC1 during embryogenesis and skotomorphogenic growth and identify 98 target genes of ABI3, representing the ABI3 regulon.

In an attempt to understand the molecular reprogramming events during androgenesis as basis for the application of double haploid technology in crop plants, we have analysed differential gene expression during **pollen embryogenesis**. Deep sequencing of the transcriptome of isolated microspores resulted in the identification of candidate genes likely to be involved in the control of this process (C. Gryzcka, D. Köszegi, A. Czihal, collaboration with research group Plant Reproductive Biology).

We have further contributed to the functional characterisation of a novel family of transcription factors, EFFECTOR OF TRANSCRIPTION (ET). ET factors function as regulators of other **transcription factors** and participate in the control of cell differentiation, including processes during plant reproduction (L.H. Diep, A.J. Johnston).

Further work, coordinated by A. J. Johnston, concerns the characterisation of a plant homologue of the mammalian tumour and cell cycle suppressor RETINOBLASTOMA (pRB) involved in the control of **cell fate of gametes**. RBR is a key component of regulatory network controlling DNA and histone methylation during gametic development. Based on a newly isolated, genetically characterised hypomorphic homozygous *rbr* mutant we investigate a novel role for RBR pathway during early germline development. Preliminary data suggest that acute reduction of RBR leads to the initiation of events similar "apomeiosis" (R. Lemcke, O. Kiroukhova, D. Köszegi; collaboration with W. Gruissem, Zürich). We have also identified putative target genes of RBR that are derepressed in this mutant as part of a novel regulatory circuit involving DNA methylation. Finally, we aim to understand the **epigenetic control of apomixis** in various *Boechera* species. We have cloned several epigenetic loci that show heterochronic gene expression in apomicitic and sexual accessions (P. Rizzo, collaboration with research group Plant Reproductive Biology). The data are anticipated to extend our knowledge on sexual and apomictic reproductive development.

Publications

Peer Reviewed Papers

2010

Aquea, F., A.J. Johnston, P. Canon, U. Grossniklaus & P. Arce-Johnson: *TRAUCO*, a *Trithorax*-group gene homologue, is required for early embryogenesis in *Arabidopsis thaliana*. J. Exp. Bot. 61 (2010) 1215-1224.

Johnston, A.J., O. Kirioukhova, P.J. Barrell, T. Rutten, J.M. Moore, R. Baskar, U. Grossniklaus & W. Gruissem: Dosage-sensitive function of *RETINOBLASTOMA RELATED* and convergent epigenetic control are required during the *Arabidopsis* life cycle. PLoS Genet. 6 (2010) e1000988.

Junker, A., A. Hartmann, F. Schreiber & H. Bäumlein: An engineer's view on regulation of seed development. Trends Plant Sci. 15 (2010) 303-307.

Schallau, A., F. Arzenton, A.J. Johnston, U. Hähnel, D. Kőszegi, F. Blattner, L. Altschmied, G. Haberer, G. Barcaccia & H. Bäumlein: Identification and genetic analysis of the APOSPORY locus in *Hypericum perforatum* L. Plant J. 62 (2010) 773-784.

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Galla, G., G. Barcaccia, A. Schallau, M. Puente Molins, H. Bäumlein & T.F. Sharbel: The cytohistological basis of apospory in *Hypericum perforatum* L. Sex. Plant Reprod. 24 (2011) 47-61.

Heckmann, S., I. Lermontova, B. Berckmans, L. De Veylder, H. Bäumlein & I. Schubert: The E2F transcription factor family regulates *CENH3* expression in *Arabidopsis thaliana*. Plant J. 68 (2011) 646-656.

Kirioukhova, O., A.J. Johnston, D. Kleen, C. Kägi, R. Baskar, J.M. Moore, H. Bäumlein, R. Gross-Hardt & U. Grossniklaus: Female gametophytic cell specification and seed development require the function of the putative *Arabidopsis* INCENP ortholog *WYRD*. Development 138 (2011) 3409-3420.

Kőszegi, D., A.J. Johnston, T. Rutten, A. Czihal, L. Altschmied, J. Kumlehn, S.E. Wust, O. Kirioukhova, J. Gheyselinck, U. Grossniklaus & H. Bäumlein: Members of the RKD transcription factor family induce an egg cell-like gene expression program. Plant J. 67 (2011) 280-291.

Lermontova, I., O. Koroleva, T. Rutten, J. Fuchs, V. Schubert, I. Moraes, D. Köszegi & I. Schubert: Knockdown of CENH3 in *Arabidopsis* reduces mitotic divisions and causes sterility by disturbed meiotic chromosome segregation. Plant J. 68 (2011) 40-50.

PhD and Diploma Theses

2010

Schallau, A.: Identification and genetic analysis of the APOSPORY locus in *Hypericum perforatum* L. (PhD Thesis) Martin-Luther-Universität Halle-Wittenberg, Naturwissenschaftliche Fakultät I, Institut für Genetik, Halle/S. (2010) 171 pp.

2011

Le, H.D.: Functional characterization of Effector of Transcription (ET) in *Arabidopsis thaliana*. (PhD Thesis) Martin-Luther-Universität Halle-Wittenberg, Naturwissenschaftliche Fakultät I, Institut für Biologie, Halle/S. (2011) 127 pp.

Lemcke, R.: The RETINOBLASTOMA pathway controls reproductive development and genome integrity in *Arabidopsis*. (Bachelor) Martin-Luther-Universität Halle-Wittenberg, Halle/S. (2011) 43 pp.

Mildner, M.: Funktionelle Charakterisierung von Eizell-aktiven RKD-Faktoren in *Arabidopsis thaliana*. (PhD Thesis) Martin-Luther-Universität Halle-Wittenberg, Halle/S. (2011) 128 pp.

Research Group: Phytoantibodies

Head: Dr. Udo Conrad

Scientists

IPK financed
Mönke, Gudrun, Dr.

Grant Positions
Weichert, Nicola, Dr. (BMBF, since 01.01.2011)
Hauptmann, Valeska (0.50 Saxony-Anhalt, till 28.02.2011)

Visiting Scientists/Scholars
Herrmann, Isabella (Martin Luther University Halle-Wittenberg, till 30.06.2010)
Hoang, Phan Trong (DLR)
Huu Cuong, Nguyen, Dr. (DAAD, 08.08.-04.10.2010)
Sarriòn Perdigones, Alejandro (Instituto de Biologia Molecular y Celular de Plantas Valencia, Spain, (17.09.-19.11.2011)

Goals

Production of recombinant fiber proteins, recombinant vaccines, recombinant therapeutic antibodies in transgenic plants, tissue- and development-specific immunomodulation of phytohormone functions in transgenic plants and molecular analysis of seed development by chromatin IP method for the molecular analysis of seed development.

Research Report

Molecular Farming experiments were performed with recombinant spider silk proteins to develop new materials for technical and medical purposes in plants. A set of dragline silk protein (MaSpI, MaSpII) and flagelliform silk (FLAG) protein expression vectors containing 2 to 4 spider silk elements and 1 ELP element has been designed and transiently expressed in tobacco (V. Hauptmann). We further developed the concept of multimeric spider silk **proteins by the transglutaminase-based dimerisation**. Here the purification of the monomers and of the dimers has been essentially improved by the **development and adaptation of a membrane-based Inverse Transition Cycling** procedure (N. Weichert, P.T. Hoang). Flagelliform spider silk-like protein expression vectors have been designed, that allow intein-based trans-splicing. Native-sized flagelliform silk multimers up to a molecular weight of 500 kDa have been produced in transiently and stably transformed tobacco leaves. Mutations in the relevant amino acid coding sequences in the intein region resulted in the expression of non-spliced monomers after transformation into tobacco, thus showing that the multimerisation is due to intein function. After affinity purification, desalting and concentration by ultrafiltration with high size exclusion (150 kDa) the FLAG protein multimers were lyophilised and could be dissolved in HFIP but not in water (N. Weichert, V. Hauptmann, M. Gils, U. Conrad). Raster scanning electron microscopic pictures of this material show extended nanofibers (M. Menzel, U. Spohn, Fraunhofer IWM Halle).

Different antigens from the bird flue virus H5N1 (hemagglutinin, neuraminidase, matrix protein) with and without ELP have been stably expressed in tobacco leaves and seeds. An **mITC technology for plant-expressed ELPylated proteins** has been developed and applied for hemagglutinin and neuraminidase. The quality of these antigens (no proteolysis, high activity in the case of neuraminidase) has been highly improved. 95 % of the antigens in the plant crude extract could be recovered using this improved purification method. Fusion of a Leucin zipper-based trimerisation motif to the C-terminus of hemagglutinin caused the expression of **hemagglutinin trimers** in tobacco plants. The expression of full-length hemagglutinin (inclusive membrane domain and cytoplasmic tail) using a secretion vector (signal peptide, no KDEL) allowed the formation and isolation of **virus-like-particles (VLPs) from tobacco** plants. These particles as well as inactivated viruses and hemagglutinin trimers were active in a standard hemagglutination assay. Immunisation studies with mice showed, that only by **immunisation with trimers** of hemagglutinin **antibodies inhibiting the activity of VLPs** in the hemagglutination assay (potentially neutralising antibodies) could be raised (P.T. Hoang, U. Conrad, J. Veits, FLI Riems, F. Rabenstein, JKI Quedlinburg). Different hemagglutinin variants (fused to ELP and to hydrophobin) have been expressed in tobacco seeds and are currently investigated according subcellular localisation (P.T. Hoang, E. Arcalis, BOKU Vienna).
Re-screening of synthetic Phage Display Libraries based on cameloid VHH led to the isolation of **new specific nanobodies against human TNFalpha** with binding behavior and TNFalpha-neutralising capacity comparable to the parental antibody (library basis), but with either completely changed CDR1 or CDR3 sequence (U. Conrad, J. Scheller, University Düsseldorf).

To understand the role of ABI3, a seed-specific transcription factor, we in more detail identified **genome-wide target genes** of this transcription factor, employing ChIP-chip technology, transcriptome analysis, qRT-PCR and a transient promoter activation assay. 98 genes were verified by at least two methods to be activated by ABI3. Most of the genes fit to functions in seed development based on gene ontology terms. Several gene functions are still unknown. The related transcription factor **FUS3 activates more than one third of the ABI3 target genes**, proofed by qRT-PCR. Within the 98 promoters of the ABI3 target genes G-box (CACGTG) – like and/or RY (CATGCA)-like motifs were discovered using the Dispom algorithm (G. Mönke, J. Keilwagen, L. Altschmied, H. Bäumlein).

In vitro binding studies of ABI3 and FUS3 to variants of the RY motif showed that one exchange of the first five nucleotides prevents binding completely. Only the last A can be partially replaced by G. *In vivo* activation studies are going on (G. Mönke, U. Conrad).

The experiments according immunomodulation of ABA functions in barley and pea are reported by the Seed Development group.

Publications

Peer Reviewed Papers

2010

Floss, D.M., M. Mockey, G. Zanello, D. Brosson, M. Diogon, R. Frutos, T. Bruel, V. Rodrigues, E. Garzon, C. Chevaleyre, M. Berri, H. Salmon, U. Conrad & L. Dedieu: Expression and immunogenicity of the mycobacterial Ag85B/ESAT-6 antigens produced in transgenic plants by Elastin-like peptide fusion strategy. J. Biomed. Biotechnol. (2010) 274346.

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Giersberg, M., D.M. Floss, S. Kipriyanov, U. Conrad & J. Scheller: Covalent dimerization of camelidae anti-human TNF-alpha single domain antibodies by the constant kappa light chain domain improves neutralizing activity. Biotechnol. Bioeng. 106 (2010) 161-166.

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Vogel, M., M. Lawson, W. Sippl, U. Conrad & W. Roos: Sanguinarine reductase – structure and mechanism of an enzyme of alkaloid detoxication. J. Biol. Chem. 285 (2010) 18397-18406.

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Conrad, U., I. Plagmann, S. Malchow, M. Sack, D.M. Floss, A.A. Kruglov, S.A. Nedospasov, S. Rose-John & J. Scheller: ELPylated anti-human TNF therapeutic single-domain antibodies for prevention of lethal septic shock. Plant Biotechnol. J. 9 (2011) 22–31.

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Phan, H.T. & U. Conrad: Membrane-based inverse transition cycling: an improved means for purifying plant-derived recombinant protein-elastin-like polypeptide fusions. Int. J. Mol. Sci. 12 (2011) 2808-2821.

Saumonneau, A., K. Rottier, U. Conrad, Y. Popineau, M. Francin-Allami & J. Gueguen: Expression of a new chimeric protein with a highly repeated sequence in tobacco cells. Plant Cell Rep. 30 (2011) 1289-1302.

Books and Book Chapters

2010

Conrad, U. & D.M. Floss: Expression of antibody fragments in transgenic plants. In: Kontermann, R. & S. Dübel (Eds.): Antibody Engineering, Vol. 2 (2nd edition). Springer-Verlag, Berlin-Heidelberg (2010) 377-386.

Floss, D.M. & U. Conrad: Expression of complete antibodies in transgenic plants. In: Kontermann, R. & S. Dübel (Eds.): Antibody Engineering, Vol. 1 (2nd edition). Springer-Verlag, Berlin-Heidelberg (2010) 489-502.

PhD and Diploma Theses

2010

Gastaldello, J.: Funktionelle Charakterisierung neuer anti hTNFα VHH cameloid nanobodies. (Bachelor Thesis) Hochschule Anhalt, Köthen (2010) 84 pp.

Kunze, M.: Charakterisierung des Abscisinsäure-Rezeptor bindenden Antikörpers anti-RCAR1. (Bachelor Thesis) Martin-Luther-Universität Halle-Wittenberg, Naturwissenschaftliche Fakultät I, Institut für Biochemie und Biotechnologie, Halle/S. (2010) 50 pp.

2011

Banik, A.: Funktionelle Charakterisierung von rekombinanten Antikörpern gegen Abszisinsäurerezeptoren. (Bachelor Thesis) Martin-Luther-Universität Halle-Wittenberg, Halle/S. (2011) 55 pp.

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Pohl, J.: Produktion von oligomeren Vogelgrippeantigenen als ELP-Fusionsproteine in Pflanzen. (Bachelor Thesis) Hochschule Anhalt, Köthen (2011) 67 pp.

Rother, E.: Herstellung und Charakterisierung von scFv´s gegen den Phytohormonrezeptor RCAR1. (Bachelor Thesis) Hochschule Mittweida, Mittweida (2011) 69 pp.

Ziermann, H.: Untersuchungen zur Sequenzspezifität der Bindung von Transkriptionsfaktoren an DNA. (Bachelor Thesis) Martin-Luther-Universität Halle-Wittenberg, Halle/S. (2011) 48 pp.

Patents

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Conrad, U. & M. Giersberg: „Fusionsantikörper". WO 2010/079149, Anmeldetag: 09.01.2009, Offenlegung: 15.07.2010, IPK Nr. 2008/10.

Conrad, U., M. Giersberg, S. Kiprijanov & S. Hähnel: "Proteolytically stable antibody formats". WO 2010/040545, Anmeldetag: 06.10.2008, Offenlegung: 15.04.2010, IPK Nr. 2008/09.

Research Group: Expression Mapping (till 31 July 2011)

Head: Dr. Lothar Altschmied

Scientists

IPK financed
Witkowicz, Justyna, Dr. (till 30.06.2010)

Visiting Scientists/Scholars
Hähnel, Urs, Dr. (Julius Kühn-Institute Quedlinburg, till 16.05.2010)

Goals

Characterisation of the physical structure of the apomeiosis locus of *Hypericum perforatum*. Analysis of promoter structure and transcription factors responsible for seed-specific gene expression in *Arabidopsis thaliana*.

Research Report

BAC clones containing the apomictic allele of the apomeiosis locus of *Hypericum perforatum* (HAPPY) had been isolated by A. Schallau and A. Czihal (Gene Regulation group), sequenced (A. Himmelbach, Genome Diversity group and S. König, Transcriptome Analysis group), and assembled (B. Steuernagel, Bioinformatics and Information Technology group). Annotation of these clones (L. Altschmied), which constitute at least 400 kbp of the apomeiosis locus, revealed, that besides pieces of genes known from the sexual allele of this locus (from plants with sexual mode of reproduction), pieces of additional genes are present within the locus. Judged on the available sequence information, none of the gene pieces in the apomeiosis locus represents a functional gene, because reading frames are interrupted by stop codons, frame shifts and transposon insertions. Hybridisation of probes derived from these additional gene pieces with high-density colony filters (D. Fiedler) of *Hypericum* BAC libraries from sexual and apomictic plants demonstrated that the additional gene pieces originate from two sexual loci. BAC clones containing these two loci were isolated from plants reproducing sexually (I. Dommes, D. Fiedler), sequenced (A. Himmelbach, Genome Diversity group and S. König, Transcriptome Analysis group) assembled (B. Steuernagel, Bioinformatics and Information Technology group), and are being annotated currently (L. Altschmied). In addition, BAC clones from apomictic plants containing all three sexual loci known to contribute to the apomeiosis locus were identified (L. Altschmied, D. Fiedler) and will be sequenced. These sequences may help to answer the question, if sexual alleles in the genome of apomictic plants do accumulate mutations according to a process known as Muller's ratchet.

Annotation of the 400 kbp HAPPY locus sequence revealed a complex pattern of repeats involving pieces of genes of the three contributing sexual loci separated by long regions containing mostly transposons. Pieces of the NPH3 gene for instance occur three times, two times in tandem and once in an inverted orientation. Despite this complicated structure and the repetitive nature of most of the sequences within the locus, a chromosome walking strategy was applied, to extend BAC coverage of the HAPPY locus. Seven BAC clones on one side and three clones on the other side of the contig were identified (D. Fiedler, L. Altschmied) using hybridisation and PCR strategies to distinguish the sexual and various apomictic alleles. The longest and least overlapping clone was chosen on either side of the contig and sequenced (A. Himmelbach, Genome Diversity and S. König, Transcriptome Analysis).

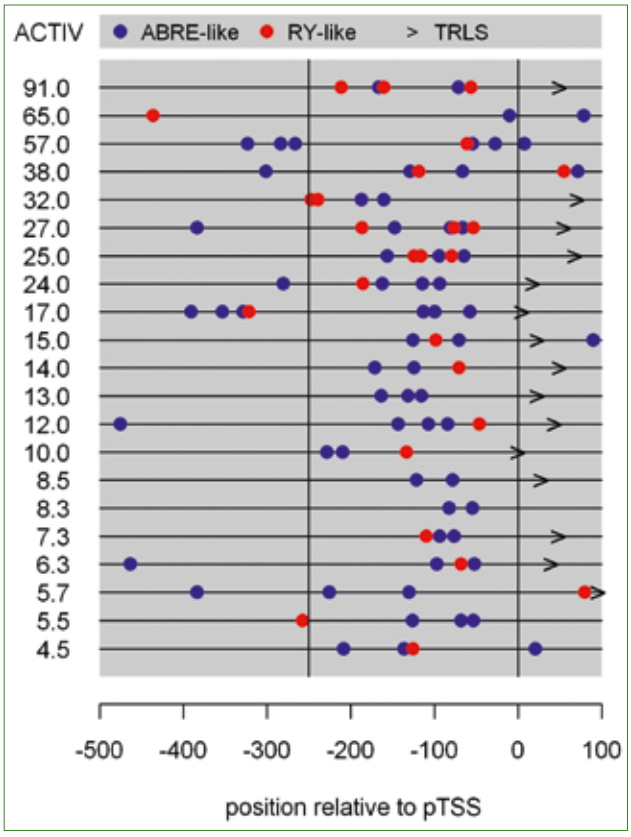

Fig. 38
Sequence motifs in 21 promoter regions of *Arabidopsis*, which were enriched by chromatin immuno-precipitation and activated by the B3-domain transcription factor ABI3 in transiently transformed protoplasts. ACTIV: ratio of reporter gene expression with and without ABI3; ABRE-like: sequence motifs with similarity to abscisic acid response elements; RY-like: sequence motifs with similarity to the RY binding site of B3-domain transcription factors; pTSS: potential transcription start site; TRLS: translation start site. (G. Mönke, Phytoantibodies; M. Seifert, Data Inspection; U. Hähnel, L. Altschmied).

To extend our work on promoters regulated by the transcription factor (TF) ABI3 and most likely, some bZIP TFs during seed development of *Arabidopsis thaliana*, we established cultivation and protoplast transformation of an embryogenic cell culture system (S. Drießlein) available from the research group Gene Regulation (Fig. 38). Three *Arabidopsis* promoters were selected based on their content of potential TF binding sites. Their fusions with a GUS reporter gene were investigated for regulation by ABI3 and the bZIP TFs EEL, ABI5, bZIP67, bZIP10, and bZIP53 in transiently tranformed protoplasts. All three promoters are regulated by ABI3, EEL, ABI5, and the combination of bZIP10 and 53, but not by bZIP10 or 53 alone (S. Drießlein, L. Altschmied). One of the selected promoters does not contain any recognisable RY element, the only confirmed binding site for ABI3, still it is regulated by ABI3. Currently, potential binding sites for bZIP factors in this promoter are mutagenised (D. Fiedler, S. Drießlein, L. Altschmied) to investigate, if ABI3 regulation depends on their presence and may be mediated by promoter bound bZIP TFs.

Publications

Peer Reviewed Papers

2010

Himmelbach, A., L. Liu, U. Zierold, L. Altschmied, H. Maucher, F. Beier, D. Müller, G. Hensel, A. Heise, A. Schützendübel, J. Kumlehn & P. Schweizer: Promoters of the barley germin-like *GER4* gene cluster enable strong transgene expression in response to pathogen attack. Plant Cell 22 (2010) 937-952.

Schallau, A., F. Arzenton, A.J. Johnston, U. Hähnel, D. Koszegi, F. Blattner, L. Altschmied, G. Haberer, G. Barcaccia & H. Bäumlein: Identification and genetic analysis of the APOSPORY locus in *Hypericum perforatum* L. Plant J. 62 (2010) 773-784.

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Kőszegi, D., A.J. Johnston, T. Rutten, A. Czihal, L. Altschmied, J. Kumlehn, S.E. Wust, O. Kirioukhova, J. Gheyselinck, U. Grossniklaus & H. Bäumlein: Members of the RKD transcription factor family induce an egg cell-like gene expression program. Plant J. 67 (2011) 280-291.

Research Group: Plant Bioinformatics

Head: Prof. Falk Schreiber

Scientists

IPK financed
Baghalian, Kambiz, Dr. (0.50, since 01.12.2011)
Hartmann, Anja (15.09.2010-28.02.2011)
Klukas, Christian, Dr. (till 30.04.2010)
Mehlhorn, Hendrik (Pakt für Forschung und Innovation, since 01.03.2011)
Rohn, Hendrik (01.03.-30.11.2011)

Grant Positions
Czauderna, Tobias (BMBF)
Grafahrend-Belau, Eva (0.50/0.75/1.00 BMBF)
Hartmann, Anja (BMBF, till 14.09.2010; since 01.03.2011)
Junker, Astrid, Dr. (1.00/0.50 BMBF)
Klapperstück, Matthias (Industry, since 01.04.2010)
Mehlhorn, Hendrik (BMBF, till 28.02.2011)
Rohn, Hendrik (BMBF, till 28.02.2011)

Visiting Scientists/Scholars
Asgari, Yasdan (University of Tehran, 22.06.-21.08.2011)
Baghalian, Kambiz, Dr. (self-financed, 03.04.-30.11.2011)
Masoudi-Nejad, Ali, Prof. (DAAD, 01.08.-10.09.2010)
Schlüter, Urte, Dr. (University of Erlangen/IPK, 18.07.-21.07.2010)
Wybrow, Michael, Dr. (Monash University, 19.08.-27.08.2010)

Goals

Representing, analysing, modelling and visualising biological networks and related data; visual analytics of multimodal biological data.

Research Report

We continued the development of our open source system **VANTED** (H. Rohn, C. Klukas, www.vanted.org, now available in version 2.0) for analysing experimental data in the context of biological networks. Novel algorithms allow easy data integration, exploration and analysis, for example, to integrate metabolic and regulatory knowledge or to identify over-representation of significantly expressed genes in pathways. VANTED has been used in many in-house and external collaborations such as investigating metabolism in *Hordeum vulgare* and *Brassica napus* (E. Grafahrend-Belau, M. Klapperstück with research groups Heterosis, Molecular Plant Nutrition, Systems Biology, MLU Halle-Wittenberg, Bayer CropScience, and *SunGene*), analysing metabolic and regulatory networks in *Beta vulgaris* (H. Mehlhorn with research group Applied Biochemistry), exploring pathway-related gene expression data for *Boechera holboellii* and *Mus musculus* (C. Klukas, H. Mehlhorn with research group Apomixis and MLU Halle-Wittenberg), and integrating multimodal data to identify metabolic processes and key genes that correlate positive with high biomass production for *Zea mays* (A. Hartmann with research group Bioinformatics and Information Technology, University Erlangen-Nürnberg, and University Düsseldorf).
In addition, several add-ons of VANTED have been developed: **Hive** (H. Rohn, www.vanted.org/hive) combines manyfold biological data types and supports the integration of spatial, structural, and kinetic models and data. Application examples include exploring image databases using biological networks, and investigating multimodal data of *Hordeum vulgare* (with research groups Heterosis and Systems Biology). **SBGN-ED** (T. Czauderna, www.sbgn-ed.org) supports the Systems Biology Graphical Notation (SBGN, www.sbgn.org) and allows the creation and editing of all three types of SBGN maps, the validation of their syntactical and semantical correctness, and the translation of already existing non-SBGN diagrams into SBGN. In 2010 and 2011 SBGN-ED won first prizes for the best SBGN software support in the annual SBGN competition. SBGN-ED has been extensively used for knowledge representation in biology, such as the RIMAS portal for *Arabidopsis thaliana*, MetaCrop for several plant species, as well as a map about plant metabolism which was awarded first prize for the best SBGN map in the 2010 SBGN competition. **CentiLib** (J. Gräßler, D. Koschützki, http://centilib.ipk-gatersleben.de) is a library for computing and investigating weighted and unweighted centralities in biological networks. CentiLib provided the algorithmical environment for investigating the structure of metabolic and gene regulatory networks in *E. coli*. **NETS** (H. Mehlhorn) is an easy to use system for integrating biological networks from various data sources and different domains. The flexible identifier mapping support includes synonyms and transitive identifier mapping paths. Experimental data can be mapped and analysed in related pathways, a methodology used, for example, to investigate differentially expressed genes in *Zea mays* and *Arabidopsis thaliana* (H. Mehlhorn, A. Junker, A. Hartmann with research groups Heterosis and Bioinformatics and Information Technology, University Erlangen-Nürnberg, and University Düsseldorf). **FluxMap** (H. Rohn, www.vanted.org/fluxmap, cooperation with research group Systems Biology) enables users to easily import and visualise simulated and measured flux data in the context of biological networks. Interactions enable switching between and comparing of different flux distributions for different species, or even enrich these flux maps by other *omics data.
The development of the **MetaCrop information system** for metabolic pathway information has been continued (M. Klapperstück, metacrop.ipk-gatersleben.de, cooperation with research groups Bioinformatics and Information Technology and Systems Biology), and MetaCrop 2.0 has been released. New features include web services, private data spaces, SBGN support,

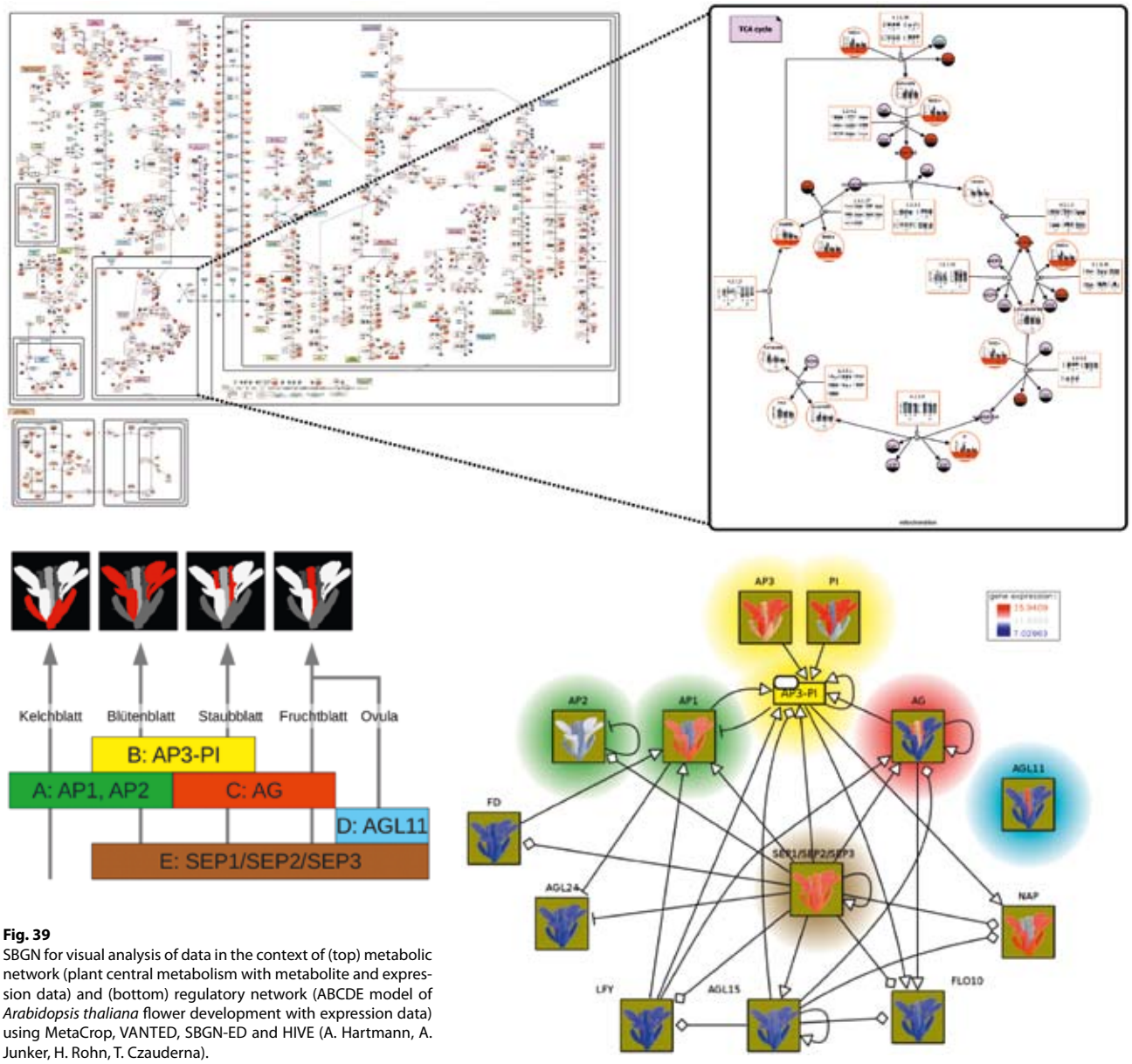

Fig. 39
SBGN for visual analysis of data in the context of (top) metabolic network (plant central metabolism with metabolite and expression data) and (bottom) regulatory network (ABCDE model of *Arabidopsis thaliana* flower development with expression data) using MetaCrop, VANTED, SBGN-ED and HIVE (A. Hartmann, A. Junker, H. Rohn, T. Czauderna).

and direct access from VANTED. Based on intensive surveys of scientific literature, the MetaCrop content has been extended to detailed information about 62 pathways based on over 1,800 publications (E. Grafahrend-Belau, A. Hartmann, A. Junker cf. Fig. 39). In addition, the **DBE2 information system** for managing biological experiment data has been further developed (H. Mehlhorn) and now provides web services and a seamless integration into VANTED. DBE2 is used in several in-house and external collaborations for managing experimental data which is analysed with the VANTED system.

Information in MetaCrop is the basis for **stoichiometric models**, and several stoichiometric, compartmented models have been developed and analysed, such as developing endosperm of *Hordeum vulgare*, developing embryo of *Medicago truncatula*, developing embryo of *Pisum sativum* and source leaf in *Zea mays* (E. Grafahrend-Belau, A. Hartmann, A. Junker with research groups Heterosis and Systems Biology). The models provide frameworks for studying metabolism *in silico* with flux balance analysis (FBA) and related methods and allow predicting flux distributions and optimal metabolic capabilities under different environmental conditions and genetic backgrounds. An example is the simulation of endosperm metabolism in Jekyll down-regulated plants and Risø13 mutants to elucidate the maternal and filial effects on sugar allocation within the barley seed, where model predictions gave new insights into the response of seed storage metabolism to variation in the supply of sucrose. Mathematical methods and models for **multiscale modelling of metabolism** combining different modelling approaches have been further developed. For an example in *Hordeum vulgare*, three stoichiometric models representing seed, source leaf, and culm have been generated (E. Grafahrend-Belau, A. Junker, cooperation with research group Systems Biology) and will be coupled, including parameters derived from a barley household model, to develop strategies aiming at the increase of the efficiency of CO_2 assimilation, solar energy fixation, and biomass production.

In an international collaboration with various partners the **Systems Biology Graphical Notation (SBGN),** representing a standard for the display and handling of biological networks, has been further developed. Several **tools and resources** were established in the group which will facilitate and exemplify the use of SBGN for biologists such as SBGN-ED, MetaCrop SBGN-pathways, RIMAS, SBGN bricks, and LibSBGN. **RIMAS** is a web-based information portal which provides a comprehensive overview of regulatory pathways and genetic interactions during *Arabidopsis thaliana* embryo and seed development (A. Junker, with research group Gene Regulation). The brick concept (adapted from Synthetic Biology) has been transferred to SBGN (A. Junker). Fundamental biological patterns are translated into a limited number of re-useable **SBGN bricks** for assembly into larger networks. A dictionary comprising an initial set of bricks has been generated and will be available for download. The use of SBGN bricks will simplify the way biologists can work with SBGN.

In collaboration with external partners several novel **algorithms for structural network analysis** and **automatic network layout** (D. Koschützki, T. Czauderna, H. Rohn) and very **efficient algorithms using parallel architectures** such as the Cell processor or GPGPUs have been developed. For the non-destructive high-throughput phenotyping system LemnaTec we continued the development of the **image analysis pipeline HTPheno** (htpheno.ipk-gatersleben.de) to compute phenotypic parameters such as plant height, plant width, and leaf area from images (A. Hartmann). The results of the analysis have been used in projects to derive biological insights, such as in drought stress during plant development in *Hordeum vulgare* (A. Hartmann with research group Genome Diversity). The development of image analysis algorithms has been transferred to the newly established research group Image Analysis (C. Klukas).

Publications

Peer Reviewed Papers

2010

Banaei Moghaddam, A.M., J. Fuchs, T. Czauderna, A. Houben & M.F. Mette: Intraspecific hybrids of *Arabidopsis thaliana* revealed no gross alterations in endopolyploidy, DNA methylation, histone modifications and transcript levels. Theor. Appl. Genet. 120 (2010) 215-226.

Czauderna, T., C. Klukas & F. Schreiber: Editing, validating, and translating of SBGN maps. Bioinformatics 26 (2010) 2340-2341.

Hippe, K., C. Colmsee, T. Czauderna, E. Grafahrend-Belau, B.H. Junker, C. Klukas, U. Scholz, F. Schreiber & S. Weise: Novel developments of the MetaCrop information system for facilitating systems biological approaches. J. Integr. Bioinform. 7 (2010) e125.

Junker, A., A. Hartmann, F. Schreiber & H. Bäumlein: An engineer's view on regulation of seed development. Trends Plant Sci. 15 (2010) 303-307.

Klukas, C. & F. Schreiber: Integration of -omics data and networks for biomedical research with VANTED. J. Integr. Bioinform. 7 (2010) 112.

Koschützki, D., B.H. Junker, J. Schwender & F. Schreiber: Structural analysis of metabolic networks based on flux centrality. J. Theor. Biol. 265 (2010) 261-269.

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Sharbel, T.F., M.L. Voigt, J.M. Corral, G. Galla, J. Kumlehn, C. Klukas, F. Schreiber, H. Vogel & B. Rotter: Apomictic and sexual ovules of *Boechera* display heterochronic global gene expression patterns. Plant Cell 22 (2010) 655-671.

Weidemann, W., C. Klukas, A. Klein, A. Simm, F. Schreiber & R. Horstkorte: Lessons from GNE-deficient embryonic stem cells: Sialic acid biosynthesis is involved in proliferation and gene expression. Glycobiology 20 (2010) 107-117.

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Hartmann, A., T. Czauderna, R. Hoffmann, N. Stein & F. Schreiber: HTPheno: An image analysis pipeline for high-throughput plant phenotyping. BMC Bioinformatics 12 (2011) 148.

Mehlhorn, H. & F. Schreiber: DBE2 – management of experimental data for the VANTED system. J. Integr. Bioinform. 8 (2011) 162.

Melkus, G., H. Rolletschek, J. Fuchs, V. Radchuk, E. Grafahrend-Belau, N. Sreenivasulu, T. Rutten, D. Weier, N. Heinzel, F. Schreiber, T. Altmann, P.M. Jakob & L. Borisjuk: Dynamic (13) C/(1) H NMR imaging uncovers sugar allocation in the living seed. Plant Biotechnol. J. 9 (2011) 1022-1037.

Rohn, H., C. Klukas & F. Schreiber: Creating views on integrated multidomain data. Bioinformatics 27 (2011) 1839-1845.

Rohn, H., C. Klukas & F. Schreiber: Visual analytics of multimodal biological data. Proceedings of the International Conference on Information Visualization Theory and Applications (IVAPP'11). SciTePress (2011) 256-261.

Rolletschek, H., G. Melkus, E. Grafahrend-Belau, J. Fuchs, N. Heinzel, F. Schreiber, P.M. Jakob & L. Borisjuk: Combined noninvasive imaging and modeling approaches reveal metabolic compartmentation in the barley endosperm. Plant Cell 23 (2011) 3041-3054.

Weise, S., J. Chen, B.H. Junker, M. Klapperstück, M. Lange, F. Schreiber & U. Scholz: Das Informationssystem MetaCrop zur Unterstützung systembiologischer Forschung an Kulturpflanzen. it – Information Technology 53 (2011) 234-240.

Books and Book Chapters

2010

Albrecht, M., A. Kerren, K. Klein, O. Kohlbacher, P. Mutzel, W. Paul, F. Schreiber & M. Wybrow: On open problems in biological network visualization. In: Eppstein, D. & E.R. Gansner (Eds.): Graph Drawing, Proc. 17th Int. Symp. on Graph Drawing, LNCS, Vol. 5849. Springer (2010) 256-267.

Schreiber, F.: Representation and analysis of biological networks with the Vanted toolsuite. In: Hofestädt, R. & N. Kolchanov (Eds.): German/Russian Network of Computational Systems Biology, Berichte aus der Medizinischen Informatik und Bioinformatik. Shaker Verlag (2010) 47-50.

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2010

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Czauderna, T., C. Klukas & F. Schreiber: SBGN-ED. http://vanted.ipk-gatersleben.de/addons/sbgn-ed (2010).

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Klukas, C. & F. Schreiber: VANTED. http://vanted.ipk-gatersleben.de (2010).

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Rohn, H., C. Klukas & F. Schreiber: HIVE. http://vanted.ipk-gatersleben.de/addons / hive (2010).

Weise, S., I. Grosse, C. Klukas, D. Koschützki, U. Scholz, F. Schreiber & B.H. Junker: Meta-All: A system for managing metabolic pathway information. http://meta-all.ipk-gatersleben.de (2010).

2011

Czauderna, T. & F. Schreiber: SBGN-ED. http://www.sbgn-ed.org (2011).

Rohn, H., C. Klukas & F. Schreiber: Vanted 2.0. http://www.vanted.org (2011).

Schreiber, F., C. Colmsee, T. Czauderna, E. Grafahrend-Belau, A. Hartmann, A. Junker, B.H. Junker, D. Koschützki, U. Scholz & S. Weise: MetaCrop 2.0. http://metacrop.ipk-gatersleben.de (2011).

van Iersel, M.P., S.E. Boyd, F. Bergmann, S. Moodie, F. Schreiber, T. Czauderna, E. Demir, N. Le Novère, A. Sorokin, H. Mi, A. Luna, U. Dogrusoz, Y. Matsuoka, A. Funahashi, H. Kitano, M.I. Aladjem, M.L. Blinov & A.C. Villéger: LibSBGN. http://libsbgn.sourceforge.net (2011).

Weise, S., I. Grosse, C. Klukas, D. Koschützki, U. Scholz, F. Schreiber & B.H. Junker: Meta-All: A system for managing metabolic pathway information. http://meta-all.ipk-gatersleben.de (2011).

PhD and Diploma Theses

2010

Grässler, J.: Optimierung und Weiterentwicklung von Algorithmen und einer Bibliothek zur Berechnung von Netzwerk-Zentralitäten. (Diploma Thesis) Martin-Luther-Universität Halle-Wittenberg, Halle/S. (2010) 59 pp.

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Fröhlich, S.: Modellprüfung biologischer Systeme. (Diploma Thesis) Martin-Luther-Universität Halle-Wittenberg, Halle/S. (2011) 100 pp.

Koschützki, D.: Zentralitätsanalyse molekularbiologischer Netzwerke. (PhD Thesis) Martin-Luther-Universität Halle-Wittenberg, Halle/S. (2011) 110 pp.

Schönherr, I.S.: Assemblierung und Analyse des *Vitis vinifera*-Genoms der Rebsorte Riesling. (Bachelor Thesis) Martin-Luther-Universität Halle-Wittenberg, Institut für Informatik, Halle/S. (2011) 40 pp.

Vogt, T.: Entwicklung und Implementierung eines Algorithmus zur Übersetzung von SBGN Process Description Diagrammen in SBGN Activity Flow Diagramme. (Diploma Thesis) Martin-Luther-Universität Halle-Wittenberg, Halle/S. (2011) 62 pp.

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Klukas, C. & F. Schreiber: Integration of -omics data and networks for biomedical research. Proc. Intl. Workshop Computational and Integrative Biology – CIB2009, 18.-20.09.2009, Hangzhou, China (2009) 14-19.

Omidi, S., F. Schreiber & A. Masoudi-Nejad: MODA: An efficient algorithm for network motif discovery in biological networks. Genes Genet. Syst. 84 (2009) 385-395.

Research Group: Data Inspection

Head: Dr. Marc Strickert (till 31 January 2010)
Head: Dr. Swetlana Friedel (since 1 February 2010)

Scientists

Grant Positions
Keilwagen, Jens, Dr. (Saxony-Anhalt)
Seifert, Michael, Dr. (Saxony-Anhalt)

Goals

Processing, visualisation and interpretation of high-dimensional biological data with modern machine learning methods.

Research Report

The Data Inspection (DI) research group financed by the Ministry of Science and Economics of Saxony-Anhalt, XP 3624HP/0606T analyses a broad spectrum of high-throughput biological data sets. Our work begins where very large and/or heterogeneous data cannot be processed any more using standard statistical methods. The DI group takes a leading role in analysing those sets with modern probabilistic modeling approaches in close cooperation with biological groups inside and outside of the IPK. In addition to advanced data analyses for different IPK groups, the main focus of the DI group is on the following areas:
(1) **computational genome comparison**, (2) **motif discovery**, (3) **reverse engineering**, and (4) **data mining in the cereals collection** of the IPK Genebank.

(1) By combining the complementary strengths in epigenetics of Dr. Vincent Colot's group (Institut de Biologie de l'Ecole Normale Supérieure, France) with machine learning techniques of our group, the aim is to identify newly inserted transposable elements (TEs). First microarray experiments are already done for investigating the DNA methylation status of TEs in a population of epigenetic recombinant inbred lines (epiRILs) of *Arabidopsis thaliana*. The huge data sets resulting from these experiments will then be analysed with help of a new class of Hidden Markov Models developed by M. Seifert (http://www.jstacs.de/index.php/PHHMM) within the frame of a DAAD bilateral project.

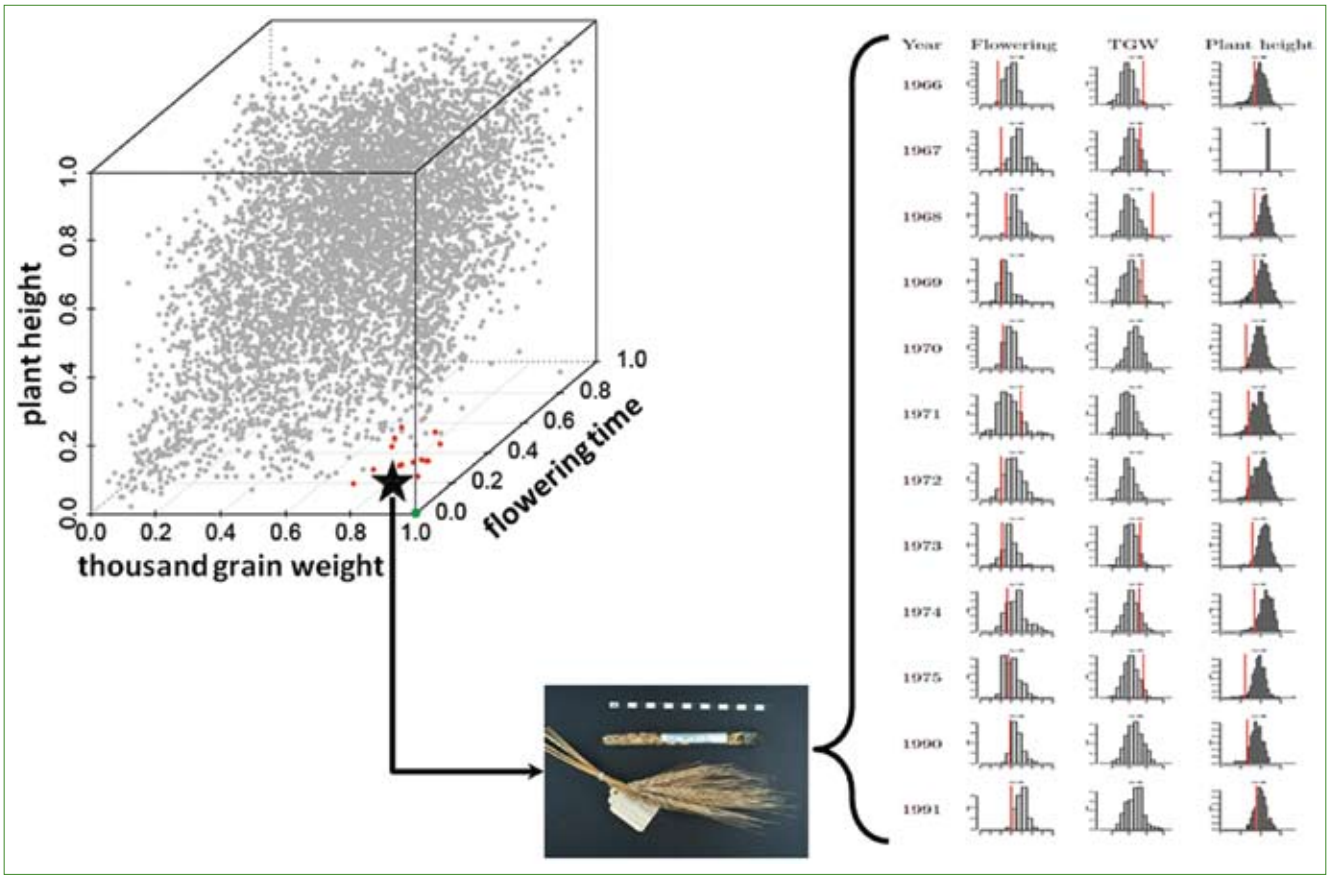

Fig. 40
The whole Genebank collection of spring barley accessions is represented in a 3-dimensional cube, where each dimension corresponds to one of three selected traits: plant height, thousand grain weight and days to flowering. Those traits are normalised according to our new statistical ranking method. This enables us to find an accession with early flowering, small plant height and high thousand grain weight, for example (indicated by the star). On the right site histograms of raw data for all cultivation years and for each trait are shown. (J. Keilwagen, S. Friedel, B. Kilian and H. Knüpffer)

(2) We developed the *de novo* motif discovery tool Dispom (http://www.jstacs.de/index.php/Dispom) for finding differentially abundant transcription factor binding sites. It models existing positional preferences of binding sites and adjusts the length of the motif in the learning process. J. Keilwagen in cooperation with colleagues from Martin Luther University Halle was able to show that the prediction performance of this tool is superior to existing tools for *de novo* motif discovery. Finally, together with the group of I. Paponov from the Albert Ludwigs University Freiburg the tool was applied for discovering binding sites enriched in promoters of auxin-responsive genes. The genes were extracted from *A. thaliana* microarray data, and a new motif was found that can be interpreted as an elongated auxin-responsive element. This result has been validated using an independent data set of auxin-responsive genes. The refined motif increased the auxin specificity by more than three orders of magnitude in genome-wide predictions compared to the canonical auxin-responsive element.

(3) With help of reverse engineering we reconstructed gene regulatory networks in *A. thaliana* under varying conditions for transcriptomic network comparison. For that we used modern information-theoretic approaches and integrated sequence analysis. Our first case study at the IPK was done together with L. Borisjuk and H. Rolletschek (research group Heterosis). We were able to show that deviations in gene regulatory interactions due to AtHb1-overexpression point to alterations in cell wall metabolism (Thiel et al. 2011).

(4) Armed with a toolkit of modern probabilistic methods, we recently focused our research on the historical IPK Genebank collection of cereals reaching back as far as 1946. The collection is one of the most important genetic resources of cereals for research and breeding. It contains a very large collection of barley and wheat accessions (~ 50,000) which we analysed first. To overcome technical and climatic biases we developed a new statistical approach for ranking the accessions. With help of this method we now can, for example, identify an optimal barley accession for any desired trait (see Fig. 40, p. 114). Based on such kind of analysis we defined groups of most contrasting accessions for an in-depth analysis. This was done together with B. Kilian from the Genome Diversity group. We were able to prove the usefulness of our methods on groups of contrasting barley accessions in a breeding approach. For the future we consider it as a big challenge to quantitatively evaluate the biodiversity in cereals. This would enable a more systematic and intelligent access to the plant genetic resources stored at the IPK Genebank for scientists and breeders world-wide.

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Books and Book Chapters

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Electronic Publications

2010

Keilwagen, J., J. Grau, A. Gohr, B. Haldemann, M. Seifert, M. Mohr, S. Posch & I. Grosse: A Java framework for statistical analysis and classification of biological sequences. http://www.jstacs.de (2010).

Oppermann, M., J. Keilwagen, H. Knüpffer, S. Friedel & A. Börner: Validation, analysis and aggregation of long-term trait observation data of genebank material. In: Weitzmann, A.L. (Ed.), Proceedings of TDWG (2010). Woods Hole, Massachusetts, USA (2010) 52-53. http://www.vliz.be/imisdocs/publications/215525.pdf (2010).

Sinha, R., T. Lenser, N. Jahn, U. Gausmann, S. Friedel, K. Szafranski, K. Huse, P. Rosenstiel, J. Hampe, S. Schuster, M. Hiller, R. Backofen & M. Platzer: Tandem Splice Site Database, TassDB2. http://gen100.imb-jena.de/TassDB2 (2010).

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Hotze, M. & S. Friedel: dCAloptimizer: A new tool for advanced codon optimization. https://www.omnifung.hki-jena.de/Rpad/dCAloptimizer.Rpad (2011).

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PhD and Diploma Theses

2010

Hotze, M.: *In silico* Sequenzoptimierung synthetischer Gene und Zuordnung des Expressionslevels über Transkriptionsanalysen am Beispiel von *Candida albicans*. (Diploma Thesis) Friedrich-Schiller-Universität, Jena (2010) 133 pp.

Keilwagen, J.: Predicting DNA binding sites using generative, discriminative, and hybrid learning principles. (PhD Thesis) Martin-Luther-Universität Halle-Wittenberg, Naturwissenschaftliche Fakultät III, Institut für Informatik, Halle/S. (2010) 131 pp.

Seifert, M.: Extensions of Hidden Markov Models for the analysis of DNA microarray data. (PhD Thesis) Martin-Luther-Universität Halle-Wittenberg, Naturwissenschaftliche Fakultät III, Institut für Informatik, Halle/S. (2010) 176 pp.

Research Group: Hybrid Wheat

Head: Dr. Mario Gils

Scientists

IPK financed
Rubtsova, Myroslava, Dr. (0.75, 01.07.-31.08.2010)

Grant Positions
Kempe, Katja, Dr. (BMBF, since 01.10.2011)
Rubtsova, Myroslava, Dr. (BMBF, till 30.06.2010; Industry, 01.09.2010-31.01.2011; BMBF, since 01.02.2011)

Goals

The establishment of a transgenic pollination control system for commercial hybrid wheat seed production.

Research Report

A split-gene approach for hybrid seed production
A precursor-T-DNA ("provector") containing two **complementary tapetum-expressed *barnase* gene fragments** is transformed into plants (see Fig. 41a). Site-specific deletions of the T-DNAs during plant development result in two alternative derivative loci, with each producing only one of the two complementary barnase precursor proteins. Crossing of plants that carry the respective complementary loci with each other leads to progeny plants harbouring the two *barnase* **gene fragments in allelic positions**. These plants are male-sterile and are used as the female crossing partners for hybrid breeding. The T1 hybrids are fertile as the *barnase* gene fragments segregate in the progeny. For the maintenance of the female crossing partner, the heterozygous plant can be crossed to a homozygous line. Given that the gene fragments conferring male sterility are linked to an herbicide tolerance gene, the heterozygous plants can be selected by applying an herbicide. The system allows for **mixed breeding** of father and mother lines. In order to increase the stability of the barnase protein complex, *barnase* gene fragments have been fused to **intein sequences** that, upon translation, covalently fuse the protein fragments autocatalytically in a process called protein-splicing.

The transformed provector constructs enable the production of **male-sterile wheat lines by *in planta* assembly of a barnase protein** (M. Gils, K. Kempe, M. Rubtsova). Male-sterility is stable over several generations and under increased temperatures, without compromising female fertility. Since the split gene system invariantly requires functional **single-copy integrations of the prolocus**, the basal vectors were modified in several steps (M. Gils). The insertion of introns for **intron-mediated enhancement of gene expression** (IME) led to a significant improvement of the split-barnase system, as been tested by transient assays in tobacco and stable transformation of wheat (M. Rubtsova, M. Gils). Three different introns were inserted into two alternative positions of the C- and N-terminal coding regions and combined in various prolocus versions (examples are given in see Fig. 41b). In oppose to the "first generation vectors", we were able to generate male-sterile wheat plants with a single-copy insertion of the prolocus. For isolocus production, a **phiC31-based site-specific recombination system** was established for wheat. The prolocus "substrate" was exposed to a phiC31 integrase encoded by a transgene that resides on a different chromosomal locus. In 34 independent lines, DNA sequences between *att* recombination sites were excised from proloci integrated in the wheat genome. We produced recombinant isoloci that were transmitted to the subsequent generation (K. Kempe, M. Rubtsova, M. Gils).

Phenotyping pollinators ("males") for hybrid wheat breeding
The objective is the development of a **semi-automatic phenotyping technology for pollination capacity** (jointly with LSA Hohenheim, J. Reif; Nordsaat GmbH, R. Schachschneider and the research group Genome Plasticity, R. Schmidt, A. Boudichevskaia). With the goal to identify suitable "father lines" for hybrid breeding, pollen traps were developed and tested in open-field trials (M. Gils, see Fig. 41c). Image analysis software facilitates a high-throughput screening of pollen amount, size and shape. By assaying several lines with different efficiency of pollen shedding, a technical proof-of-concept could be achieved.

Production of doubled haploid winter wheat
An anther culture-based technology for winter wheat was developed that regenerated high numbers of green and fertile doubled haploid plants **(DHs) from a colchicine-free anther-culture approach** with a frequency of >60 % (M. Rubtsova, in collaboration with Saaten-Union Biotec GmbH, H. Gnad, J. Weyen). Our results indicate that the external application of auxins in the induction media plays an important role for the ploidy switch.

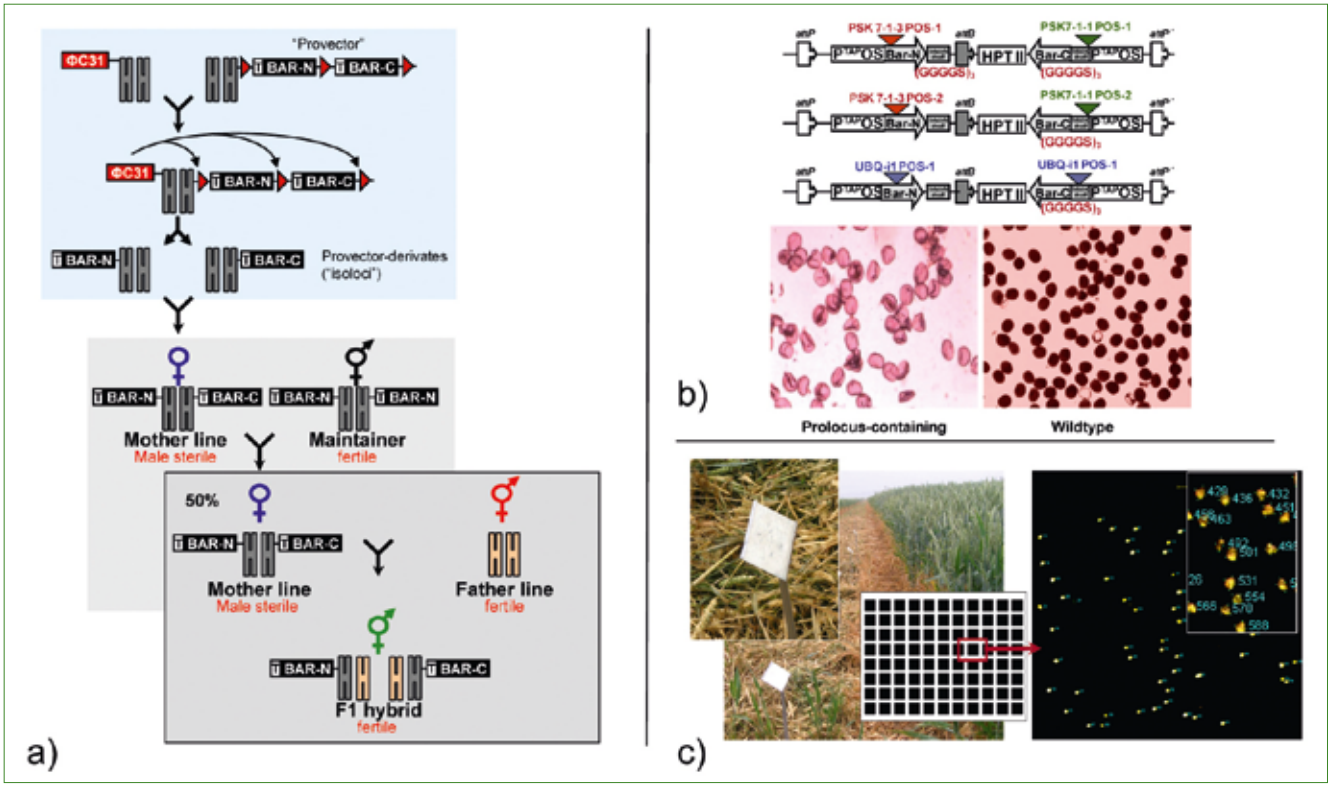

Fig. 41
a) The split-gene approach for hybrid seed production. Tapetum-specific promoter. b) A single-copy prolocus integration results in male-sterile wheat plants. c) Measurement of pollination capacities under open-field conditions and analysis of pollen size and shape (M. Gils).

Further technologies and tools developed in collaborative activities

The intein technology was used for the production of **spider silk protein multimers** in transgenic tobacco plants (jointly with U. Conrad, see report of the research group Phytoantibodies). Furthermore, **new putative intein sequences** have been identified by a database screen (in collaboration with the research group Plant Bioinformatics, F. Schreiber, H. Mehlhorn). We cloned vectors for transient assays that allow a rapid validation of the candidate sequences.

Functional phiC31-based recombination systems were established for barley (M. Rubtsova, in collaboration with the research group Plant Reproductive Biology, J. Kumlehn, E. Kapusi). A **site-specific transgene integration** system that is based on interspecific hybrids (wheat × pearl millet) is currently under development (in collaboration with Saaten-Union Biotec, J. Weyen).

Publications

Peer Reviewed Papers

2010

Kempe, K., M. Rubtsova, C. Berger, J. Kumlehn, C. Schollmeier & M. Gils: Transgene excision from wheat chromosomes by phage phiC31 integrase. Plant Mol. Biol. 72 (2010) 673-687.

2011

Kempe, K. & M. Gils: Pollination control technologies for hybrid breeding. Mol. Breed. 27 (2011) 417-437.

Research Group: Image Analysis (since 1 May 2010)

Head: Dr. Christian Klukas

Scientists

IPK financed
Entzian, Alexander (0.50/1.00, since 15.09.2010)

Goals

The research group Image Analysis focused on the development and establishment of an information system for the storage and analysis of high-throughput image data. The available infrastructure for the automated movement and imaging of plants enables researchers to collect huge amounts of image data (captured are visible light, near-infrared spectra and fluorescence). Newly developed or adapted image analysis and data integration methods as well as the usage of existing software packages enable to support researchers in investigating developmental changes and differences in selected phenotypic properties of plants.

Research Report

In 2010 and 2011 the group worked on establishing and developing the foundation for the automatic analysis of image datasets, derived from three different camera systems (visible light, fluorescence, near-infrared). The first step was the analysis of existing data structures in the LemnaTec database system and development of an access module that transforms these data sets on-demand into a form, suitable for the image analysis within the "Integrated Analysis Platform" (IAP). The newly developed Java-based information system IAP serves as a hub, providing its users multiple, easily via a web browser accessible functions for (1) investigating captured images, weight- and watering data sets within the LemnaTec database system, (2) transferring such data for long-term archival into the hierarchical storage management system (HSM) which is operated by the Bioinformatics and Information Technology group (BIT), (3) downloading complete data sets onto the researchers PCs and to (4) initiate the automated image analysis of experiments.

Automated image analysis functions have been implemented within IAP to access barley and maize plant growth (height, width, projected area, digital biomass and more) as well as to characterise relative differences in plant photosynthesis and water content by calculating intensity histograms for foreground (plant) pixels of the fluorescence and near-infrared images. The foreground/background separation has been implemented appropriately by developing new automated calibration procedures which consider and correct for the fluctuating positions of marker points, colour temperatures and noise levels. The robustness and accuracy of the image analysis procedures for barley and maize have been validated in the frame of two test runs in the automated greenhouse, suitable for maize plants.
Image analysis results may be exported as data tables or accessed using automatically generated reports (PDF files), providing parameter descriptions and diagrams showing parameter value changes over time for the different treatments and genotypes in the particular experiment under investigation. These report files are generated on demand using the statistics tool 'R' as well as the document preparation system 'LaTeX'. The IAP system incorporates the open source VANTED system and the publicly available open source image-processing library ImageJ as core libraries (C. Klukas and A. Entzian).

During 2010 and 2011 the collaboration with Prof. M. Chen from the College of Life Sciences, Zhejiang University, China has been further developed. The support in form of a travel and research grant from the National Natural Science Foundation of China (NSFC), under the frame of the "Research Fund for International Young Scientists" made it possible to work on the project "Joint development and improvement of bioinformatic tools for storage, integration and analysis of biological pathways and network-integrated visualisation of experiment data". Within this collaboration two joint publications have been completed and future joint research projects have been drafted (C. Klukas).

In collaboration with Prof. F. Schreiber and the group Plant Bioinformatics (PBI) a number of projects, for example dealing with multi-omics data integration (HIVE) and advanced data exploration techniques have been completed and resulted in joint publications (C. Klukas).

Publications

Peer Reviewed Papers

2010

Czauderna, T., C. Klukas & F. Schreiber: Editing, validating, and translating of SBGN maps. Bioinformatics 26 (2010) 2340-2341.

Hippe, K., C. Colmsee, T. Czauderna, E. Grafahrend-Belau, B.H. Junker, C. Klukas, U. Scholz, F. Schreiber & S. Weise: Novel developments of the MetaCrop information system for facilitating systems biological approaches. J. Integr. Bioinform. 7 (2010) e125.

Klukas, C. & F. Schreiber: Integration of -omics data and networks for biomedical research with VANTED. J. Integr. Bioinform. 7 (2010) 112.

Sharbel, T.F., M.L. Voigt, J.M. Corral, G. Galla, J. Kumlehn, C. Klukas, F. Schreiber, H. Vogel & B. Rotter: Apomictic and sexual ovules of *Boechera* display heterochronic global gene expression patterns. Plant Cell 22 (2010) 655-671.

Weidemann, W., C. Klukas, A. Klein, A. Simm, F. Schreiber & R. Horstkorte: Lessons from GNE-deficient embryonic stem cells: Sialic acid biosynthesis is involved in proliferation and gene expression. Glycobiology 20 (2010) 107-117.

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Huang, D., Y. Huang, Y. Bai, D. Chen, R. Hofestädt, C. Klukas & M. Chen: MyBioNet: interactively visualise, edit and merge biological networks on the Web. Bioinformatics 27 (2011) 3321-3322.

Rohn, H., C. Klukas & F. Schreiber: Creating views on integrated multidomain data. Bioinformatics 27 (2011) 1839-1845.

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Other Papers

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Huang, D., Y. Huang, C. Klukas, R. Hofestädt & M. Chen: PBSK Browser: navigate biological pathways of PSI-MI, BioPAX, SBML and KGML formats. Proceedings of the IEEE International Conference on Bioinformatics and Biomedicine Workshops (BIBMW 2010), 18.-21.12.2010, Hongkong, China (2010) 13-18.

Electronic Publications

2010

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Rohn, H., C. Klukas & F. Schreiber: HIVE. http://vanted.ipk-gatersleben.de/addons/hive (2010).

Weise, S., I. Grosse, C. Klukas, D. Koschützki, U. Scholz, F. Schreiber & B.H. Junker: Meta-All: A system for managing metabolic pathway information. http://meta-all.ipk-gatersleben.de (2010).

2011

Rohn, H., C. Klukas & F. Schreiber: Vanted 2.0. http://www.vanted.org (2011).

Weise, S., I. Grosse, C. Klukas, D. Koschützki, U. Scholz, F. Schreiber & B.H. Junker: Meta-All: A system for managing metabolic pathway information. http://meta-all.ipk-gatersleben.de (2011).

Research Group: Stress Genomics (since 1 November 2010)

Head: Dr. Nese Sreenivasulu

Scientists

IPK financed
Venkatasubbu, Thirulogachandar (0.50, since 17.04.2011)

Grant Positions
Govind, Geetha, Dr. (1.00/0.75 BMBF, since 29.11.2010)
Harshavardhan, Vokkaliga Thammegowda (0.50 BMBF, 01.11.-31.12.2010; since 01.07.2011)
Kalladan, Rajesh (0.50 Industry, since 01.04.2011)
Seiler, Christiane, Dr. (0.75 BMBF, since 01.05.2011)

Visiting Scientists/Scholars
Palakolanu, Sudhakar Reddy, Dr. (DAAD, since 06.11.2011)
Prasad, Manoj, Dr. (DLR, 18.11.-27.11.2010)
Seiler, Christiane, Dr. (self-financed, 01.11.2010-30.04.2011)
Strickert, Marc, Dr. (self-financed, since 01.11.2010)

Goals

Revealing the molecular mechanisms of yield stability under terminal drought with focus on altered grain number and seed filling efficiency.

Research Report

To understand these mechanisms integrative genomics approaches will be used to explore (a) natural genetic variation in barley by studying introgression line populations with wild barley accession donor, (b) mapping populations created from selected breeding lines of stay-green and remobilisation and (c) GMO plants of achieving ABA homeostasis using drought-induced promoters active during the generative phase. The aforementioned genetic material will be used to understand mechanisms of spikelet fertility influencing grain number as well reaching enhanced yield stability and uncompromised seed quality during grain filling under drought stress.

The BC3 double haploid *Hordeum spontaneum* 584 (BC3 DH Hs584) population containing 70 introgression lines was assessed for its performance (yield, thousand grain weight and starch content) under terminal drought and a total of 28 major QTLs (LOD score ≥3) with the hot-spot QTL on chromosome 1, 2 and 3 were detected (K. Rajesh in collaboration with M. Röder, research group Gene and Genome Mapping). Better performing introgression lines possessing a segment of the Hs584 introgression in the hot-spot QTL region (depicting minimised yield loss under terminal drought) and sensitive introgression lines (with severe yield penalty under terminal drought) have been selected to study differential responses of drought tolerance by throughput genomics platform. It includes transcriptome, metabolome and enzymatic analyses together with sophisticated bioinformatic tools, which enabled the identification of favourable alleles and regulatory networks underlying improved performance (V.T. Harshavardhan, K. Rajesh, M. Strickert in collaboration with H. Rolletschek, research group Heterosis).

We have used a stay-green type and a normally senescing type from elite commercial breeding lines of barley (*Hordeum vulgare*) to investigate ABA signalling under conditions of post-anthesis drought. **The drought sensitive, senescing line produces much more abscisic acid (ABA) than the stay-green type under stress conditions in its source (flag leaf) and sink (developing seeds) tissue. In the senescing line, ABA catabolism to phaseic acid (PA), dihydrophaseic acid (DPA) and ABA sequestration as glucose ester (ABA-GE) are also very active under prolonged drought stress indicating the higher flux of ABA production**. We annotated all pertinent gene/transcript sequences of barley that are potentially involved in ABA signalling and identified enriched motifs from the extracted 5′ upstream regions. **The ABA receptor genes were much more responsive to drought in the senescing line than in the stay-green line acting under ABA dosage dependent manner leading to altered PP2C to RCAR ratio at the transcriptional level and ABA sensitivity**. The other genes were in general induced in both lines albeit to various extents. Notably, PKABA1 that is known to phosphorylate the transcription factor ABF1 in wheat was highly induced by stress in the senescing line as compared to the stay-green line. **Taken together, the drought sensitive and tolerant lines of barley were found to differ in their ABA homeostasis and in the ABA signalling pathway, impacting water use efficiency and finally grain weight under terminal drought** (C. Seiler, see Fig. 42, p. 122).

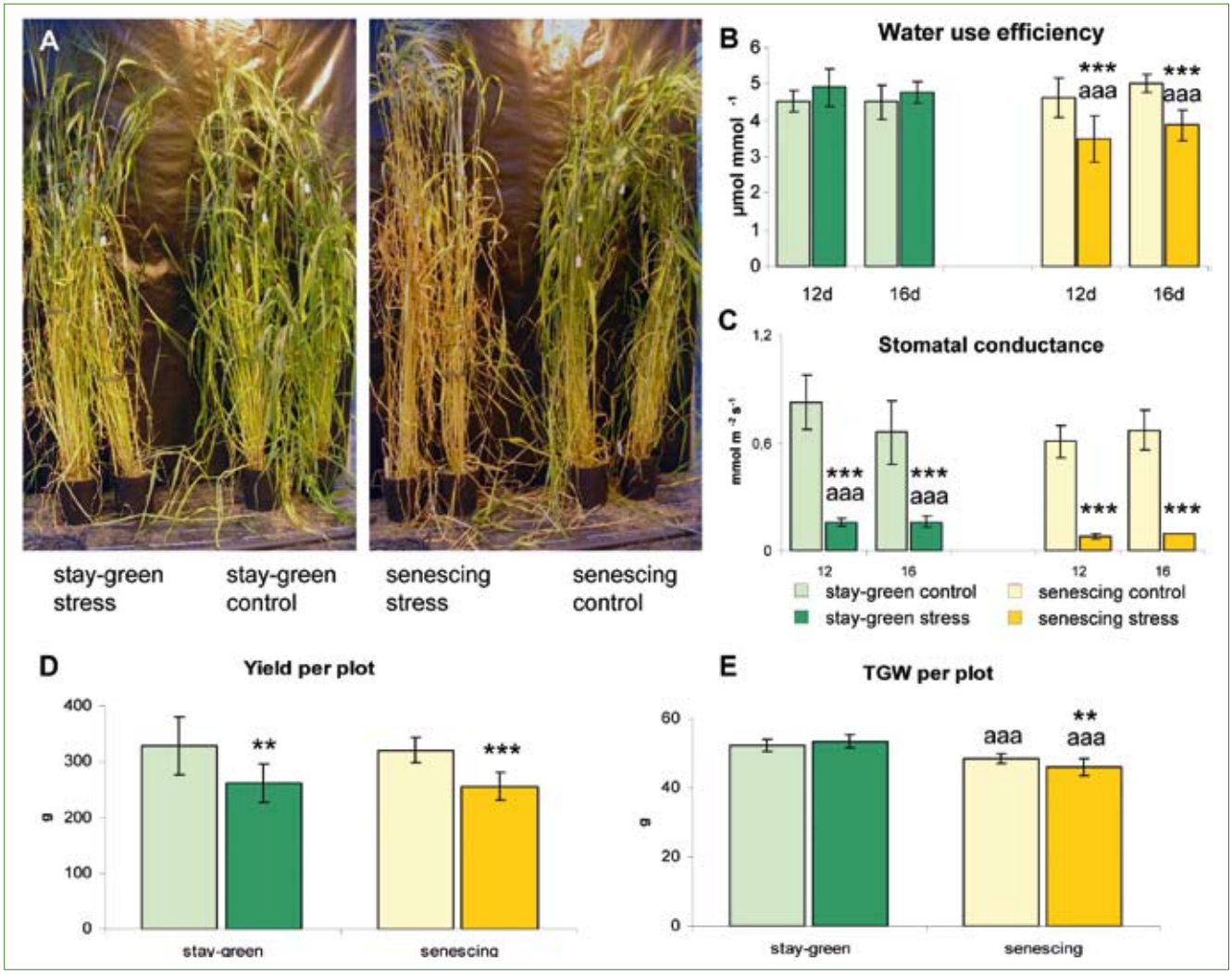

Fig. 42
Phenotype and yield characteristics of two contrasting barley genotypes under control and drought stress conditions. A: Plants of the stay-green (left picture) and senescing (right picture) genotype after 3 weeks of stress and respective control plants. B; C: Water use efficiency (assimilation / transpiration) and stomatal conductance of the two genotypes measured in flag leaf at 12 and 16 days after flowering (d). D, E: Yield and Thousand Grain Weight (TGW) calculated per plot consisting of 50 plants each. Asterisks indicate statistical significant differences between control and stress treatment with $p \leq 0.01$ (**) and $p \leq 0.001$ (***). Triple "a" indicates differences between stay-green and senescing line with $p \leq 0.001$ (C. Seiler and K. Rajesh).

Using this contrasting "stay-green" and efficient remobilisation lines, a double haploid (DH) population is created. Comprehensive screening of a DH population will result in identifying improved barley lines with improved seed set and grain yield under drought stress. By implementing complementary genomic and genetic approaches we will identify genomic regions influencing improved seed set under drought. More specifically, the selected contrasting lines will be characterised using genome-wide transcriptome, targeted metabolite and hormome profiling to define the basis of genetic networks to increase drought tolerance (N. Sreenivasulu in cooperation with N. von Wirén, research group Molecular Plant Nutrition). Using the same set of DH population, we will assess the malting efficiency from drought-stressed seed pool and identify potential regulators (N. Sreenivasulu in cooperation with A. Graner, research group Genome Diversity).

Further, the function of ABA in flag leaf and seeds under terminal drought has been tested to verify its role in drought tolerance in GMO barley using 16 different constructs by manipulating different nodes of ABA biosynthesis and degradation pathways using a set of drought inducible promoters. Transgenic barley plants are developed to manipulate the levels of ABA in source (flag leaf) and sink (developing barley grain) and to alter ABA hypersensitivity in seed tissues using a set of drought inducible promoters to study its impact on seed filling efficiency under terminal drought. **Under severe stress the transgenic lines performed significantly better than WT with enhanced grain weight by maintaining higher relative leaf water content and photosynthesis due to maintained ABA homeostasis. Taken together, the drought sensitive (WT) and tolerant lines (GMO) of barley were found to differ in their ABA homeostasis and in the ABA signalling pathway, impacting water use efficiency and finally grain weight under terminal drought** (V.T. Harshavardhan, C. Seiler in collaboration with J. Kumlehn, research group Plant Reproductive Biology).

Publications

Peer Reviewed Papers

2010

Lohse, M., A. Nunes-Nesi, P. Krüger, A. Nagel, J. Hannemann, F.M. Giorgi, L. Childs, S. Osorio, D. Walther, J. Selbig, N. Sreenivasulu, M. Stitt, A.R. Fernie & B. Usadel: Robin: an intuitive wizard application for R-based expression microarray quality assessment and analysis. Plant Physiol. 153 (2010) 642-651.

Sharma, S., N. Sreenivasulu, V.T. Harshavardhan, C. Seiler, S. Sharma, Z.N. Khalil, E. Akhunov, S.K. Sehgal & M.S. Röder: Delineating the structural, functional and evolutionary relationships of sucrose phosphate synthase gene family II in wheat and related grasses. BMC Plant Biol. 10 (2010) 134.

Sreenivasulu, N., L. Borisjuk, B.H. Junker, H.P. Mock, H. Rolletschek, U. Seiffert, W. Weschke & U. Wobus: Barley grain development toward an integrative view. Int. Rev. Cell Mol. Biol. 281 (2010) 49-89.

Sreenivasulu, N., V. Radchuk, A. Alawady, L. Borisjuk, D. Weier, N. Staroske, J. Fuchs, O. Miersch, M. Strickert, B. Usadel, U. Wobus, B. Grimm, H. Weber & W. Weschke: De-regulation of abscisic acid contents causes abnormal endosperm development in the barley mutant *seg8*. Plant J. 64 (2010) 589-603.

Weichert, N., I. Saalbach, H. Weichert, S. Kohl, A. Erban, J. Kopka, B. Hause, A. Varshney, N. Sreenivasulu, M. Strickert, J. Kumlehn, W. Weschke & H. Weber: Increasing sucrose uptake capacity of wheat grains stimulates storage protein synthesis. Plant Physiol. 152 (2010) 698-710.

2011

Govind, G., C. Seiler, U. Wobus & N. Sreenivasulu: Importance of ABA homeostasis under terminal drought stress in regulating grain filling events. Plant Signal. Behav. 6 (2011) 1228-1231.

Lata, C., S. Jha, V. Dixit, N. Sreenivasulu & M. Prasad: Differential antioxidative responses to dehydration-induced oxidative stress in core set of foxtail millet cultivars [*Setaria italica* (L.)]. Protoplasma 248 (2011) 817-828.

Melkus, G., H. Rolletschek, J. Fuchs, V. Radchuk, E. Grafahrend-Belau, N. Sreenivasulu, T. Rutten, D. Weier, N. Heinzel, F. Schreiber, T. Altmann, P.M. Jakob & L. Borisjuk: Dynamic (13) C/(1) H NMR imaging uncovers sugar allocation in the living seed. Plant Biotechnol. J. 9 (2011) 1022-1037.

Puranik, S., S. Jha, P.S. Srivastava, N. Sreenivasulu & M. Prasad: Comparative transcriptome analysis of contrasting foxtail millet cultivars in response to short-term salinity stress. J. Plant Physiol. 168 (2011) 280-287.

Seiler, C., V.T. Harshavardhan, K. Rajesh, P.S. Reddy, M. Strickert, H. Rolletschek, U. Scholz, U. Wobus & N. Sreenivasulu: ABA biosynthesis and degradation contributing to ABA homeostasis during barley seed development under control and terminal drought-stress conditions. J. Exp. Bot. 62 (2011) 2615-32.

Worch, S., K. Rajesh, V.T. Harshavardhan, C. Pietsch, V. Korzun, L. Kuntze, A. Börner, U. Wobus, M.S. Röder & N. Sreenivasulu: Haplotyping, linkage mapping and expression analysis of barley genes regulated by terminal drought stress influencing seed quality. BMC Plant Biol. 11 (2011) 1.

Books and Book Chapters

2010

Sreenivasulu, N., R. Sunkar, U. Wobus & M. Strickert: Array platforms and bioinformatics tools for the analysis of plant transcriptome in response to abiotic stress. In: Sunkar, R. (Ed.): Plant Stress Tolerance – Methods and Protocols. Methods Mol. Biol., Vol. 639. Humana Press (2010) 71-93.

Weber, H., N. Sreenivasulu & W. Weschke: Molecular physiology of seed maturation and seed storage protein biosynthesis. In: Pua, E.-C. & M.R. Davey (Eds.): Plant Developmental Biology – Biotechnological Perspectives, Vol. 2. Springer, Berlin (2010) 83-104.

Other Papers

2010

Sreenivasulu, N., M.S. Röder & U. Wobus: Trockenstress – eine Suche nach den Ursachen und nach neuen Wegen zur Züchtung trockentoleranter Getreide. GenomXPress 4 (2010) 4-6.

PhD and Diploma Thesis

2011

Kock, V.: Salinity tolerance mechanisms in barley. (Master Thesis) Wageningen UR-Plant Breeding, Wageningen/The Netherlands (2011) 44 pp.

Abteilung Physiologie und Zellbiologie/
Department of Physiology and Cell Biology

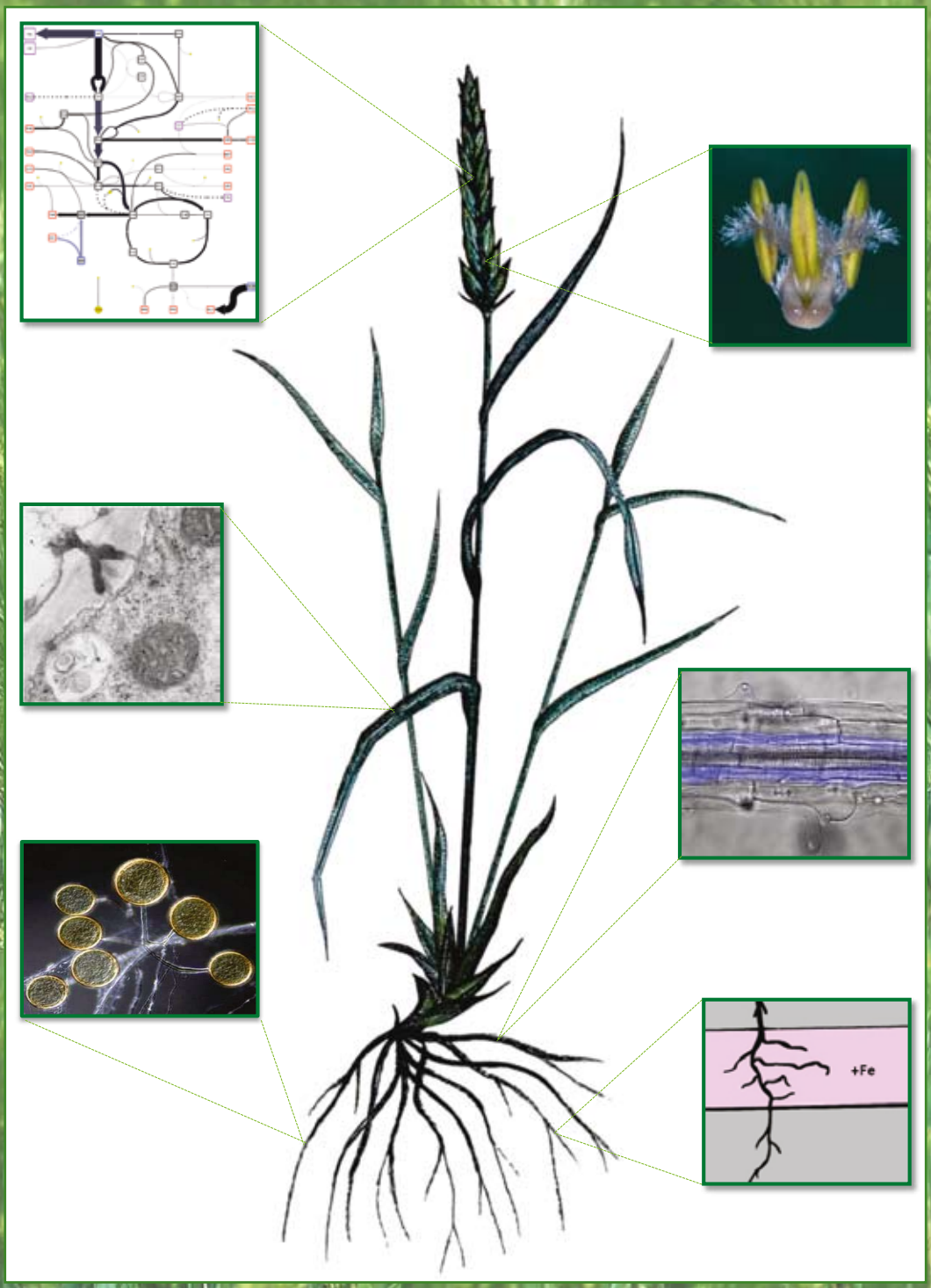

Abb. 43
Ausgewählte Forschungsthemen in der Abteilung Physiologie und Zellbiologie.
Fig. 43
Selected research topics of the Department of Physiology and Cell Biology.

Abteilung Physiologie und Zellbiologie

Leiter: Prof. Dr. Nicolaus von Wirén

Allgemeine Forschungsziele

Aufklärung der Regulation von Stoffwechselvorgängen und Entwicklungsprozessen in Pflanzen und in ihren heterologen Expressionssystemen, mit dem vorrangigen Ziel agronomisch relevante Merkmale in Nutzpflanzen oder biotechnologische Verfahrensweisen zu verbessern.

Entwicklung im Berichtszeitraum

Von den sechs Arbeitsgruppen der Abteilung Physiologie und Zellbiologie arbeiten drei mit einem vorwiegend biochemisch-physiologischen Methodenspektrum zum Metabolismus und Sensing von Pflanzennährstoffen (Arbeitsgruppe Molekulare Pflanzenernährung), zur Regulation vom Sekundärstoffwechsel und der physiologischen Bedeutung von Sekundärmetaboliten unter Stress (Arbeitsgruppe Angewandte Biochemie) und zu Systemeigenschaften des Primärmetabolismus (Arbeitsgruppe Systembiologie). Diese Arbeitsgruppen erweitern damit auch das Spektrum an physiologisch oder morphologisch erfassbaren Merkmalen, die beim Screening verschiedener Genotypen auch in Projekten anderer Abteilungen aufgenommen werden. Die anderen drei Arbeitsgruppen wenden dagegen vorwiegend Methoden aus der Entwicklungsbiologie und Biotechnologie an: Die Arbeitsgruppe Strukturelle Zellbiologie setzt licht- und elektronenmikroskopische Verfahren zur Beschreibung ultra-/struktureller Veränderungen in Pflanzengeweben ein, während die Arbeitsgruppe Pflanzliche Reproduktionsbiologie Entwicklungsprozesse, die mit der sexuellen und asexuellen Fortpflanzung assoziiert sind, aufklärt und in die Verbesserung biotechnologischer Verfahren einbringt. Die Arbeitsgruppe Hefegenetik nutzt Hefen als Wirt für die Produktion rekombinanter Proteine, als Gendonor und Biokatalysator oder als mikrobielle Komponente für Biosensoren zur Analyse von Umweltparametern und für die Überwachung von Futter- und Nahrungsmitteln. Daneben analysiert sie arbuskuläre Mykorrhizapilze bezüglich ihrer Interaktion mit Pflanzenwurzeln und deren Auswirkung auf das Pflanzenwachstum unter Stressbedingungen.

In den letzten beiden Jahren wurde die breite technische Plattform der Abteilung weiter ausgebaut. Neu etabliert wurden u.a. eine komplette Mineralstoffanalytik mit automatischem Probenverdau, ICP-OES, Sektorfeld-ICP-MS und Isotopenverhältnis-Massenspektrometrie (Ag Molekulare Pflanzenernährung), eine Konfokale Lasermikroskopie mit Spinning-Disk zum „live-cell imaging“ und ein MALDI-TOF-Gerät, das neben der Proteinidentifizierung auch für MS-basiertes Imaging genutzt wird (Ag Angewandte Biochemie). Die Etablierung einer UPLC-MS/MS-basierten Plattform zur Bestimmung von Phytohormonen und zwei komplementärer LC-MS/MS-basierten Plattformen zur Analyse von isotopenmarkierten Primärmetaboliten befinden sich derzeit noch im Aufbau.

Department of Physiology and Cell Biology

Head: Prof. Nicolaus von Wirén

Research Goals

The common aim in the department is the improvement of agronomically relevant traits in crops and of biotechnological applications by an improved adaptation and regulation of metabolic pathways and developmental processes in plants or in unicellular expression systems.

Developments in 2010 and 2011

Out of the six research groups in the Physiology and Cell Biology department, three groups mainly employ a biochemical-physiologically oriented range of methods to investigate the metabolism and sensing of nutrients (Molecular Plant Nutrition group), the regulation of secondary metabolism and the physiological function of secondary metabolites under stress (Applied Biochemistry group), and system properties of primary metabolism (Systems Biology group). Thereby, these groups also enlarge the methodological scope of physiologically and morphologically measurable traits, which are monitored in screening projects within and outside the department. The other three research groups primarily employ developmental and biotechnological methods: the Structural Cell Biology group employs light and electron microscopy to describe ultra-/structural changes in plant tissues, while the Plant Reproductive Biology group characterises developmental processes which are associated with sexual or asexual reproduction for the improvement of biotechnological applications. The Yeast Genetics group employs different yeast strains as hosts for recombinant protein production, as gene donor and biocatalysts for new biotechnological products and as microbial components in biosensors for environmental monitoring or food and feed control. Moreover, arbuscular mycorrhizal fungi are used to analyse fungal-root interactions and their effect on plant growth under stress conditions.

The past two years have also been used to enlarge the technical platform in the department. Newly established approaches include the mineral element analysis including automated sample digestion, ICP-OES, sector field ICP-MS and isotope ratio-mass spectrometry (Molecular Plant Nutrition), a spinning-disc confocal laser scanning microscopy for live-cell imaging (Structural Cell Biology) and a MALDI-TOF system which is used for protein identification and MS-based imaging of metabolites and proteins (Applied Biochemistry). A UPLC-MS/MS-based platform for phytohormone analysis and two complementary LC-MS/MS-based platforms for the analysis of isotope-labeled primary metabolites are currently being set up.

These platforms will also be used to advance common departmental research projects, such as the identification of barley genotypes or genes increasing salt tolerance, of secondary metabolites increasing nutrient efficiency or of substances and processes regulating pollen embryogenesis.

Diese Plattformen wurden auch zur Bearbeitung arbeitsgruppenübergreifender Projekte in der Abteilung eingesetzt, wie z. B. zur Identifizierung von Gerstengenotypen und -genen, die die Salztoleranz erhöhen, von Sekundärmetaboliten, die die Mineralstoffeffizienz verbessern oder von Substanzen und Prozessen, die die Pollenembryogenese steuern.

Hervorzuheben sind folgende Entwicklungen:
Mit der Untersuchung **morphogenetischer Wirkungen von Nährstoffen** wurde in der Arbeitsgruppe Molekulare Pflanzenernährung ein neuer Forschungsschwerpunkt etabliert. Dabei liegt der Fokus auf Veränderungen in der Architektur von Seitenwurzeln bei zeitlich oder räumlich wechselndem Nährstoffangebot. Über die quantitative Erfassung unterschiedlicher Parameter der Seitenwurzellänge und -anzahl konnte gezeigt werden, dass lokales Ammoniumangebot die Seitenwurzelbildung stimuliert, wogegen lokales Nitratangebot v. a. die Seitenwurzellänge erhöht. Damit wirken Ammonium und Nitrat komplementär auf die Seitenwurzelentwicklung (Lima et al. 2010, Plant Cell). Im Fall eines lokal begrenzten Fe-Angebots erhöhen Seitenwurzeln wiederum ihr Längenwachstum. Diese Anpassung beruht auf einer lokalen Expression des Auxintransporters AUX1, der basipetal transportiertes Auxin in die sich streckenden Seitenwurzeln leitet (Giehl et al. 2011, Plant Cell).
Die dabei gewonnenen Erkenntnisse tragen auch zu einem besseren Verständnis der **Adventivwurzelbildung** bei Petunien bei. Gezieltes Nährstoffangebot und Dunkelbehandlungen stärken die Adventivwurzelbildung der Stecklinge über eine veränderte systemische Signaltransduktion bzw. Source-Sink-Beziehungen (Breuillin et al. 2010, Plant J.; Klopotek et al. 2010, J. Plant Physiol.). Solche Behandlungen können somit zu einer erweiterten Wertschöpfung im kommerziellen Gartenbau beitragen.

Untersuchungen zur Biosynthese und Funktion von Sekundärmetaboliten. In der Arbeitsgruppe Angewandte Biochemie wurden die Arbeiten zur Aufklärung der gesundheitsfördernden Wirkung von Flavonoiden in der menschlichen Ernährung im Rahmen des EU-Projekts ATHENA fortgesetzt. Vorangehende Arbeiten hatten in Tierversuchen gezeigt, dass Anthocyan-angereichertes Futter gesundheitsfördernd wirkt. Im Mittelpunkt der derzeitigen Versuche stehen die phytochemische Charakterisierung von Pflanzenmaterial und die präparative Aufreinigung strukturell definierter Anthocyane für weiterführende medizinische Studien in Zusammenarbeit mit den Projektpartnern.
Ein Kandidatengen, das in die Regulation der Coumarin-Akkumulation in *Arabidopsis*-Wurzeln eingreift, wurde weiter charakterisiert. Mit Hilfe der Fluoreszenzmikroskopie wurde eine gewebespezifische Akkumulation der Coumarine nachgewiesen. Für das weitergehende Verständnis der Biosynthese der Coumarine im Kontext des allgemeinen Phenylpropanstoffwechsels werden derzeit gewebespezifische Untersuchungen durchgeführt.

Untersuchungen zur Salztoleranz in Gerste. In Kreuzungspopulationen von Gerste, deren Elternlinien eine unterschiedliche Salztoleranz aufweisen, konnten wir durch Proteomanalysen

Some highlights that deserve particular attention are the following:
The Molecular Plant Nutrition group has recently established a new key area with investigations on the **morphogenetic impact of nutrients** on plants. The focus of this research highlights changes in the architecture of lateral roots under spatially and temporarily changing nutrient supplies. In *Arabidopsis*, the quantitative assessment of different root measures showed that local ammonium supply stimulates lateral root initiation, whereas local nitrate enhances lateral root length. Thus, ammonium and nitrate shape lateral root development in a complementary manner (Lima et al. 2010, Plant Cell). In the case of localised Fe supply, lateral roots also elongate into Fe-rich patches. This process is triggered by the local expression of the auxin transporter AUX1 that increases the flux of basipetally translocated auxin into elongating lateral roots (Giehl et al. 2011, Plant Cell).
These new insights into the regulation of lateral root development will also be used to improve the understanding and manipulation of **adventitious root formation** in *Petunia*. In *Petunia* shoot cuttings, nutrient supply or dark treatments can alter systemic signaling or source-sink relations, which are relevant for adventitious root formation and may provide an added value in commercial horticulture (Breuillin et al. 2010, Plant J.; Klopotek et al. 2010, J. Plant Physiol.).

Biosynthesis and functions of secondary metabolites. Within the frame of the EU project ATHENA the Applied Biochemistry group has continued phytochemical research directed towards beneficial health effects of flavonoids as part of the human diet. Previous experiments using animal model systems have shown protective effects of an anthocyanin-enriched diet. On-going research aims at the phytochemical characterisation of novel plant material as well as the preparative isolation of selected anthocyanins for further medicinal studies in cooperation with the project partners.
A candidate gene involved in the control of coumarin accumulation in *Arabidopsis* roots has been further characterised. Using fluorescence microscopy, a tissue-specific accumulation of coumarins could be demonstrated. For a deeper understanding of the biosynthesis of coumarins and related control mechanisms within the context of the general phenylpropanoid metabolism, tissue-specific gene expression studies are performed.

Mechanisms of salt tolerance in barley. Mapping populations with contrasting salt tolerance of their parental lines have been studied. By using proteome approaches (total root proteome, plasma membrane fractions) a number of candidates has been identified, which are functionally characterised. Further candidates were obtained by complementing a salt-sensitive yeast strain with a cDNA library prepared from the salt-tolerant parental line Morex.
Functional analysis includes the study of related *Arabidopsis* knock-out mutants. In barley, the expression of candidate proteins will be studied at high temporal and spatial resolution. A further aspect will be the analysis of phytohormone profiles and changes of their patterns in response to salt stress in contrasting genotypes.

(Gesamtproteom, Plasmamembran-Fraktionen) eine Reihe von Kandidatengenen identifizieren, welche funktionell näher untersucht werden. Weitere Kandidaten wurden durch Komplementation eines salzsensitiven Hefestamms mit cDNA aus Wurzeln einer salztoleranteren Elternlinie (Morex) gewonnen. Mit der funktionellen Charakterisierung von *Arabidopsis* Knock-out-Mutanten wurde begonnen. Weitere Arbeiten in ausgewählten Gerstenlinien mit kontrastierender Salztoleranz umfassen die gewebespezifische Expression der Kandidatengene, die Analyse von Gen-Expressionsmustern sowie Änderungen in Phytohormonprofilen unter Salzstress.

Erweiterung der Transformationsplattform. Die für Getreidearten bereits seit einigen Jahren außerordentlich leistungsfähige Transformationsplattform der Arbeitsgruppe Pflanzliche Reproduktionsbiologie wurde durch die Etablierung effizienter und reproduzierbarer Methoden für das Poaceen-Modell *Brachypodium distachyon* sowie für *Boechera polyantha*, eine zweikeimblättrige Modellart für die Apomixis-Forschung, erweitert. Beide Methoden stellen Innovationen dar und werden bereits für die funktionelle Validierung diverser Kandidatengene eingesetzt. Darüber hinaus ist in einem abteilungsübergreifenden Ansatz durch Agrobakterien-vermittelte Integration von Telomersequenzen und daraus folgende gezielte Verkürzung von Chromosomen bei *Arabidopsis* und Gerste ein bedeutender Fortschritt hin zur Entwicklung von Minichromosomen gelungen, die als praktikable pflanzliche Vektoren die Grundlage einer zukünftigen Generation gentechnisch verbesserter Kulturpflanzen darstellen könnten.

Aufklärung struktureller Mechanismen der Pollenembryogenese in Gerste. Trotz des enormen Potenzials der Pollenembryogenese für die Grundlagenforschung, die Biotechnologie und kommerzielle Aspekte der Ertragssteigerung bei Nutzpflanzen sind deren grundlegende Mechanismen weitgehend unbekannt. Zum besseren Verständnis der initialen Mechanismen der Pollenembryogenese hat die Arbeitsgruppe Strukturelle Zellbiologie im Rahmen des Verbundvorhabens GABI-POEM vergleichende zellbiologische Untersuchungen der gametophytischen und embryogenen Pollenentwicklung durchgeführt. Die Verwendung transgener Gerstenlinien mit einer GFP-Expression im Zellkern und die Entwicklung einer speziellen Probenkammer für das *Live Cell Imaging* ermöglichten zum ersten Mal die Visualisierung der gesamten Entwicklung des Pollens während der Pollenembryogenese in hoher zeitlicher Auflösung. Dabei unterliefen zwei der neun beobachteten Entwicklungstypen in heterogenen Pollenkulturen Pollenembryogenese (Fig. 46, S. 136). Es wurde beobachtet, dass die erste Mitose sowohl symmetrisch als auch asymmetrisch erfolgen kann. Die Ergebnisse der Ultrastrukturanalysen und des Live Cell Imaging zeigten, dass es sich bei der Kernfusion, die zu jedem Zeitpunkt der Entwicklung stattfinden kann (Fig. 47, S. 137), um den entscheidenden Mechanismus zur Genomverdopplung während der Pollenembryogenese handelt. Diese umfangreichen neuen Kenntnisse zur Initiation der Pollenembryogenese in Gerste und die Optimierung bzw. Entwicklung neuer zellbiologischer Methoden könnten zur Etablierung

Extension and improvement of the transformation platform. The transformation platform for cereals, which is already well established in the Plant Reproductive Biology group, has been extended by efficient and reproducible methods for the Poaceae model species *Brachypodium distachyon* as well as for *Boechera polyantha*, which is a dicotyledonous experimental model for apomixis research. Both methods represent true innovations and are being already employed for the functional validation of various candidate genes. In a joint project conducted along with two groups of the Cytogenetics and Genome Analysis department the Plant Reproductive Biology group has also been successful in a first crucial step towards the establishment of minichromosomes. More specifically, chromosomal truncations were achieved in *Arabidopsis* and barley by *Agrobacterium*-mediated integration of telomer sequences. Minichromosomes are regarded as viable and advantageous plant vectors for the development of a future generation of genetically engineered crops.

Characterisation of the initial mechanisms of pollen embryogenesis in barley. The unique potential of pollen embryogenesis for basic research, biotechnology and commercial crop improvement is in strong contrast to the poor understanding of its underlying biological processes. To understand the initial mechanisms of pollen embryogenesis, a comparative cell biological study has been conducted to identify structural markers and features of the embryogenic and gametophytic pathway. The use of a transgenic barley line with GFP expression in the nucleus and the development of a custom-made chamber for live-cell imaging allowed for the first time the monitoring of pollen embryogenesis from the stage of vacuolated immature uni-nucleate barley pollen to the development of multicellular structures at high temporal resolution. Nine different developmental types were described for the highly heterogenic pollen culture, with two types undergoing pollen embryogenesis (Fig. 46, p. 136). The first mitosis either proceeded symmetrically or asymmetrically. Ultrastructural and live-cell imaging showed that nuclear fusion, which is the crucial mechanism of genome doubling during barley pollen embryogenesis, can occur at any developmental stage (Fig. 47, p. 137). This new achievement on the initial mechanisms of pollen embryogenesis in barley as well as on the optimisation and development of new cell biological tools may stimulate the knowledge-based establishment of double haploids in recalcitrant genotypes or other economically important crop plants and will eventually allow the identification of key genes in this process. In addition, the newly established methods of pollen fixation and live-cell imaging will also be useful to study other developmental processes in plants.

The Yeast Genetics group succeeded in the **system-biological modelling of the tannic acid degradation pathway** in the non-conventional yeast *Arxula adeninivorans*. The completely sequenced and annotated genome of this yeast in combination with genetic and biotechnical tools (selection of respective mutants, fusion products, mitotic segregants and transformants) allowed the identification and characterisation of all enzymes

Doppelhaploider in weiteren Genotypen als auch in wirtschaftlich relevanten Kulturpflanzen führen und die Identifizierung beteiligter Gene ermöglichen. Darüber hinaus sind die neu entwickelten bzw. optimierten zellbiologischen Methoden in vielen Bereichen der Pflanzenforschung anwendbar.

Mit der **systembiologischen Modellierung des Abbauweges von Tanninen** gelang der Arbeitsgruppe Hefegenetik am Beispiel der Hefe *Arxula adeninivorans* die Aufklärung eines bisher noch unbekannten eukaryotischen Stoffwechselweges. Das komplett am IPK sequenzierte und annotierte Genom dieser Hefe in Kombination mit genetischen und gentechnischen Tools (Herstellung entsprechender Mutanten, Fusionsprodukte, mitotischer Segreganten und Transformanten) erlaubte sowohl die Identifizierung als auch Charakterisierung aller Enzyme (einschließlich deren Gene) dieses für die Grundlagenforschung und die biotechnologische Forschung äußerst bedeutenden Stoffwechsels. So ist *Arxula* die bisher einzig bekannte Hefe, die zwei Tannasen mit unterschiedlichen Substratspektren sezerniert und damit sowohl kondensierte als auch hydrolysierbare Tannine über Gallussäure, Pyrogallol und 2-Hydroxymukonsäure zu Succinat abbauen kann. Bei all diesen Genen handelt es sich um Tannin- bzw. Gallussäure-induzierbare Gene.

Im Biosensorlabor der Arbeitsgruppe Hefegenetik wurden **neue Biosensoren** entwickelt und validiert, mit denen sich arbuskuläre Mykorrhizapilze und phytopathogene Viren an Pflanzen einerseits sowie Hormonaktivitäten und Pharmazeutika in Umweltproben und Tieren andererseits schnell, eindeutig und reproduzierbar nachweisen lassen. So gelang die Etablierung von auf Mikrotiterplatten-Assays bzw. auf der SPR-Plattform beruhenden Hochdurchsatzverfahren zur Analyse der Interaktion von arbuskulären Mykorrhizapilzen mit Wurzeln bzw. zum Nachweis von phytopathogenen RNA-Viren an Weizen und Kartoffelpflanzen.

Etablierung von Methoden zur Analyse von Stoffwechselflüssen. In der Arbeitsgruppe Systembiologie wurde eine Methode zur Bestimmung von intrazellulären Reaktionsraten im zentralen Stoffwechsel von Leguminosen- und Getreidesamen aufgesetzt. Diese Methode der metabolischen Stoffflussanalyse (MFA) ermöglicht die Erstellung von sehr detaillierten Flusskarten, die auch zyklische, parallele, und bidirektionale Flüsse beinhalten. Da Stoffflüsse nicht direkt gemessen werden können, werden in dieser Methode Markierungsexperimente simuliert, die mit entsprechenden Laborexperimenten verglichen werden. Die Parameter in den Modellen werden dann in einem iterativen Prozess angepasst, um Experiment und Simulation ähnlicher werden zu lassen. Die Etablierung der Methode setzt profunde interdisziplinäre Kenntnisse in Biochemie, Mathematik und Informatik voraus. MFA wird momentan in verschiedenen Drittmittelprojekten angewendet.

Nicolaus von Wirén, November 2011

(including the respective genes) of this important pathway. So far, *Arxula* is the first yeast containing two secretory tannases with different substrate spectra. It is able to digest condensed and hydrolysable tannic acids via gallic acid, pyrogallol and 2-hydroxy mucoic acid to succinate. All genes involved in this pathway are inducible by tannic acid and gallic acid.

In the biosensor laboratory of the Yeast Genetics group, **new biosensors** have been developed and validated for the fast and reproducible detection of arbuscular mycorrhiza fungi (AMF) and of phytopathogenic viruses on plants as well as of hormonal activities and pharmaceuticals in environmental samples and animals. Based on DNA-DNA or DNA-RNA hybridisations high-throughput microtiter plate assays and SPR chips have been established for analyses of mycorrhizal-plant root interactions or the detection of phytopathogenic RNA viruses in wheat and potato.

Establishment of methods for metabolic flux analysis in plant seeds. In the Systems Biology group, a method for determining intracellular reaction rates in central metabolism has been implemented, adapted to legume and cereal seeds, and optimised and partly automated to yield a competitive throughput. This method, named Metabolic Flux Analysis (MFA), allows the generation of highly detailed flux maps which include cyclic, parallel, and bidirectional fluxes. As metabolic fluxes cannot be measured directly, the method relies on simulations of feeding experiments with stable isotopes, which are then compared to respective laboratory experiments. By adjusting the parameters of the model, simulation and experiment are brought closer together in an iterative manner. Setting up the method requires expertise in biochemistry, mathematics, and computer science. MFA is currently being applied in several BMBF-funded projects.

Nicolaus von Wirén, November 2011

Research Group: Molecular Plant Nutrition

Head: Prof. Nicolaus von Wirén

Scientists

IPK financed
Ahkami, Amirhossein (0.50, till 31.03.2010)
Bauer, Bernhard (0.50)
Bohner, Anne (0.50 / 1.00)
Gruber, Benjamin D., Dr.
Hajirezaei, Mohammad R., Dr.
Hettwer Giehl, Ricardo Fabiano (0.50/1.00, since 01.04.2011)
Weishaar, Claudia (0.50, till 30.09.2011)

Grant Positions
Bohner, Anne (0.50 BMBF, 01.08.-30.09.2011)
Boylu, Baris (0.50 BMBF, since 01.09.2011)
Donath, Sebastian (0.50 DFG)
Eggert, Kai, Dr. (BMBF, since 01.08.2011)
Eroglu, Seckin (0.50 BMBF, since 08.10.2010)
Ghaffari, Mohammad Reza (0.50 BMBF)
Hosseini, Seyed Abdollah (0.50 BMBF, since 20.06.2011)
Kim, Young-Min (0.50 DFG, till 31.07.2010)
Köber, Julia Verena (0.50 DFG, 01.04.2010-31.03.2011)
Lingam, Brahmasivasenkar (0.50 Pakt für Forschung und Innovation, since 01.06.2011)
Manasse Laginha, Alberto (0.50 DFG, since 01.01.2011)
Schmid, Nicole (0.50 BMBF)
Shi, Rongli, Dr. (0.75 DFG, since 17.11.2010)
Ye, Fanghua (0.50 IZN, since 05.05.2010)

Visiting Scientists/Scholars
Ahkami, Amirhossein (University Hohenheim, 01.04.-30.09.2010)
Alvarez, Maria (BMBF, 11.09.-21.09.2010)
Barunawati, Nunun (Indonesian government)
Boylu, Baris (self-financed, 26.08.-31.08.2011)
Carillo, Nestor, Prof. (DFG, 09.09.-23.09.2010; IPK, 12.05.-17.05.2011)
Duan, Fengying (Chinese government, since 01.11.2010)
Fedoseyenko, Dmitriy (self-financed, 01.01.-31.12.2010; 01.07.-31.07.2011)
Ghaboli, Medhi (Ministry of Science, Research and Technology Iran, since 05.08.2011)
Ghorbani Javid, Majid (Ministry of Science, Research and Technology Iran, 11.03.-10.09.2010)
Hettwer Giehl, Ricardo Fabiano (CAPES, 03.05.2010-31.03.2011)
Isik, Zeynep (Fellowship of University Hohenheim, 18.03.-26.03.2010)
Kim, Young-Min (self-financed, since 01.02.2011)
Monteoliva, Mariela (BMBF, 14.11.-20.12.2010)
Schmidt, Susanne (Humboldt fellowship, 14.05.-30.06.2011)
Takahashi, Michiko, Prof. Dr. (self-financed, 22.04.-21.09.2011)
Tognetti, Vanessa, Dr. (IPK, 12.05.-17.05.2011)
Yuan, Linxing, Prof. (Robert Bosch Foundation, 12.08.-02.09.2011)
Zurbriggen, Mathias, Dr. (DFG, 21.06.-30.06.2010; 29.08.-23.09.2010)

Goals

Characterisation of morphological and physiological responses of plants subjected to biotic and abiotic stress conditions with a strong focus on changing nutrient supplies, and identification of rate-limiting steps in carbohydrate and nutrient metabolism of stressed plants.

Research Report

Nutrient sensing. Changes in the architecture of lateral roots in response to a localised supply of nutrients are regarded as a morphological read-out for nutrient sensing. We used horizontally- or vertically-split agar plates with localised nitrogen supplies to describe lateral root growth into nitrogen-containing agar patches. We observed that localised ammonium supply strongly stimulated lateral root branching in *Arabidopsis*, leading to a phenotype with highly branched, higher-order lateral roots, while localised nitrate supply mainly enhanced lateral root elongation. Thus, ammonium and nitrate act in a complementary manner to shape lateral root development. An analysis of *Arabidopsis* mutants defective in single or multiple AMT-type ammonium transporters then revealed that AMT1;3 had a particularly strong impact on lateral root initiation. ^{15}N-labeled ammonium uptake studies indicated that ammonium-triggered lateral root branching was not a nutritional response. Thus AMT1;3, which is expressed in the rhizodermis and cortex, acts upstream of an ammonium sensing event that stimulates the initiation of lateral roots (Lima et al. 2010, Plant Cell).
We have meanwhile extended our approach to other nutrients and observed that lateral root development is not a common response to localised nutrient supplies. When we conducted an in-depth analysis for lateral root responses to localised Fe supply, a local upregulation of the auxin transporter AUX1 was found to be a prerequisite for a local auxin accumulation in lateral root apices (Fig. 44, p. 130). This auxin mainly derives from the rootward auxin stream and promotes the elongation of lateral roots (Giehl et al. 2011, Plant Cell). Currently, we search for *Arabidopsis* mutants affected in targeted lateral root responses and investigate root developmental processes, in which nutrients alter phytohormone signalling pathways (Dr. B. Gruber, Dr. Ricardo Giehl).

To establish a screening platform for the selection of barley genotypes with rapid **root growth under field conditions**, we have developed a fertilisation device for the deep placement of fertiliser bands in different depths. These bands provide nutrients that are otherwise limiting for plants growing on these plots. As soon as the roots of individual plants reach a fertiliser band, they regreen and change light-absorbing properties.

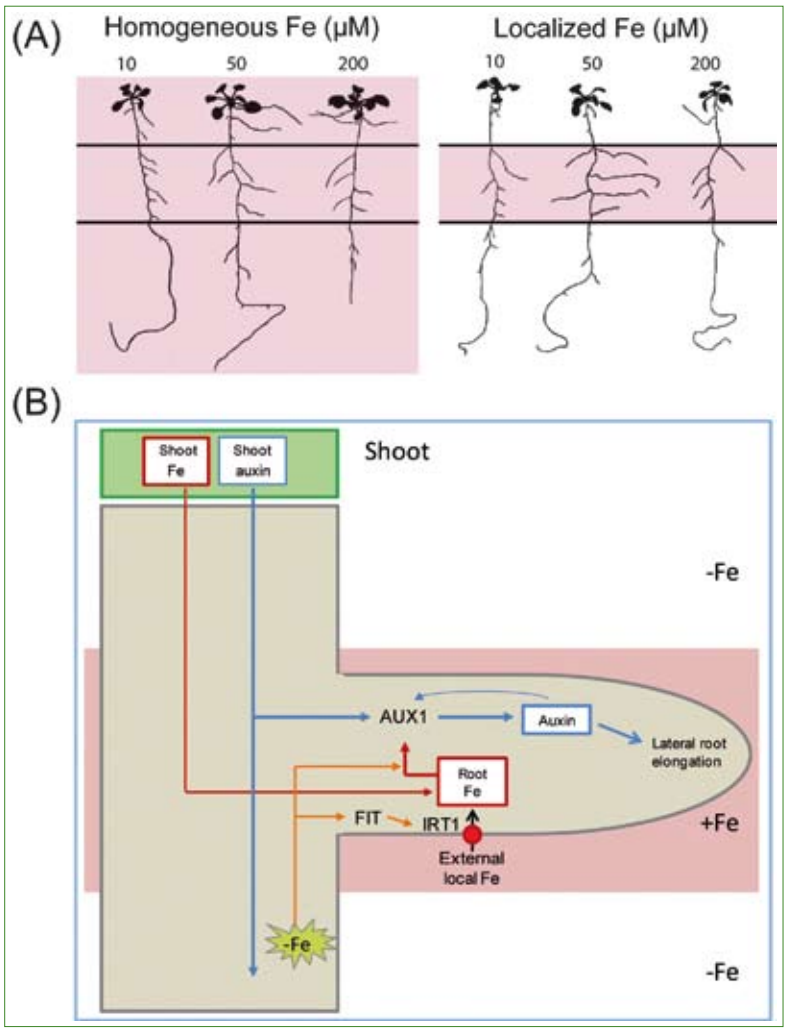

Fig. 44
The regulation of lateral root development by localised availability of Fe.
(A) Root architecture of *Arabidopsis thaliana* plants in response to Fe supply. Seedlings were grown on half-strength MS medium without Fe for 7 days before transferring to segmented agar plates containing half-strength MS and 75 µM ferrozine. Fe(III)-EDTA (µM) was added at the indicated concentrations to all three segments (homogeneous supply) or only to the middle segment (localised supply). Plants were scanned after 15 days of growth on Fe treatments and representative plants are shown. Horizontal lines represent the borders between the three segments.
(B) Model for the regulation of lateral root development under localised availability of Fe.
Uptake of Fe via the high-affinity Fe^{2+} transporter IRT1 increases the symplastic root Fe pool, which can be replenished by Fe derived from the shoot or other parts of the root. The local enrichment in symplastic root Fe leads to an upregulation of the auxin importer AUX1 channelling auxin from the rootward auxin stream towards the lateral root tip. This response is re-inforced by the integration of systemic Fe deficiency signals originated from other parts of the root. Increased rootward auxin movement in lateral roots triggers the longitudinal elongation of mature cells, subsequently resulting in enhanced lateral root elongation.

A regular recording of hyperspectral data from these plants allows us to detect when genotypes reach a fertiliser band and to set up a ranking of lines according to their root penetration rate (B. Baylu, B. Bauer).

Plant growth-promoting rhizobacteria. In an EU-funded cooperation a *Raoultella terrigena* strain had been isolated from the rhizosphere of wheat and found to promote plant growth in field studies. Since the reproducibility of yield increases by inoculating this or other plant growth-promoting bacteria is still variable, we established an *Arabidopsis* growth assay with vertically oriented agar plates, in which *Raoultella* stimulates root and shoot growth by more than twofold. However, this growth effect depends on the supplied nitrogen form and on the buffer capacity of the medium. Recently, we conducted a transcriptome analysis of inoculated versus non-inoculated roots and shoots and found several genes that show a particularly strong induction or repression after inoculation. After qPCR verification, T-DNA insertion lines for these genes have been isolated and are currently being characterised for their growth response to *Raoultella*. Within a Leibniz Association-funded PAKT project with the IPB Halle we aim at identifying *Arabidopsis* genes that determine the plant's responsiveness to growth-promoting bacteria (S. Lingam).

In our role as coordinator of a DFG research group on **nitrogen remobilisation in senescing plants**, we focused on the role of ammonium and urea transport in senescing leaves as in *Arabidopsis* the ammonium and urea transporter genes *AMT1;1* and *DUR3* are upregulated during senescence. We have now found that DUR3 mainly serves for urea retrieval from the leaf apoplast, thereby safeguarding urea-N that may otherwise be lost. With the successful establishment of an isotope ratio mass spectrometry, retranslocation studies with ^{15}N-labeled substrates have been undertaken in transgenic *Arabidopsis* and barley plants with deregulated expression of ammonium and urea transporter genes to determine the retranslocation efficiency of different phloem-mobile N forms. Moreover, polyamine measurements have been undertaken, since this class of putative phytohormones strongly responds to ammonium nutrition and senescence and might have a regulatory impact on the development of leaf senescence (A. Bohner, S. Donath).

In parallel, field-grown wheat plants that were senescing at different stages were used to collect leaf and spike material for the analysis of N and metal micronutrients. Together with gene expression studies and the analysis of metals and potential chelators in senescing leaves, this approach showed that phytosiderophores and citrate play an important role for **Fe mobilisation in senescing source leaves as a prerequisite for Fe retranslocation** to sink organs (R. Shi, N. Barunawati).

Iron efficiency strongly relies on the genetically determined ability of plants to increase Fe acquisition in the rhizosphere either by Fe(III) reduction and Fe^{2+} uptake, as in strategy I plants, or by the release of phytosiderophores and subsequent Fe(III)-phytosiderophore uptake, as in graminaceous (strategy II) plants. To identify genes controlling Fe acquisition in *Arabidopsis*, a collection of 7,000 *Arabidopsis* T-DNA insertion lines has been screened on a self-made calcareous substrate for phenotypes that show less or more severe Fe deficiency-induced chlorosis than wild type plants. This approach led to the identification of two lines that suffer from Fe deficiency-induced chlorosis more than wild-type plants and are defective either in a gene involved in the phenylpropanoid pathway or another gene encoding a MYB-type transcription factor. In the frame of a Plant-KBBE project, these genes will be further characterised for their role in Fe efficiency using reverse genetic approaches (N. Schmid, S. Eroglu).

Hexokinases are central enzymes in glycolysis that phosphorylate glucose and related hexoses and thereby can fulfil sensing functions in carbohydrate metabolism. In tobacco, six hexokinase isoforms have been identified and silenced in transgenic plants. Only RNAi lines of NtHXK1 showed chlorosis, severely damaged mesophyll tissue and an excess accumulation of starch. Metabolite analyses and functional studies indicated that the loss of activity of this cytosolic hexokinase blocked downstream processing of glucose and causing starch accumulation in chloroplasts. This study indicates a central function of NtHXK1 in primary carbon metabolism that can be primarily explained by its catalytic activity (Y.-M. Kim, M. Hajirezaei).

The expression of a **bacterial flavodoxin** in *Arabidopsis*, tobacco, potato or barley improves plant tolerance to biotic and abiotic stresses. To circumvent the complex phenotypes resulting from stress exposure, we generated transgenic tobacco lines, in which ferredoxin is knocked-down by RNA interference. Silenced lines exhibited arrested growth, diffuse or variegated leaf chlorosis and inhibited photosynthesis. Chloroplast or nuclear transformation of these plants with a cyanobacterial flavodoxin gene restored photosynthetic activity and the wild-type phenotype. In addition, these transgenics were more tolerant than wild-type plants to oxidative stress imposed by the redox-cycling herbicide methyl viologen. These results show that cyanobacterial flavodoxin is able to functionally replace plant-endogenous ferredoxin and suggest that the superior stability of flavodoxin and its more efficient cycling of reduction equivalents enhance stress tolerance (Blanco et al. 2011, Plant J.).

Publications

Peer Reviewed Papers

2010

Breuillin, F., J. Schramm, M. Hajirezaei, A. Ahkami, P. Favre, U. Druege, B. Hause, M. Bucher, T. Kretzschmar, E. Bossolini, C. Kuhlemeier, E. Martinoia, P. Franken, U. Scholz & D. Reinhardt: Phosphate systemically inhibits development of arbuscular mycorrhiza in *Petunia hybrida* and represses genes involved in mycorrhizal functioning. Plant J. 64 (2010) 1002-1017.

El-Banna, A., M.R. Hajirezaei, J. Wissing, Z. Ali, L. Vaas, E. Heine-Dobbernack, H.J. Jacobsen, H.M. Schumacher & H. Kiesecker: Over-expression of PR-10a leads to increased salt and osmotic tolerance in potato cell cultures. J. Biotechnol. 150 (2010) 277-287.

Graff, L., P. Obrdlik, L. Yuan, D. Loque, W.B. Frommer & N. von Wirén: N-terminal cysteines affect oligomer stability of the allosterically regulated ammonium transporter LeAMT1;1. J. Exp. Bot. 62 (2010) 1361-1373.

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Lima, J.E., S. Kojima, H. Takahashi & N. von Wirén: Ammonium triggers lateral root branching in *Arabidopsis* in an AMMONIUM TRANSPORTER1;3-dependent manner. Plant Cell 22 (2010) 3621-3633.

Riebeseel, E., R.E. Häusler, R. Radchuk, T. Meitzel, M.R. Hajirezaei, R.J. Neil Emery, H. Küster, A. Nunes-Nesi, A.R. Fernie, W. Weschke & H. Weber: The 2-oxoglutarate/malate translocator mediates amino acid and storage protein biosynthesis in pea embryos. Plant J. 61 (2010) 350-363.

Zurbriggen, M., N. Carrillo & M. Hajirezaei: Engineering the future. Development of transgenic plants with enhanced tolerance to adverse environments. Biotechnol. Genet. Eng. Rev. 27 (2010) 33-56.

Zurbriggen, M.D., N. Carrillo & M.R. Hajirezaei: ROS signaling in the hypersensitive response: When, where and what for? Plant Signal. Behav. 5 (2010) 393-396.

2011

Bazargani, M.M., E. Sarhadi, A.A. Bushehri, A. Matros, H.P. Mock, M.R. Naghavi, V. Hajihoseini, M. Mardi, M.R. Hajirezaei, F. Moradi, B. Ehdaie & G.H. Salekdeh: A proteomics view on the role of drought-induced senescence and oxidative stress defense in enhanced stem reserves remobilization in wheat. J. Proteomics 74 (2011) 1959-1973.

Blanco, N.E., R.D. Ceccoli, M.E. Segretin, H.O. Poli, I. Voss, M. Melzer, F.F. Bravo-Almonacid, R. Scheibe, M.R. Hajirezaei & N. Carrillo: Cyanobacterial flavodoxin complements ferredoxin deficiency in knocked-down transgenic tobacco plants. Plant J. 65 (2011) 922-935.

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Graff, L., P. Obrdlik, L. Yuan, D. Loqué, W.B. Frommer & N. von Wirén: N-terminal cysteines affect oligomer stability of the allosterically regulated ammonium transporter LeAMT1;1. J. Exp. Bot. 62 (2011) 1361-1373.

Köster, J., H. Hayen, N. von Wirén & G. Weber: Isoelectric focusing of small non-covalent metal species from plants. Electrophoresis 32 (2011) 772-781.

Köster, J., R. Shi, N. von Wirén & G. Weber: Evaluation of different column types for the hydrophilic interaction chromatographic separation of iron-citrate and copper-histidine species from plants. J. Chromatogr. A 1218 (2011) 4934-4943.

von Wirén, N.: Grand challenges in plant nutrition. Front. Plant Sci. 2 (2011) 4; doi:10.3389/fpls.2011.00004.

Other Papers

2010

Bauer, B.: Winterweizenanbau – Bestandesaufbau im Frühjahr auf den Sortentyp abstimmen? Innovation 1 (2010) 16-18.

Bauer, B.: Qualitätsweizen produzieren – An welchen Schrauben ist zu drehen, um auch bei hohen Erträgen sichere Eiweißgehalte zu erzielen? Getreidemagazin 2 (2010) 112-114.

Lemke, R., M. Hajirezaei, B.H. Junker, J. Müller, B. Usadel, M. Leps & F. Schreiber: MMM – Mehrskalen-Stoffwechselmodelle zur Systembiologie in Getreiden – ein integrativer Ansatz für die Biomasseforschung. Systembiologie.de 2 (2010) 51-53.

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2010

Ahkami, A.: Molecular physiology of Adventitious Root Formation (ARF) in *Petunia hybrida* cuttings. (PhD Thesis) Martin-Luther-Universität Halle-Wittenberg, Naturwissenschaftliche Fakultät I, Halle/S. (2010) 150 pp.

2011

Bohner, A.: Membrane transport and long-distance translocation of urea in *Arabidopsis thaliana*. (PhD Thesis) Universität Hohenheim, Stuttgart (2011) 109 pp.

Giehl, R.F.H.: Identification of regulatory factors determining nutrient acquisition in *Arabidopsis*. (PhD Thesis) Universität Hohenheim, Stuttgart (2011) 157 pp.

Lutz, U.: The role of the transcription factor ANAC020 in iron nutrition and flowering time regulation in *Arabidopsis thaliana*. (Diploma Thesis) Universität Hohenheim, Stuttgart (2011) 90 pp.

Vorrath, I.: Genotypische Unterschiede beim Einfluss der N-Form auf die Metabolitzusammensetzung in Weizen. (Master Thesis) Hochschule Anhalt, Bernburg (2011) 45 pp.

Weishaar, C.: Impact of the plant growth-promoting rhizobacterium *Raoutella terrigena* TFi08N on plant growth and root architecture. (PhD Thesis) Martin-Luther-Universität Halle-Wittenberg, Halle / S. (2011) 97 pp.

Additional Publications 2009

Bauer, B. & N. von Wirén: Ansätze aus der Pflanzenernährung zur genetischen Anpassung von Kulturpflanzen an den Klimawandel. Vortr. Pflanzenzücht. 81 (2009) 63-70.

Lanquar, V., D. Loque, F. Hormann, L.X. Yuan, A. Bohner, W.R. Engelsberger, S. Lalonde, W.X. Schulze, N. von Wirén & W.B. Frommer: Feedback inhibition of ammonium uptake by a phospho-dependent allosteric mechanism in *Arabidopsis*. Plant Cell 21 (2009) 3610-3622.

Research Group: Applied Biochemistry

Head: Dr. Hans-Peter Mock

Scientists

IPK financed
Döll, Stefanie (0.50, since 01.12.2011)
Matros, Andrea, Dr. (till 30.11.2011)
Peukert, Manuela (0.50, since 01.12.2011)

Grant Positions
Dittbrenner, Anke (Industry)
Döll, Stefanie (0.50 Industry, till 30.05.2010 and 01.03.-30.06.2011; 0.50 BMBF, 31.05.2010-28.02.2011 and 01.07.-30.11.2011)
Hedtmann, Christiane (0.50 Industry, 01.04.-30.06.2011; 0.50 BMBF, 01.07.-31.12.2011)
Kaspar, Stephanie (0.50/1.00 BMBF, till 31.03.2011)
Lippmann, Rico (0.50 BMBF)
Matros, Andrea, Dr. (BMBF, since 01.12.2011)
Merx, Kathleen (0.50 BMBF, till 28.02.2011)
Peukert, Manuela (0.50 DFG, till 30.11.2011)
Tandron, Yudelsy Antonia, Dr. (0.50 BMBF, till 30.06.2010)

Visiting Scientists/Scholars
Capdesuner Ruiz, Yanelis Karina (DAAD scholarship, till 29.08.2010; 16.06.-10.12.2011)
Eick, Manuela (self-financed, 18.07.-30.07.2010)
Fila, Jan (EU COST, 02.03.-28.03.2010; self-financed, 14.11.-27.11.2010; DAAD, 31.07.-18.09.2011)
Hashemi, Amenehsadat (Ministry of Science, Research and Technology Iran, 19.06.-18.12.2011)
Huerta Ocampo, José Àngel (self-financed, 04.04.-30.11.2011)
Janmohammadi, Mohsen (Research scholar Iran, till 22.04.2010)
Lattanzio, Giuseppe (self-financed, 01.08.-22.11.2010)
Mazzucotelli, Elisabeth, Dr. (EU COST, 18.04.-28.05.2010)
Witzel, Katja, Dr. (self-financed, 08.11.-26.11.2010; 16.05.-20.05.2011; 01.11.-08.11.2011)
Yadav, Sunita (DAAD fellowship, 01.09.-30.11.2011)

Goals

The main research interest of the group is the biosynthesis and regulation of secondary metabolism in plants. Protective functions against abiotic and biotic stresses but also to the potential health effects of these metabolites as a part of the human diet are important aspects. A major goal is to gain further insights into regulatory programmes and mechanism of resource allocation into different branches of secondary metabolism. Proteome approaches are applied to study the integration of secondary metabolism into overall cellular defence mechanisms.

Research Report

Within the EU **ATHENA** project the group is responsible for the phytochemical characterisation of plant materials. Plant tissues are profiled for **flavonoids and related phenylpropanoids with potentially beneficial health effects** by using HPLC-UV-MS. Plant materials studied comprise transgenic tomato fruits with ectopic expression of transcription factors regulating anthocyanin biosynthesis, maize, blood orange accessions, grape cell cultures as well as barley and wheat lines. A major goal of the project is to study the effects of individual anthocyanins in feeding studies using animal model systems. For this purpose, preparative isolation of anthocyanins from different sources has been started by adopting HPLC methods to a larger scale (A. Dittbrenner, A. Matros; collaboration with ATHENA partners).
The biochemical and molecular analysis of exudates biosynthesis in **glandular trichomes of tobacco** varieties has been continued. Methods for analysis of diterpenoids and for sucrose esters have been applied to quantify the amounts of individual diterpenoids and of sucrose esters in exudates of about forty tobacco accessions. Next generation sequencing technique was applied to sequence trichome cDNA libraries generated for three selected accessions. Data are currently used to perform array experiments with a larger set of accessions (Y. Capdesuner, Y. Tandron, R. Lippmann, A. Matros).

The functional characterisation of a putative regulatory factor of **coumarin biosynthesis** was continued. Knock-out mutant and wild-type plants were grown under conditions favouring coumarin accumulation and array experiments were performed to compare the expression profiles as a means to further characterise the regulatory context of the candidate gene. Potential involvement of coumarins in iron nutrition is studied in collaboration with the group of N. von Wirén (D. Berreth, S. Döll).

The functional characterisation of the stress-induced co-chaperone protein STINT and related STIAT proteins in *Arabidopsis* has been continued. A major focus of recent research was the potential **phosphorylation** of these co-chaperones. Methods for the isolation of phosphorylated STINT or STIAT proteins have been introduced. Putative phosphorylation sites have been identified by mass spectrometry (S. Endress, C. Hedtmann).

A major area of research in the group has been the study of changes in **proteome patterns** during **barley seed development**. The multiplexed LC-MS analysis of individual barley grain tissues isolated by laser capture micro-dissection combined with pressure catapulting (LMPC), allowed for the identification of several proteins showing tissue-specificity in their expression. Results underline the distinct biological functions of the two investigated tissues within the developing barley grain (S. Kaspar, K. Merx, A. Matros; collaboration with W. Weschke). In parallel, an

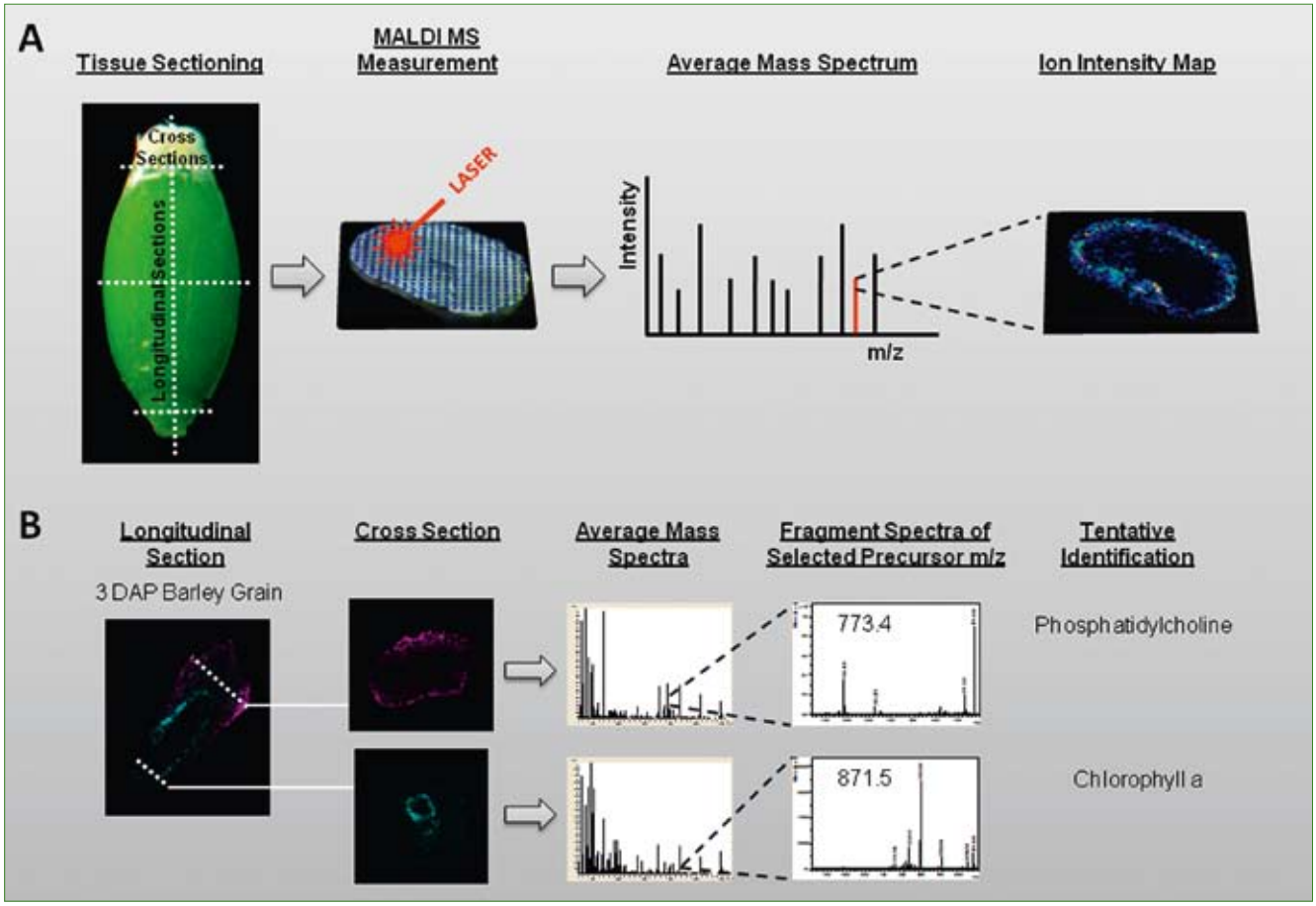

Fig. 45
Matrix-assisted laser desorption/ionisation mass spectrometric imaging (MALDI-MSI) analysis of immature barley (*Hordeum vulgare*) grain tissues.
A) Representative scheme of MALDI-MSI approach. First cryo-sections from barley grains are prepared and a suitable matrix is applied onto the tissue section. The data are acquired by rasterising the complete tissue section with a laser-beam and capturing the full mass spectrum at each irradiation point with a MALDI-TOF device. An average mass spectrum is obtained and ion intensity maps are used to infer the distribution of distinct *m / z* values over the tissue.
B) Examples from analyses of 30 µm sections of 3-d after pollination (DAP) developing barley grains are shown. The multi-ion image shows molecular masses *m/z* 773.4 (mangenta) and *m / z* 871.5 (turquoise) from a longitudinal section (left). Also corresponding selected-ion images and the respective average mass spectra from cross sections are shown (centre). Identification of underlying molecular compounds was based on MS fragmentation analysis directly from the cryo-sections.

MALDI-MS imaging platform able to profile developing barley grains has been established. The protein compositions of grains sampled shortly after fertilisation have displayed either tissue-specific or co-localised protein expression patterns. Currently, LMPC and on-tissue digestion are being used to determine the identity of the underlying proteins. In addition, funding by the DFG has been provided for the development of **MALDI-MS imaging of metabolites** in developing barley grains (see Fig. 45). Protocols for detecting small molecules in cryo-dissected immature barley grains have been introduced and were successfully transferred to tobacco root tissue (M. Peukert, A. Matros). The resulting data set revealed reproducible metabolite distributions specific to various tissues as well to different developmental stages of barley seeds. A number of these signals were tentatively identified as being derived from oligosaccharides and phospholipids (M. Peukert, A. Matros; collaboration with W. Weschke).

The project on **salt stress responses in barley** mapping populations with contrasting tolerances has been continued (K. Witzel, A. Matros; collaboration with A. Börner and all groups of the Physiology and Cell Biology department). Novel candidates associated with the higher salt tolerance of the Morex variety have been revealed by comparative analysis of the root plasma membrane proteome of plants from both parental lines grown under salt stress. The proteome of the plasma membrane fraction was analysed by multiplexed LC-MS of peptides resulting from digestion with trypsin; complementary datasets were obtained by using elastase for protein digestion. The full root proteome approach was performed in a kinetic manner for the parental lines of the Steptoe-Morex population. Several candidates associated with the higher tolerance of the Morex cultivar were found in more than one of the studies, including the earlier data from the complementation of a salt-sensitive *Saccharomyces* strain. Functional characterisation of candidates has been continued using different approaches, such as analysis of *Arabidopsis* KO lines and targeted studies in yeast and barley. A particular set of candidates point to the significance of plasma membrane proteome as well as lipid composition and to the involvement of control by specific phytohormones.

A novel project aims at elucidating the potential of *Euphorbia lathyris* for generation of biofuels. This plant grows on marginal soils thereby not competing with crops and is characterised by the accumulation of **energy-rich triterpenoids** (EULAFUEL; R. Lippmann).

Publications

Peer Reviewed Papers

2010

Agarwal, R., A. Matros, M. Melzer, H.P. Mock & J.K. Sainis: Heterogeneity in thylakoid membrane proteome of *Synechocystis* 6803. J. Proteomics 73 (2010) 976-991.

Kaspar, S., A. Matros & H.P. Mock: Proteome and flavonoid analysis reveals distinct responses of epidermal tissue and whole leaves upon UV-B radiation of barley (*Hordeum vulgare* L.) seedlings. J. Proteome Res. 9 (2010) 2402-2411.

Kaspar, S., D. Weier, W. Weschke, H.P. Mock & A. Matros: Protein analysis of laser capture micro-dissected tissues revealed cell-type specific biological functions in developing barley grains. Anal. Bioanal. Chem. 398 (2010) 2883-2893.

Sreenivasulu, N., L. Borisjuk, B.H. Junker, H.P. Mock, H. Rolletschek, U. Seiffert, W. Weschke & U. Wobus: Barley grain development toward an integrative view. Int. Rev. Cell Mol. Biol. 281 (2010) 49-89.

Witzel, K., A. Weidner, G.K. Surabhi, R.K. Varshney, G. Kunze, G.H. Buck-Sorlin, A. Börner & H.P. Mock: Comparative analysis of the grain proteome fraction in barley genotypes with contrasting salinity tolerance during germination. Plant Cell Environ. 33 (2010) 211-222.

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Bazargani, M.M., E. Sarhadi, A.A. Bushehri, A. Matros, H.P. Mock, M.R. Naghavi, V. Hajihoseini, M. Mardi, M.R. Hajirezaei, F. Moradi, B. Ehdaie & G.H. Salekdeh: A proteomics view on the role of drought-induced senescence and oxidative stress defense in enhanced stem reserves remobilization in wheat. J. Proteomics 74 (2011) 1959-1973.

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Books and Book Chapters

2011

Matros, A., S. Kaspar, S. Tenzer, M. Kipping, U. Seiffert & H.P. Mock: Label-free liquid chromatography-based quantitative proteomics: challenges and recent developments. In: Rancourt, G.C. (Ed.): Proteomics: Methods, applications and limitations (Protein biochemistry, synthesis, structure and cellular functions). Nova Science Publishers Inc., New York (2011) 103-136.

Møller, A.L.B., K. Witzel, A. Vertommen, V. Barkholt, B. Svennson, S. Carpentier, H.-P. Mock & C. Finnie: Plant plasma membrane proteomics: challenges and possibilities. In: Ivanov, A.R. & A.V. Lazarev (Eds.): Sample preparation in biological mass spectrometry. Springer, Dordrecht etc. (2011) 411-434.

Other Papers

2010

Seiffert, U., F. Bollenbeck, H.P. Mock & A. Matros: Clustering of crop phenotypes by means of hyperspectral signatures using artificial neural networks. Proceedings of the 2nd IEEE Workshop on Hyperspectral Imaging and Signal Processing: Evolution in Remote Sensing WHISPERS 2010, Reykjavik/Iceland, IEEE Press (2010) 31-34.

PhD and Diploma Theses

2010

del Rocio Moya Ruiz, M.: Expression differencial de proteinas radiculares del trigo (*Triticum aestivum* L.) a la adhesion de *Azospirillum brasiliense* Cd. (Master Thesis) La Paz/Mexico (2010) 105 pp.

2011

Berreth, D.-C.: Analyse der gewebespezifischen Expression von Genen der Stressabwehr in *Arabidopsis*-Wurzeln mit besonderer Berücksichtigung von Genen des Phenylpropanstoffwechsels. (Master Thesis) Fakultät Naturwissenschaften, Universität Hohenheim, Hohenheim (2011) 99 pp.

Kaspar, S.: Analysis of isolated barley tissues using proteomic approaches. (PhD Thesis) Martin-Luther-Universität Halle-Wittenberg, Halle/S. (2011) 224 pp.

Lange, H.: Modifikation von Anthocyanseitenketten mit Hilfe rekombinant exprimierter Proteine. (Bachelor Thesis) Hochschule Anhalt, Köthen (2011) 75 pp.

Research Group: Structural Cell Biology

Head: Dr. Michael Melzer

Scientists

IPK financed
Rutten, Twan, Dr.

Grant Positions
Daghma, Diaa El-Din (0.50 BMBF, till 30.11.2010)

Visiting Scientists/Scholars
Andersen, Louise, Prof. (self-financed, 28.04.-17.05.2011)
Ghoniem, Ahmed Eisa Mahmoud (Cairo University, 10.10.-09.11.2010)
Marzec, Marek (EU-UPGOW, till 29.03.2010; DAAD, 01.04.-21.04.2011, 02.06.-28.06.2011 and 29.09.-20.10.2011)
Pandey, Pooja (DAAD-Siemens fellowship, 24.09.-30.09.2011)

Goals

As core facility for light and electron microscopy the Structural Cell Biology group on the one hand provides practical and theoretical advice to other groups that wish to address research problems by microscopy and conducts own research projects on the other hand. In various cooperations with internal and external research groups we focus mainly on ultrastructural characterisation, monitoring of cell dynamic processes and the spatial distribution of macromolecules in plants using sophisticated cell biological techniques of confocal laser scanning microscopy (CLSM), spinning disc microscopy (SDM), scanning electron microscopy (SEM) and transmission electron microscopy (TEM).

Research Report

To understand the **initial mechanisms of pollen embryogenesis in barley** (D. S. Daghma, GABI-POEM), various cell biological methods have been used to identify **structural markers** and features of the embryogenic and gametophytic pathway. Ultrastructural observations showed that both gametophytic and embryogenic pollen contain a large central vacuole, which persisted beyond the first pollen mitosis. The gametophytic pathway is characterised by the gradual decreasing of the large central vacuole, while in pollen embryogenesis this central vacuole was gradually replaced by many small ones. As compared to embryogenic pollen, gametophytic pollen had a higher density of ribosomes, rough endoplasmic reticulum, and organelles such as mitochondria and dictyosomes. The development of a custom-made live cell imaging chamber and the use of transgenic barley lines with GFP expression in the nucleus for the first time allowed the **visualisation of POEM from the vacuolated immature uni-nucleate barley pollen until the development of multicellular structures** at high temporal resolution. **Nine different developmental types** of cultured pollen have been determined (Fig. 46) including two pathways characteristic for pollen undergoing POEM. **Ultrastructural and live-cell imaging results identified nuclear fusion as the crucial mechanism of genome doubling** during barley pollen embryogenesis. It can occur at any developmental stage during pollen embryogenesis and multiple fusions may lead to variable ploidy level in multicellular structures (Fig. 47, p. 137). **The first mitosis** of the uninucleate microspores **can be symmetric or asymmetric**. Although this is important for the future pathway we found that it is not a key trigger of POEM. The advanced experimental set up and the comprehensive information on the initial mechanisms of POEM will eventually allow functional validation of genes putatively involved in POEM and therefore stimulate a knowledge-based establishment of the commercially useful haploid technology in numerous plant species.

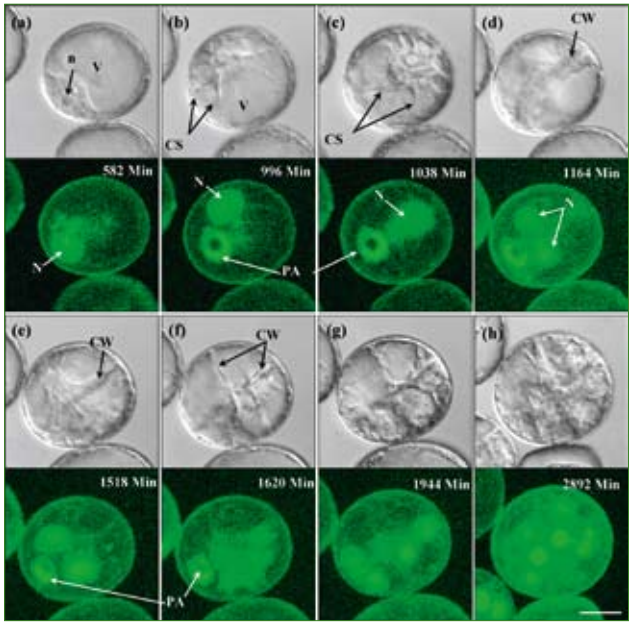

Fig. 46
Time lapse of type I development (embryogenic pollen). CLSM images shown in DIC and nuclear GFP fluorescence. (a) Uni-nucleate pollen grain with the nucleus close to the pollen aperture. (b, c) Migration of the nucleus to a semi-central position and formation of cytoplasmic strands. The blurred fluorescence signal seen in (c) indicates the disruption of the nuclear envelope before mitosis. (d) Newly formed cell wall (DIC) and two daughter nuclei (GFP) after mitosis. (e) Appearance of cytoplasmic strands indicating imminent second mitosis. (f, g) Newly formed cell walls (DIC) separate four cells (GFP) contained within the original exine. (h) Additional cycles of mitosis have created multicellular structure. CS, cytoplasmic strands; CW, cell wall; N, nucleus; n, nucleolus; PA, pollen aperture. Bar = 20 µm (D. S. Daghma, T. Rutten, G. Hensel, J. Kumlehn and M. Melzer).

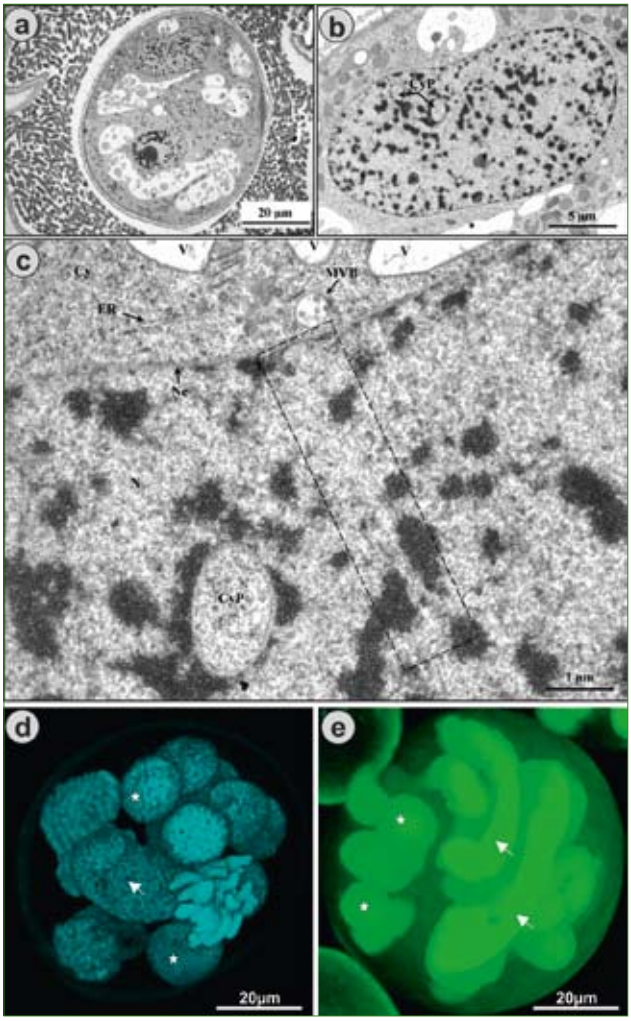

Fig. 47
Nuclear fusion in multicellular structures 7 days after initiation of POEM. Transmission electron microscopy (a-c) and confocal laser scanning microscopy (d-e). (a-b) Elongated nucleus with clear median constriction. (c) Detail of nucleus cytoplasmic pockets and a narrow median band (dashed box) marking the site of fusion. (d) DAPI staining. (e) GFP expression in nuclei with highly polyploid nuclei (arrows) next to small likely haploid nuclei (stars). Cy, cytoplasm; CyP, cytoplasmic pocket; ER, endoplasmic reticulum; MVB, multi vesicles body; N, nucleus; Ne, Nuclear envelope; V, vacuole (D. S. Daghma, T. Rutten, G. Hensel, J. Kumlehn and M. Melzer).

In collaboration with the research group Gene Regulation (D. Köszegi, M. Michael) a break-through was realised in elucidating the role of the **egg cell-specific transcription factors AtRKD1 and AtRKD2**. Permanent induction of these factors arrest the function of the shoot apical meristem and cause the initiation of axillary meristems. Expression analysis of the meristem-specific **transcription factors WUSCHEL and CLAVATA** tagged with GUS or GFP showed that meristematic identity was not altered in the arrested shoot apical meristem. However, studies with the auxin-inducible promoter DR5 revealed that the auxin gradient typical for normal meristems, was absent in plants overexpressing ATRKD1 or AtRKD2. The conclusion that **AtRKD1 and AtRKD2 may play a role in regulating auxin** gradients is supported by recent publications showing locally produced auxin gradients to be essential for the correct cellular organisation within the female gametophyte.

In the centromeres of all eukaryotes, the normal histone H3 is replaced with a centromere-specific variant, CENH3 in plants. The presence of CENH3 is believed to be important for the assembly of the kinetochore on the centromere which is responsible for a correct chromosome segregation during nuclear division. In collaboration with the research group Karyotype Evolution (I. Lermontova) the **dynamics of CENH3 in root tip cells** of *Arabidopsis thaliana* were investigated. Using live cell imaging approaches we were able to confirm a plant-specific behaviour of CENH3 dynamics during the cell cycle. In animals CENH3 is stable throughout the cell cycle until the anaphase. During this short time of increased mobility, just before the end of mitosis, animal cells duplicate their CENH3 content. In *Arabidopsis* root tip **cells expressing YFP-tagged CENH3**, fluorescence intensity together with CENH3 content remained stationary for at least three to four hours prior to mitosis. A mere 7 % of the total protein content was mobile during this time, indicating a slow turnover that may compensate for damaged molecules, or the presence of two separate CENH3 populations which have yet to be identified. After mitosis each daughter nucleus contained exactly half of the fluorescence intensity of the mother nucleus. These data prove that in ***Arabidopsis* CENH3 loading must happen very early in G2**. The loading process itself, our analysis indicates, may last no more than 30 min. To follow CENH3 dynamics during the complete cell cycle of single cells in real time, long-term observations using a recently acquired spinning disc microscope will be carried out.

Together with the research group Molecular Plant Nutrition (M. Hajirezaei) and the Institute of Molecular and Cell Biology of the National University of Rosario, Argentina (M. Zurbriggen, N. Blanco, N. Carillo) we continued our structural characterisation of transgenic tobacco plants expressing a cyanobacterial flavodoxin (Fld).

In a joint project (DAAD) with the Dept. of Genetics, Katowice, Poland (I. Szarejko, M. Marzec) we are working on the **structural and molecular characterisation of barley root epidermal cells** for the identification of new **genes involved in root hair development** in *Hordeum vulgare*. Preliminary studies have shown a different localisation pattern of arabinogalactans in epidermal cells of control and hairless mutant barley plants.

Publications

Peer Reviewed Papers

2010

Agarwal, R., A. Matros, M. Melzer, H.P. Mock & J.K. Sainis: Heterogeneity in thylakoid membrane proteome of *Synechocystis* 6803. J. Proteomics 73 (2010) 976-991.

Arsova, B., U. Hoja, M. Wimmelbacher, E. Greiner, S. Üstün, M. Melzer, K. Petersen, W. Lein & F. Börnke: Plastidial thioredoxin z interacts with two fructokinase-like proteins in a thiol-dependent manner: Evidence for an essential role in chloroplast development in *Arabidopsis* and *Nicotiana benthamiana*. Plant Cell 22 (2010) 1498-1515.

Johnston, A.J., O. Kirioukhova, P.J. Barrell, T. Rutten, J.M. Moore, R. Baskar, U. Grossniklaus & W. Gruissem: Dosage-sensitive function of *RETINOBLASTOMA RELATED* and convergent epigenetic control are required during the *Arabidopsis* life cycle. PLoS Genet. 6 (2010) e1000988.

Kotseruba, V., K. Pistrick, F.R. Blattner, K. Kumke, O. Weiss, T. Rutten, J. Fuchs, T. Endo, S. Nasuda, A. Ghukasyan & A. Houben: The evolution of the hexaploid grass *Zingeria kochii* (Mez) Tzvel. (2n=12) was accompanied by complex hybridization and uniparental loss of ribosomal DNA. Mol. Phylogenet. Evol. 56 (2010) 146-155.

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Blanco, N.E., R.D. Ceccoli, M.E. Segretin, H.O. Poli, I. Voss, M. Melzer, F.F. Bravo-Almonacid, R. Scheibe, M.R. Hajirezaei & N. Carrillo: Cyanobacterial flavodoxin complements ferredoxin deficiency in knocked-down transgenic tobacco plants. Plant J. 65 (2011) 922-935.

Czarnecki, O., B. Hedtke, M. Melzer, M. Rothbart, A. Richter, Y. Schröter, T. Pfannschmidt & B. Grimm: An *Arabidopsis* GluTR-binding protein mediates spatial separation of 5-aminolevulinic acid synthesis in chloroplasts. Plant Cell 23 (2011) 4476-4491.

Daghma, D.S., J. Kumlehn & M. Melzer: The use of cyanobacteria as filler in nitrocellulose capillaries improves ultrastructural preservation of immature barley pollen upon high pressure freezing. J. Microsc. 244 (2011) 79-84.

Karimi Ashtiyani, R., A.M. Banaei Moghaddam, V. Schubert, T. Rutten, J. Fuchs, D. Demidov, F.R. Blattner & A. Houben: AtHaspin phosphorylates histone H3 at threonine 3 during mitosis and contributes to embryonic patterning in *Arabidopsis*. Plant J. 68 (2011) 443-454.

Köszegi, D., A.J. Johnston, T. Rutten, A. Czihal, L. Altschmied, J. Kumlehn, S.E. Wust, O. Kirioukhova, J. Gheyselinck, U. Grossniklaus & H. Bäumlein: Members of the RKD transcription factor family induce an egg cell-like gene expression program. Plant J. 67 (2011) 280-291.

Lermontova, I., O. Koroleva, T. Rutten, J. Fuchs, V. Schubert, I. Moraes, D. Köszegi & I. Schubert: Knockdown of CENH3 in *Arabidopsis* reduces mitotic divisions and causes sterility by disturbed meiotic chromosome segregation. Plant J. 68 (2011) 40-50.

Lermontova, I., T. Rutten & I. Schubert: Deposition, turnover, and release of CENH3 at *Arabidopsis* centromeres. Chromosoma 120 (2011) 633-640.

Melkus, G., H. Rolletschek, J. Fuchs, V. Radchuk, E. Grafahrend-Belau, N. Sreenivasulu, T. Rutten, D. Weier, N. Heinzel, F. Schreiber, T. Altmann, P.M. Jakob & L. Borisjuk: Dynamic (13) C/(1) H NMR imaging uncovers sugar allocation in the living seed. Plant Biotechnol. J. 9 (2011) 1022-1037.

Rudolph, M., A. Schlereth, M. Körner, K. Feussner, E. Berndt, M. Melzer, E. Hornung & I. Feussner: The lipoxygenase-dependent oxygenation of lipid body membranes is promoted by a patatin-type phospholipase in cucumber cotyledons. J. Exp. Bot. 62 (2011) 749-760.

Tschiersch, H., L. Borisjuk, T. Rutten & H. Rolletschek: Gradients of seed photosynthesis and its role for oxygen balancing. Biosystems 103 (2011) 302-308.

PhD and Diploma Theses

2011

Daghma, D.S.: Structural changes during the initiation of pollen embryogenesis in barley (*Hordeum vulgare* L.). (PhD Thesis) Martin-Luther-Universität Halle-Wittenberg, Halle/S. (2011) 167 pp.

Research Group: Plant Reproductive Biology

Head: Dr. Jochen Kumlehn

Scientists

IPK financed
Daghma, Diaa El-Din (0.50 Pakt für Forschung und Innovation, 01.07.-31.12.2011)
Goedeke, Stefanie (0.50 Pakt für Forschung und Innovation, till 31.03.2010)
Gurushidze, Maia, Dr. (0.25, till 31.08.2010; 0.50/0.75, 01.04.-31.08.2011)
Hensel, Götz, Dr. (Pakt für Forschung und Innovation, 01.09.2010-28.02.2011)
Kapusi, Eszter (Pakt für Forschung und Innovation, till 31.05.2011)
Rizzo, Paride (0.50, 01.01.-31.03.2010)
Saalbach, Isolde, Dr. (0.50)

Grant Positions
Berger, Carolin, Dr. (BMBF, till 23.09.2010)
Bruchmüller, Astrid (0.50 Overhead, till 31.03.2010)
Gurushidze, Maia, Dr. (0.50/0.75 BMBF, till 30.04.2011; 0.25 Overhead, 01.05.-31.08.2011; 0.50/1.00 BMBF, since 01.09.2011)
Guse, Tilo (0.50 Industry)
Hensel, Götz, Dr. (BMBF, till 31.08.2010; since 01.03.2011)
Kastner, Christine (0.50 BMBF)
Pencs, Stefanie (BMBF, since 01.11.2011)
Plasun, Katarzyna (0.50 BMBF, till 31.08.2010, 0.50 Overhead, 01.09.-31.12.2010)
Riechen, Jan (0.50 BMBF, till 31.01.2011)
Rizzo, Paride (0.50 Overhead, 01.04.-30.09.2010; 0.50 BMBF, 01.10.-31.12.2010)

Visiting Scientists/Scholars
Bini, Federica, Dr. (self-financed, since 01.09.2011)
Cambra, Inés (University of Madrid, 11.04.-14.07.2011; IPK, 15.08.-14.09.2011)
Gajecka, Monika (ERASMUS fellowship, 06.06.-05.09.2011)
Goedeke, Stefanie (self-financed, 01.04.-31.12.2010)
Hiekel, Stefan (IPK, 10.10.-30.11.2011)
Plasun, Katarzyna (self-financed, since 01.01.2011)
Pourkheirandish, Mohammad, Dr. (NIAS, 03.01.-08.01.2011)
Perera, Prasanthi, Dr. (CIAT, 23.09.-23.10.2011)
Szyrajew, Katarzyna (ERASMUS fellowship, 19.09.-18.12.2011)
Tedeschi, Francesca, Dr. (University of Tuscia, 01.10.2010-30.09.2011)
Zahid Abbas, Malik (Fellowship of Higher Education Commission, 17.06.-16.12.2010)

Goals

The major interest of the Plant Reproductive Biology group centers around the establishment and implementation of enabling technologies such as genetic transformation, micro-dissection of live cells and the generation of true-breeding plants so as to facilitate applied research as well as crop improvement approaches. Taking advantage of the resultant technological platform, further research projects aim to elucidate mechanisms of sexual and asexual plant reproduction, plant-pathogen interactions, as well as many other aspects of crop plant performance.

Research Report

Pollen embryogenesis is a viable means to produce populations of entirely true-breeding plants. Whereas those plants are highly valuable both in research and practical breeding, the molecular processes that are crucial for the initiation of pollen embryogenesis are largely unkown. In cooperation with KWS SAAT AG and the IPK research groups Structural Cell Biology, Gene Regulation, Applied Biochemistry as well as Bioinformatics and Information Technology, we have thus been pursuing an integrated research approach that encompasses ultrastructural studies, time-lapse microscopy as well as comparative transcript, metabolite and protein profiling using the model species tobacco and barley. To this end, the PRB group has been providing highly specific samples of developmental stages of both regular pollen development and pollen embryogenesis, which was achieved by improvements in pollen treatment, purification of pollen populations, and individual pollen selection. Deep sequencing of mRNA isolated from those samples has resulted in a unique resource for the **identification and functional validation of genes putatively involved in the developmental switch from pollen maturation towards embryogenesis**. The long-term goal of this work is to facilitate knowledge-based development of haploid technology broadly applicable in crop plants (D.S. Daghma, G. Hensel, I. Otto).

Among the Triticeae cereals, **rye** is considered to be the most recalcitrant as to pollen embryogenesis. In a bilateral project with the plant breeding station KWS Lochow, we have recently succeeded to establish embryogenic pollen cultures and to generate **doubled haploid lines** in this species (C. Bollmann, S. Hiekel). Moreover, we were the first to generate plants via the pollen embryogenesis pathway in the Poaceae model species ***Brachypodium distachyon***. However, in the most important plant model *Arabidopsis*, our efforts to establish haploid technology have failed so far. Though we were able to develop a highly efficient method to produce plants from *in vitro* cultivated anthers, these lines proved by molecular markers to originate from somatic cells of the anther rather than from haploid pollen grains (B. Melzer, K. Plasun, I. Otto, P. Hoffmeister).

Conventional TILLING (Targeting Induced Local Lesions in Genomes) populations derive from mutagenic treatment of diploid tissues, which results in the formation of heterozygotic mutations and chimeric primary mutant lines. Therefore, we have pursued a novel approach where haploid single cells, i.e. isolated immature pollen **(microspores) of barley, are used** as a target **for chemical mutagenesis**. This enables us **to generate homozygous**, non-chimeric primary **mutant lines** that can be instantly identified by phenotype and reproduced without any segregation. A short-awned, as well as a dwarf phenotype did not segregate in the M2 generation indicating that the respective mutations had already been homozygous and non-chimeric in the primary mutant plants. To evaluate the frequency of induced mutations, embryogenic pollen cultures of transgenic cv. Igri lines carrying a homozygous, single-copy green fluorescence protein (GFP) gene were subjected to mutagenesis treatment. It was demonstrated that GFP knock-out mutations can be already visually detected in haploid pollen-derived embryo populations (Fig. 48). (M. Gurushidze, F. Bini, E. Kugelmann, I. Otto).

The PRB group's **transformation** platform that includes ***Agrobacterium*-based** methods for barley, wild barley (*Hordeum spontaneum*), wheat, rye, triticale, maize and tef has been extended to the emerging monocot model species ***Brachypodium distachyon***. This was achieved by a novel method that rests on the formation of **regenerable callus on segments of primary shoots** from mature, *in vitro* germinated grains. This method has the major advantages that there is no need to continuously grow donor plants to provide recipient explants used for the gene transfer, and that the dissection of shoot segments is much more straightforward than the isolation of the tiny immature embryos of *Brachypodium* (B. Melzer, T. Guse, Ch. Kastner, C. Berger, E. Kapusi, G. Hensel).

To study molecular genetic mechanisms functionally associated with apomixis, the genus *Boechera* is an ideal model system. As it is characterised by naturally occurring diploid apomictic and sexual forms, gene expression of both reproductive modes can be compared without the confounding effects of polyploidy. In co-operation with the Apomixis group, we have **isolated ovules from sexual and apomictic accessions at different stages of development to identify differentially expressed genes** after deep sequencing of respective cDNA libraries. To allow for the **functional validation of candidate genes** associated with apomictic reproduction, we recently succeeded as the first to establish a **transformation method for *Boechera polyantha***. The protocol rests on the inoculation of petiols of *in vitro* germinated seedlings with *Agrobacterium* (S. Freist, I. Otto, G. Hensel).

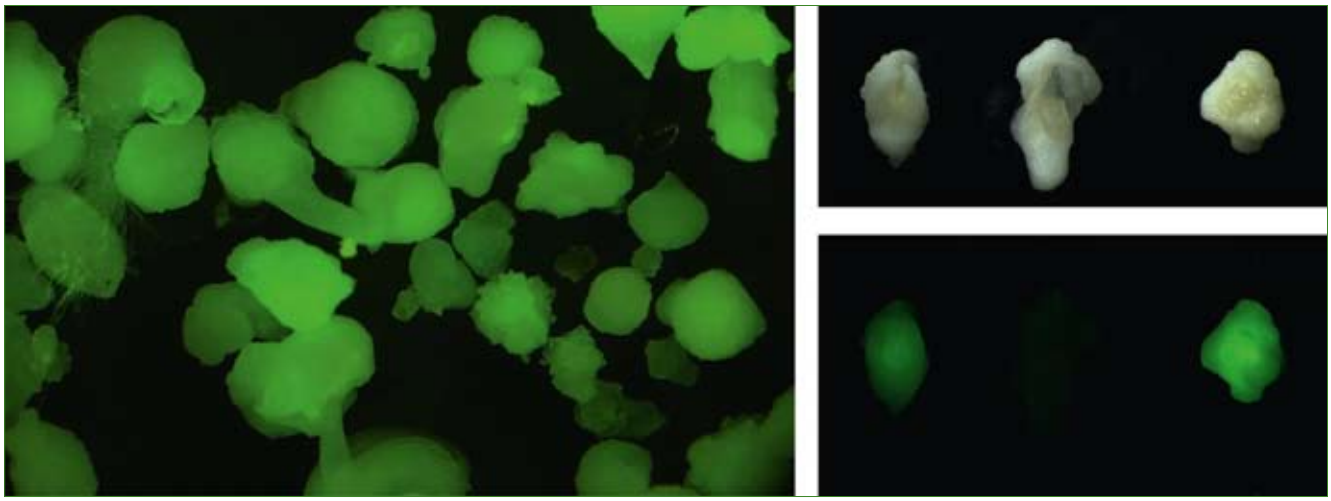

Fig. 48
Mutagenisation via ethane methyl sulfonate treatment of isolated barley microspores derived from a transgenic line carrying a single GFP copy at homozygous state. left: embryogenic pollen culture from non-treated microspores with GFP being consistently expressed in all embryo-like structures. right: pollen-derived embryos following EMS-treatment of microspores, upper right: embryos under white light, lower right: excitation of the same objects with far blue light reveals that the GFP gene appears to be knocked out in the individuum placed in the centre, while the left and right ones show fluorescence (Photos: M. Gurushidze and J. Kumlehn).

Engineered minichromosomes open up the opportunity to simultaneously transfer and stably express multiple transgenes in plants without recombination of the genetic background. In collaboration with the research groups Chromosome Structure and Function and Epigenetics, we have **truncated *Arabidopsis* and barley chromosomes via integration of telomere sequences** using *Agrobacterium*, which is a first crucial step in a top-down approach towards the development of minichromosomes. In barley, *de novo* formation of telomeres was found in tetraploid plants only, indicating that the recovery of shortened chromosomes is facilitated by genetic redundancy. **Truncated chromosomes were transmissible in sexual reproduction**, but were inherited at rates lower than expected according to the Mendelian rules (E. Kapusi, G. Hensel, S. Knüpffer, C. Marthe).

In collaboration with the Technical University Munich we previously showed that the barley ROP G-protein RACB is required for full susceptibility of the leaf epidermis to invasion by the biotrophic fungus *Blumeria graminis* f. sp. *hordei*. More recently, we demonstrated that the **barley** MICROTUBULE-ASSOCIATED ROP-GTPASE ACTIVATING PROTEIN **(MAGAP1) labelled with GFP** decorated cortical microtubules and was recruited by activated RACB to the cell periphery. Under fungal attack, MAGAP1-labelled microtubules establish a polarised network at sites of successful defence. These results suggest that RACB and MAGAP1 might be antagonistic players in cytoskeleton organisation in the context of fungal infection. In a further approach with the same collaboration partner, transgenic barley plants carrying an ***HvBI-1* RNA-interference** (RNAi) construct were generated. These lines had reduced levels of *HvBI-1* transcript and showed enhanced resistance to penetration by *B. graminis hordei*. Reactive oxygen species (ROS) also play an important role in plant-pathogen interactions. Prominent sources of ROS are respiratory burst oxidase homologs (RBOH) whose function is still poorly understood. Again in collaboration with the Technical University Munich, transgenic **barley RNAi-lines** were generated, which showed reduced expression of the **HvRBOHF2** isoform of NADPH oxidases, failed to establish penetration resistance to *B. graminis hordei* and to control leaf cell death (G. Hensel, C. Marthe).

RNAi is an established means of knocking down genes in plants and fungi. Both sequence-specificity as well as systemic spreading of gene silencing is essentially mediated by small interfering RNAs. Considering that there is intimate cellular contact between plants and fungal pathogens during infection, we hypothesised that fungal genes may effectively be targeted by small RNAs derived from appropriately designed hairpin constructs expressed by host plant cells. This phenomenon that was coined **host-induced gene silencing** (HIGS) has been investigated in cooperation with the Transcriptome Analysis group employing the barley-powdery mildew pathosystem. Transgenic barley lines were generated using a hairpin **RNAi** construct based on a fragment of the ***B. graminis hordei*** glucanosyltransferase 1 **(*GTF1*)** gene. GTFs are specifically found in fungi where they are involved in cell elongation and virulence. In T1-populations obtained, colony formation of *B. graminis hordei* was significantly reduced. The results suggest uptake of RNA molecules by the powdery mildew fungus from attacked plant cells, which may cause knock-down of targeted fungal genes and reduced disease severity. Thanks to its potentially high specificity, the huge array of candidate target genes, and the fact that the protection mechanism acts without any further gene product being required, this novel principle holds a promise for future applications to effectively combat fungal diseases of crop plants (G. Hensel, G. Zimmermann, A. Knospe, C. Marthe).

To functionally validate maize genes with regard to their role in the interaction with *Ustilago maydis*, a virus-induced gene silencing (VIGS) system based on the Brome Mosaic Virus (BMV) was established in maize by our cooperation partners at the MPI in Marburg. Using this system, transient knock-down of the *terpene synthase 6/11* (*TPS6/11*) gene that had been found to be significantly upregulated upon *U. maydis* infection resulted in increased severity of disease symptoms. In order to confirm these results and to demonstrate the value of the newly established VIGS system, we produced stably transgenic maize lines carrying a ubiquitously expressed *TPS6/11* RNAi-construct. Plants where *TPS6/11* expression was effectively silenced also showed significantly increased levels of *U. maydis* colonisation associated with increased tumor formation and extended chlorosis, as was found in the respective VIGS experiment (Ch. Kastner, S. Wolf, H. Büchner).

Publications

Peer Reviewed Papers

2010

Eichmann, R., M. Bischof, C. Weis, J. Shaw, C. Lacomme, P. Schweizer, D. Douchkov, G. Hensel, J. Kumlehn & R. Hückelhoven: BAX INHIBITOR-1 is required for full susceptibility of barley to powdery mildew. Mol. Plant Microbe Interact. 23 (2010) 1217-1227.

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Books and Book Chapters

2010

Kumlehn, J., G. Zimmermann, C. Berger, C. Marthe & G. Hensel: Characters of transgenic plants and their application in plant production – *Triticeae* cereals. In: Kempken, F. & C. Jung (Eds.): Genetic modification of plants – Agriculture, Horticulture & Forestry. Springer-Verlag, Berlin-Heidelberg (2010) 287-306.

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Hensel, G.: Genetic transformation of *Triticeae* cereals for molecular farming. In: Alvarez, M. (Ed.): Genetic Transformation. ISBN: 978-953-307-364-4, InTech (2011) 171-190, Available from: http://www.intechopen.com/articles/show/title/genetic-transformation-of-triticeae-cereals-for-molecular-farming.

PhD and Diploma Theses

2010

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Kapusi, E.: Elimination of selectable markers genes via segregation of uncoupled T-DNAs in populations of doubled haploid barley. (PhD Thesis) Martin-Luther-Universität Halle-Wittenberg, Naturwissenschaftliche Fakultät I, Halle/S. (2010) 103 pp.

2011

Melzer, B.: Transformation von *Brachypodium distachyon* durch den Agrobacterium-vermittelten Gentransfer in Sprosssegmentkallus. (Diploma Thesis) Hochschule Mittweida, (2011) 166 pp.

Research Group: Yeast Genetics

Head: Prof. Gotthard Kunze

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Pham, Thi Minh Ha (0.50, since 01.08.2011)
Sedzielewska, Kinga Anna (0.50, since 01.04.2011)
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Kasprzak, Jakub (0.50 Industry, since 15.11.2011)
Körner, Martina, Dr. (AIF, till 23.06.2010)
Riechen, Jan (0.50/1.00 Industry, since 01.07.2011)
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Sedzielewska, Kinga Anna (0.50 Overhead, 15.09.2010-31.03.2011)
Trautwein, Anke (0.50 AIF, till 30.11.2011)
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Alvaro Benito, Miguel (CBMSO scholarship Madrid, 23.08.-26.11.2010)
Baronian, Keith, Prof. (self-financed, 17.06.-28.06.2010)
Lemanski, Tabias Samuel (ComEAST, 08.02.-07.05.2010)
Nutz, Sabine (IPK, 01.02.-04.03.2011)
Ordenes, Viviana, Dr. (self-financed, 11.10.-25.10.2010)
Pham, Thi Minh Ha (MOET Vietnam, till 31.07.2011)
Sashidar, Burla, Dr. (DLR, 08.04.-28.06.2010)
Sedzielewska, Kinga Anna (AMykor GmbH, till 14.09.2010)
Toro Nahuelpan, Mauricio (Fellowship of Bayer Foundation, 19.08.2010-03.03.2011)
Yelchuri, Ravi Kumar (BMBF, 16.11.-10.12.2010)

Goals

The research of the Yeast Genetics group focuses on the development of yeast as a model organism to study **osmo- and salt tolerance**. Yeast is a valuable tool to characterise metabolic pathways in eukaryotes and is able to synthesise **biotechnologically interesting products**. In addition they are used as microbial compounds of **biosensors**. Yeast species that are used are *Saccharomyces cerevisiae* and **non-*Saccharomyces* yeasts** such as *Arxula adeninivorans* and *Hansenula polymorpha.* Both are completely sequenced and have annotated genomes. Yeast and filamentous fungi serve as sources for genes suitable for metabolic redesign of plants in order to improve the quality of end products or to develop recombinant microbes as biosensors to detect environmental pollutions. Moreover **arbuscular mycorrhizal fungi (AMF)** are in the centre of interest to analyse and optimise fungus-plant root interactions. They are used as a gene source to produce biotechnologically interesting AMF proteins improving plant growth even under stress conditions.

Research Report

Arxula adeninivorans is an attractive non-pathogenic organism for basic and applied research. Its biotechnological application results from special and remarkable characteristics, such as immense broad range of sole carbon and nitrogen sources, interesting temperature-dependent dimorphism, extreme thermo-, osmo- and salt tolerance, excellent growth and secretion characteristics. The genome of *Arxula* is completely sequenced and annotated enabling to explore and exploit new pathways such as the **metabolism of tannic acid, purine and n-butanol**. Furthermore *A. adeninivorans* is used as host for the synthesis of special products such as recombinant glycosylated secretory proteins. It serves as a suitable biocatalyst for the synthesis of biotechnological interesting products such as n-butanol, because all essential prerequisites and components for heterologous gene expression are available. Several specialised methods have been established (**transformation/expression platform Xplor®2, gene disruption, protoplast fusion, mitotic segregation**) and industrial strains were constructed. These strains are suitable producers of **enzymes to substitute chemical synthesis steps by biochemical steps** (1), to produce the **glycoprotein glomalin** as potential formulation additive, soil conditioner and product for the pharmacology (2), to **improve the biogas content** (3) and to produce **food with low purine content** (4). Other biotechnological application fields for *Arxula* cells are the **accumulation of metal ions**, **production of biobutanol** and its use as **biocatalyst of a microbial fuel cell (MFC)** that produces high levels of a reduced molecule to shuttle electrons from the cell to the electrode. This can serve as an alternative for conventional energy production in the future (D. Jankowska, A. Trautwein, M. Schwarz, E. Böer, U. Hähnel, J. Riechen, K. Florschütz, S. Worch, A. Kahlo, M. Kunze, K. Giese, M. Benito Alvaro, J.B. del Pino).

In addition *A. adeninivorans* is used as model organism for plants. Investigations in the field of osmo- and salt tolerance are performed within the intergroup project "Molecular analysis of salt tolerance in barley". This group focuses on the key pathways for osmo- and salt tolerance and on the identification of **compatible solutes** in barley and yeast. Barley and *A. adeninivorans* cDNA sequences encoding for products improving osmo- and salt tolerance are identified by complementation

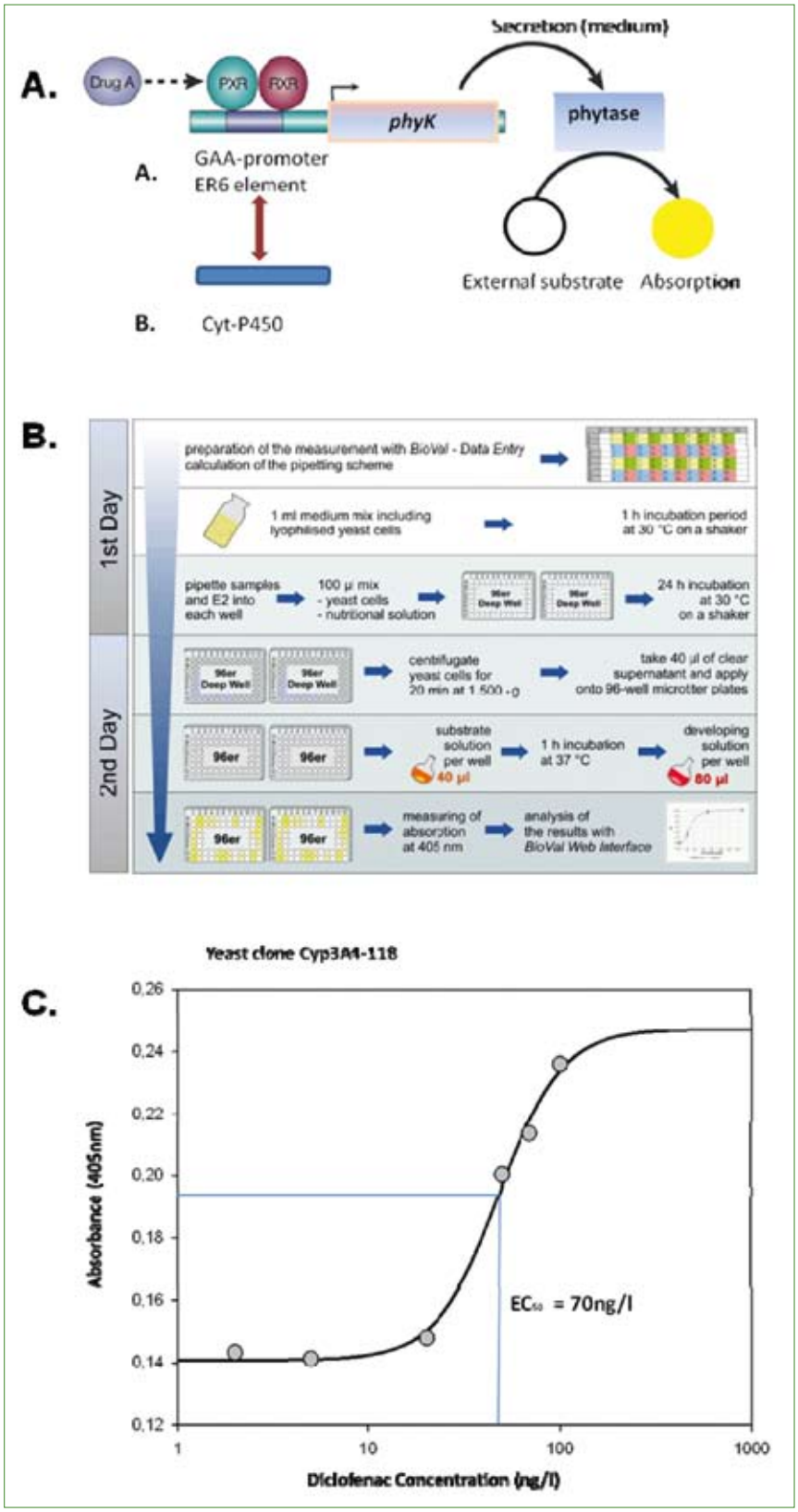

Fig. 49

A. Activation of reporter gene expression.
After binding of a xenobiotic element (Drug A) to the PX receptor, the receptor heterodimerises with its partner RXR and binds to the xenobiotic response element (ER6) located on the modified GAA-promoter. Alternatively, the human Cyp3A4 promoter was used to initiate specific reporter gene expression (Cyp3A4 yeast clones) in yeast cells.

B. Schematic illustration of the yeast biosensor workflow.

C. Reaction of the new biosensor cells exposed to different Diclofenac concentrations.
Cells were incubated over night in different Diclofenac concentrations at 30°C under constant shaking conditions. Afterwards the activity of the secreted phytase was determined by a colorimetric enzyme assay.

of the osmo- and salt-sensitive yeast *S. cerevisiae*. The analysis of the selected *A. adeninivorans* genes including gene products demonstrate that the HOG pathway is induced by two ways: (1) by phosphorylation of relevant enzymes as shown for yeast with moderate resistance and (2) by induction of HOG genes, such as *ASLN1, AYPD1, ASSK1, ASTE20,* the MAPKK kinases *ASTE11* and *ASSK2*, the MAPK kinase *APBS2* and the MAP kinase *AHOG1*. The phosphorylated Ahog1p induces the expression of genes encoding the synthesis of **compatible solutes**, such as glycerol, erythritol and mannitol. Whereas the levels of glycerol and erythritol correlate directly with the osmolarity of the culture media, intracellular mannitol is accumulated to a very high extent and is relatively independent of the medium osmolarity. This effect, together with the combination of phosporylation and gene induction, seems to provide better adaptation during transition from low to high osmolarity conditions (A. Trautwein, M. Dähne, E. Böer, P. Mock – Applied Biochemistry group, M. Melzer –Structural Cell Biology group).

Yeasts are also used as **microbial sensor compound for the detection of hormone activities (estrogenic, androgenic, progesteronic, glucocorticoidic activities), dioxins as well as pharmaceuticals** in tap water, mineral water, waste water, urine and blood serum. Sensors are based on recombinant *A. adeninivorans* cells which include the respective human receptors (hERα, hAR, hPR, hGR, AHR, PXR / RXR) and are designed as estrogen/androgen/progesterone/glucocorticoid/dioxin/pharmaceutical screen assays with biochemical measurement as well as microbial biosensors with an amperometric detection method. The **estrogen and androgen screen assay (A-YES and A-YAS assay)** have been validated for its suitability to measure estrogens and estrogen-like substances as well as androgens and androgen-like substances in samples of tap water, mineral water, urine and different wastewater treatment plants which have high matrix effects. With detection limits of approx. 0.5 ng l^{-1} for 17 ß-estradiol (E2) and 80 ng l^{-1} for 5α-dihydrotestosterone (DHT) the assays are applicable for a range of 0.5 to 80 ng l^{-1} effective E2 and 80 – 400 ng l^{-1} DHT concentrations, respectively. First assays (A-YES®_aqua, A-YAS®_aqua, A_YES®_aqua_salutaris) based on these sensor compounds are commercialised already. A parallel receptor functionalised microchips based on the **surface plasmon resonance technique** is established, which detect receptor-ligand interactions. Therefore the respective recombinant receptors are produced by the Xplor®2 transformation/expression platform in yeast (M. Giersberg, P. Thi Minh Ha, T. Gerlach, A. Chamas, C. Kaiser, A. Nieter, J. Saß, H. Greif, – see Fig. 49, p. 144).

Beside yeasts, **arbuscular mycorrhizal fungi (AMF)** are in the focus of the research group. They are able to establish a symbiotic relationship with 70 - 90 % of land plant species and obviously, this interaction has a major impact on the entire soil ecosystem. They improve the uptake of phosphorus and nitrogen by plants and are essential to protect plants against root pathogens and able to improve salt and drought tolerance. DNA content of AMF strains were determined by flow cytometry and confirmed afterwards by Feulgen densitometry. Furthermore, fluorescence *in situ* hybridisation (FISH) was used to determine the number of rDNA loci per genome. The two analysed *Glomus* isolates (AMykor and DAOM 197198) belong to *Glomus irregulare* species, have a genome size of approximately 150 Mb and obtained 1 or 2 rDNA loci per genome. For the taxonomic analysis of AMF, for the identification and classification of mycorrhiza residing on plant roots and the detection of **phytopathogenic viruses** on barley and potato biosensors based on DNA-DNA and DNA-RNA hybridisation, as well as antibody-antigen interaction have been developed and adapted. Based on DNA hybridisation, detection assays in the 96-well format and microchips based on the **surface plasmon resonance technique,** are able to analyse the mycorrhizal content in plant populations and phytopathogenic viruses in plants. The microtiter plate assay has been validated and applied in the analysis of the mycorrhizal content in a wood population growing under extreme conditions (K. Florschütz, K. Sedzielewska, D. Kleemann, A. Schröter, G. Oswald – Fig. 50, p. 146).

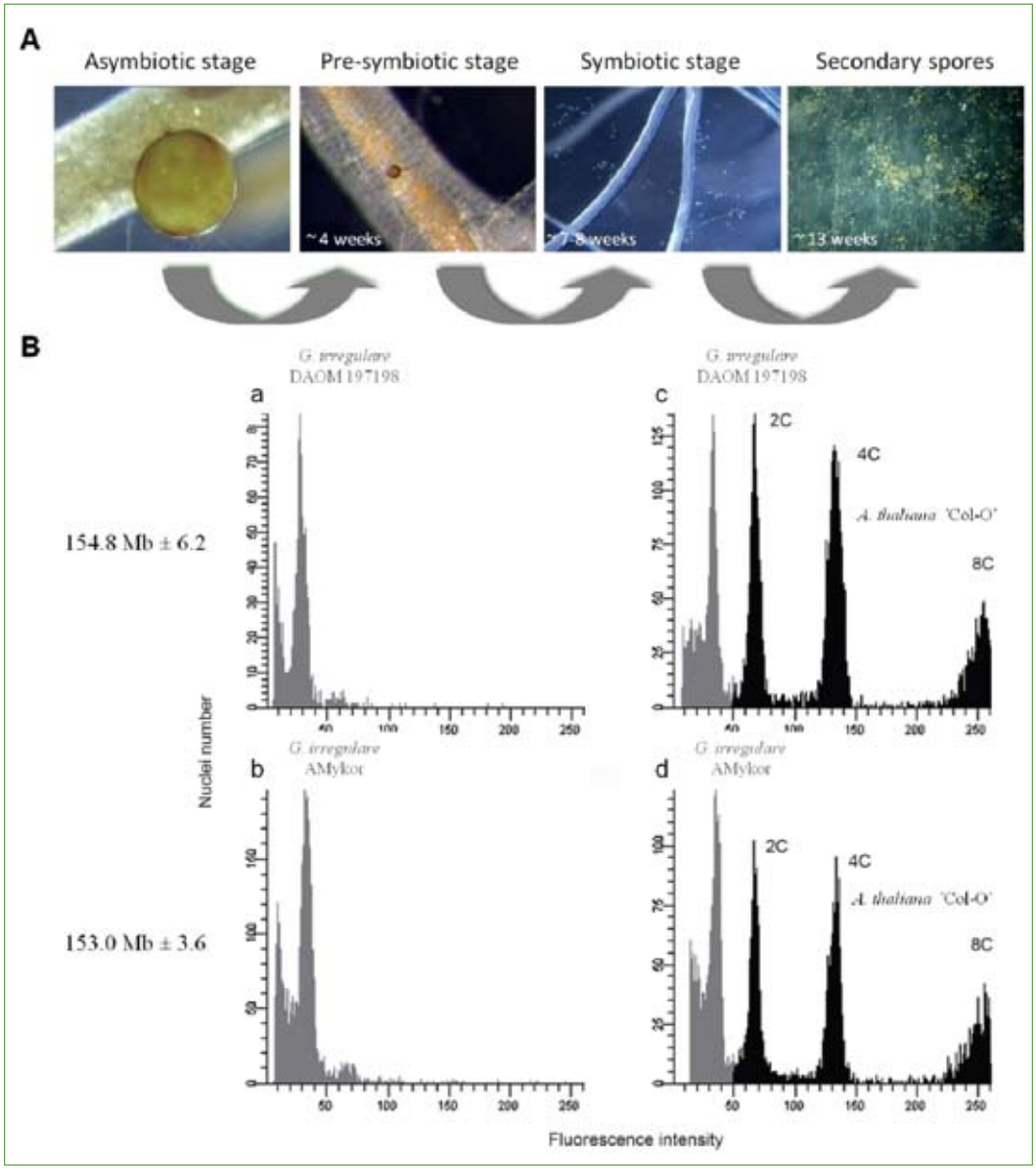

Fig. 50
A Life cycle of an arbuscular mycorrhizal fungus belonging to *Glomus irregulare* species.
B Histograms of relative fluorescence intensities obtained after flow cytometry analysis of propidium iodide-stained nuclei of (a) *G. irregulare* DAOM197198, (b) *G. irregulare* AMykor, (c) *G. irregulare* DAOM197198 (grey) with internal reference standard *A. thaliana* 'Col-O' (black), (d) *G. irregulare* AMykor (grey) with internal reference standard *A. thaliana* 'Col-O' (black). Due to endoreduplication occurring in *A. thaliana* leaf tissue nuclei (Galbraith et al., 1991), different ploidy levels are detectable. The first peak represents 2C nuclei with a DNA content of 0.32 pg. Fluorescence intensity of nuclei is expressed in arbitrary units (linear scale).

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2010

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Radchuk, R., U. Conrad, I. Saalbach, M. Giersberg, R.J. Emery, H. Küster, A. Nunes-Nesi, A.R. Fernie, W. Weschke & H. Weber: Abscisic acid deficiency of developing pea embryos achieved by immunomodulation attenuates developmental phase transition and storage metabolism. Plant J. 64 (2010) 715-730.

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Böer, E., F.S. Breuer, M. Weniger, S. Denter, M. Piontek & G. Kunze: Large-scale production of tannase using the yeast *Arxula adeninivorans*. Appl. Microbiol. Biotechnol. 92 (2011) 105-114.

Chelikani, V., F.J. Rawson, A.J. Downard, R. Gooneratne, G. Kunze, N. Pasco & K.H.R. Baronian: Electrochemical detection of oestrogen binding protein interaction with oestrogen in *Candida albicans* cell lysate. Biosens. Bioelectron. 26 (2011) 3737-3741.

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Sędzielewska, K.A., J. Fuchs, E.M. Temsch, K. Baronian, R. Watzke & G. Kunze: Estimation of the *Glomus intraradices* nuclear DNA content. New Phytol. 192 (2011) 794-797.

Singh, B., G. Kunze & T. Satyanarayana: Developments in biochemical aspects and biotechnological applications of microbial phytases. Biotechnol. Mol. Biol. Rev. 6 (2011) 69-87.

Worch, S., K. Rajesh, V.T. Harshavardhan, C. Pietsch, V. Korzun, L. Kuntze, A. Börner, U. Wobus, M.S. Röder & N. Sreenivasulu: Haplotyping, linkage mapping and expression analysis of barley genes regulated by terminal drought stress influencing seed quality. BMC Plant Biol. 11 (2011) 1.

Books and Book Chapters

2010

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Florschütz, K., F. Sonntag, A. Schröter, S. Schmieder, U. Klotzbach & G. Kunze: On-Chip-Nachweis von phytopathogenen RNA-Viren und miRNA mittels Oberflächenplasmonenresonanz. In: Proc. Sensorforschung für Medizin und Technik. Sensor + Test (2011) 35-40.

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PhD and Diploma Theses

2010

Kaiser, C.: Etablierung eines auf Hefezellen basierenden Assays zur Erfassung östrogener Wirkungen im Rahmen der Umwelt-, Nahrungs- und Futtermittelanalytik. (PhD Thesis) Ernst-Moritz-Arndt-Universität, Greifswald (2010) 175 pp.

Klemann, D.: Genetic diversity of arbuscular mycorrhizal fungi (AMP) and the influence of AMF on salt tolerance in *Medicago truncatula*. (Master Thesis) Universität Hohenheim, Hohenheim (2010) 98 pp.

Molitor, R.: Isolation und Charakterisierung der aus *Arxula adeninivorans* stammenden Gallussäure-Decarboxylase (GSDC)- und Dihydroxybenzoate-Decarboxylase (ADBC)-Gene. (Bachelor Thesis) Hochschule Anhalt (FH), Köthen (2010) 84 pp.

Nieter, A.: Entwicklung eines auf Hefezellen basierenden Biosensors zum Nachweis von Substanzen mit glucocorticoider Wirkung. (Bachelor Thesis) Martin-Luther-Universität Halle-Wittenberg, Halle/S. (2010) 49 pp.

2011

Dähne, M.: Untersuchungen des HOG-Pathways bei Hefen. (Bachelor Thesis) Hochschule Anhalt (FH), Köthen (2011) 59 pp.

Giese, K.: Tanninabbau in *Arxula adeninivorans* – Charakterisierung und Funktionsanalyse der Tannase 2 (Atan2p). (Bachelor Thesis) Hochschule Anhalt (FH), Köthen (2011) 104 pp.

Greif, H.: Nachweis der Pregnan-X-(PXR)-, Retinoid-X-(RXR)-Rezeptor Heterodimerisierung durch bimolekulare Fluoreszenz-Komplementation. (Bachelor Thesis) Hochschule Anhalt (FH), Köthen (2011) 83 pp.

Kahlo, A.: Enzyme als Biokatalysatoren zur Synthese von Zuckerderivaten für die Biomedizin und Biotechnologie. (Bachelor Thesis) Hochschule Anhalt (FH), Köthen (2011) 77 pp.

Patents

2010

Kunze, G., K. Florschütz, R. Watzke, K. Watzke & R. Hacker: „Verfahren zum Nachweis von Mykhorrizapilzen". Anmeldetag: 21.04.2009, Offenlegung: 08.12.2010, IPK Nr. 2009 / 03.

Kunze, G., K. Florschütz & M. Körner: „Biosensor und Verfahren zur Regelung einer Wasseraufbereitungsanlage". Anmeldetag: 25.06.2009, Offenlegung: 30.12.2010, IPK Nr. 2009 / 05.

Research Group: Systems Biology

Head: Dr. Björn Junker

Scientists

IPK financed
Bundtzen, Sophie, Dr. (0.50, 01.06.-31.12.2011)
Poskar, Hart, Dr. (01.02.-14.05.2010)

Grant Positions
Baker, Syed Murtuza (0.50 BMBF)
Bundtzen, Sophie, Dr. (0.50 Industry, 15.11.2010-31.05.2011)
Franke, Mathias (0.50 BMBF)
Hüge, Jan, Dr. (BMBF, since 01.08.2010)
Krach, Christian, Dr. (BMBF)
Liiving, Tiina (0.50 BMBF)
Poskar, Hart, Dr. (Industry, since 15.05.2010)
Schallau, Kai, Dr. (BMBF, till 31.10.2011)

Goals

Understanding the dynamics of plant metabolic pathways, especially in seeds of crop plants, by a combination of computer modeling and biochemical analysis.

Research Report

The major scientific focus of the group is the **metabolism of plant seeds**, which is investigated by applying systems biology methods. **Mathematical models** of metabolism are created, and the **experimental data** necessary for these models is generated. Thus, the work is divided approximately 50/50 into experimental methods for data generation and theoretical methods for data processing and prediction.

The group is funded by a 5-year **BMBF** grant as a **FORSYS-Partner Junior Research Group** since Juli 2008. In the last two years, several state-of-the-art methods have been established and are now used as the work horses of the group. The main method is steady-state **metabolic flux analysis**, in which computational models of plant metabolism are enriched by stable isotope labelling data obtained from the lab. This method has been applied to investigate metabolic processes taking place at the filling stage in **legume seeds**, especially pea (*Pisum sativum*) and barrel medic (*Medicago truncatula*), as well as **cereal seeds**, above all barley (*Hordeum vulgare*) and rice (*Oryza sativa*).

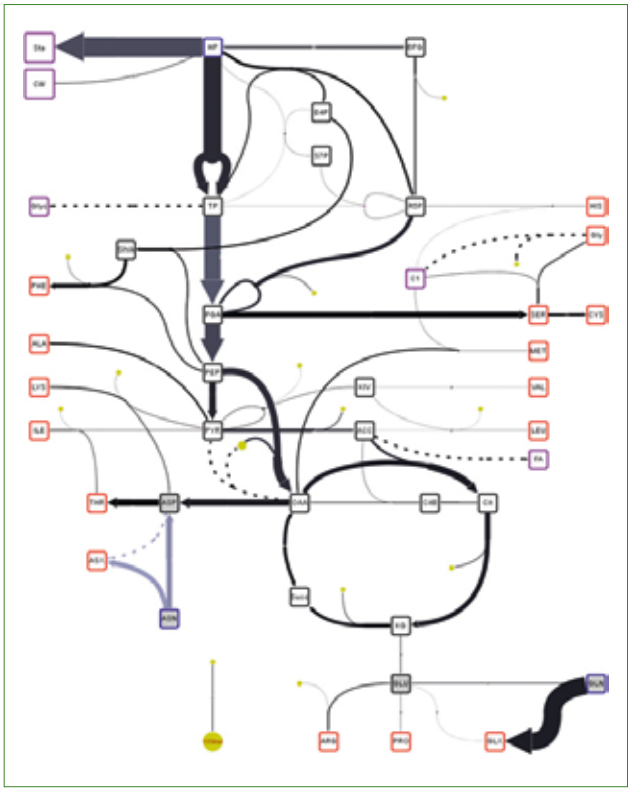

Fig. 51
A map of intracellular metabolic fluxes of developing pea seeds (H. Poskar, C. Krach).

For steady-state metabolic flux analysis several experimental and computational parts of the method had to be established in the group: embryo cultures, stable isotope feeding experiments and sample preparation (N. Schäfer, F. Kellner, L. Fichtmüller), analysis by GC-MS (J. Hüge), automatic data extraction and correction for natural isotope abundance (H. Poskar, M. Franke), as well as model creation for pea and *Medicago* central metabolism (C. Krach). The resulting flux maps cover large parts of central metabolism and resolve cyclic and parallel fluxes (see Fig. 51).
Due to the highly complex and laborious nature of steady-state metabolic flux analysis, in the past the method has been applied to small numbers of genotypes or treatments (usually not more than 3 per study). We have significantly increased the throughput of the method by using lab automation, simplifying the laboratory protocols, and automating the computational pipeline from data extraction to flux modelling. Currently, we have studies under way for flux comparison of more than 100 genotypes. Thus, the screening of medium-scale plant populations for individuals with desired flux phenotypes is now possible.

In the reported period, several stoichiometric and kinetic models have been set up for seed metabolism of different species (K. Schallau, S. Weber, K. Lotz, S.M. Baker), covering central metabolism of the seeds. These models are constantly filled by experimental data, which is derived from metabolite and enzyme measurements (N. Schäfer, F. Kellner, V. Peter). For pea seeds, we have set up a non-aqueous technique to analyse metabolites and enzymes in a sub-cellular way (T. Liiving). For the kinetic models, parameters that could not be measured may be estimated by a new computational pipeline for parameter identifiability analysis and parameter estimation with an improved algorithm tailored for biochemical data (S.M. Baker). With the help of the kinetic models, targets for metabolic engineering can be predicted to improve seed composition. We have started to verify the predicted strategies by generating the respective genetic constructs and transforming them into plants. First results from these plants will be obtained in 2012.

Publications

Peer Reviewed Papers

2010

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Floss, D.M., K. Schallau, S. Rose-John, U. Conrad & J. Scheller: Elastin-like polypeptides revolutionize recombinant protein expression and their biomedical application. Trends Biotechnol. 28 (2010) 37-45.

Hippe, K., C. Colmsee, T. Czauderna, E. Grafahrend-Belau, B.H. Junker, C. Klukas, U. Scholz, F. Schreiber & S. Weise: Novel developments of the MetaCrop information system for facilitating systems biological approaches. J. Integr. Bioinform. 7 (2010) e125.

Koschützki, D., B.H. Junker, J. Schwender & F. Schreiber: Structural analysis of metabolic networks based on flux centrality. J. Theor. Biol. 265 (2010) 261-269.

Schallau, K. & B.H. Junker: Simulating plant metabolic pathways with enzyme-kinetic models. Plant Physiol. 152 (2010) 1763-1771.

Sreenivasulu, N., L. Borisjuk, B.H. Junker, H.P. Mock, H. Rolletschek, U. Seiffert, W. Weschke & U. Wobus: Barley grain development toward an integrative view. Int. Rev. Cell Mol. Biol. 281 (2010) 49-89.

2011

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Huege, J., J. Goetze, D. Schwarz, H. Bauwe, M. Hagemann & J. Kopka: Modulation of the major paths of carbon in photorespiratory mutants of *Synechocystis*. PLoS One 6 (2011) e16278.

Junker, B.H.: Steady-state-^{13}C-Flussanalysen in Pflanzen. Biospektrum 17 (2011) 230-232.

Weise, S., J. Chen, B.H. Junker, M. Klapperstück, M. Lange, F. Schreiber & U. Scholz: Das Informationssystem MetaCrop zur Unterstützung systembiologischer Forschung an Kulturpflanzen. it - Information Technology 53 (2011) 234-240.

Books and Book Chapters

2010

Baker, S.M., H. Poskar & B.H. Junker: Unscented Kalman filter for estimation of multiple parameters in kinetic models. In: Nykter, M., P. Ruusuvuori, C. Carlberg & O. Yli-Harja (Eds.): Proc. 7th Intl. Conf. on Computational Systems Biology (WCSB2010), June 16-18, Luxembourg. Tampere International Center for Signal Processing. TICSP series 51 (2010) 19-22.

2011

Liiving, T., S.M. Baker & B.H. Junker: Biochemical fundamentals. In: Koch, I., W. Reisig & F. Schreiber (Eds.): Modeling in systems biology: the petri net approach. Springer Book Series Computational Biology, Vol. 16. Springer, New York, USA (2011) 19-36.

Schuster, S. & B.H. Junker: Topological analysis of metabolic and regulatory networks. In: Koch, I., W. Reisig & F. Schreiber (Eds.): Modeling in systems biology: the petri net approach. Springer Book Series Computational Biology, Vol. 16. Springer, New York, USA (2011) 209-224.

Other Papers

2010

Baker, S.M. & B.H. Junker: Adaptive unscented Kalman filter for estimation of parameters in kinetic metabolic models. Proc. 4th Int. Conf. on Computational Systems Biology (2010) 185-186.

Lemke, R., M. Hajirezaei, B.H. Junker, J. Müller, B. Usadel, M. Leps & F. Schreiber: MMM – Mehrskalen-Stoffwechselmodelle zur Systembiologie in Getreiden – ein integrativer Ansatz für die Biomasseforschung. Systembiologie.de 2 (2010) 51-53.

Electronic Publications

2010

Grafahrend-Belau, E., S. Weise, D. Koschützki, U. Scholz, B.H. Junker & F. Schreiber: MetaCrop – A detailed database of crop plant metabolism. http://metacrop.ipk-gatersleben.de (2010).

Weise, S., I. Grosse, C. Klukas, D. Koschützki, U. Scholz, F. Schreiber & B.H. Junker: Meta-All: A system for managing metabolic pathway information. http://meta-all.ipk-gatersleben.de (2010).

2011

Schreiber, F., C. Colmsee, T. Czauderna, E. Grafahrend-Belau, A. Hartmann, A. Junker, B.H. Junker, D. Koschützki, U. Scholz & S. Weise: MetaCrop 2.0. http://metacrop.ipk-gatersleben.de (2011).

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PhD and Diploma Theses

2011

Peter, V.: Vorhersage der subzellulären Verteilung von Enzymaktivitäten im Erbsensamen auf Basis von Expressionsdaten. (Bachelor Thesis) Hochschule Mittweida (2011) 79 pp.

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Pflanzengenom-Ressourcen-Centrum (PGRC)

Koordinator: Dr. habil. Patrick Schweizer

Das Pflanzengenom-Ressourcen-Centrum (PGRC; http://pgrc.ipk-gatersleben.de/) des IPK erbrachte in den Jahren 2010 und 2011 Serviceleistungen für interne Nutzer und externe Kooperationspartner, diente als wissenschaftlich-technische Plattform am IPK und koordinierte das internationale Forschungsnetzwerk BarleyGenomeNet (http://www.barleynet.org) für Genomforschung der Gerste. Die Organisation des PGRC befindet sich momentan in einem Prozess der Erneuerung, wie unten stehend weiter ausgeführt werden soll.

Für den wissenschaftlichen Forschritt der zum PGRC gehörenden Arbeitsgruppen wird auf die Jahresberichte der jeweiligen Gruppen verwiesen.

1. Service:
Die Serviceleistungen des PGRC wurden 2010 um SNP-Analyse unter Verwendung des VeraCode-Systems der Firma Illumina und 2011 um Populationsaufbau/Erhalt für Gerste, Weizen und (bei Bedarf) für *Arabidopsis thaliana* erweitert. Hingegen wird TILLING der Gerste nach Beendigung der entsprechenden Drittmittelförderung (GABI-TILL) nicht, wie ursprünglich erwogen, in der Form eines PGRC-Service weitergeführt, sondern soll allenfalls an einen kommerziellen Serviceprovider ausgelagert werden. Der entsprechende Einsatz von PGRC-Personal wurde beendet und stellte somit eine Projektunterstützung dar, die diversen internen und externen Nutzern der TILLING-Plattform zugutekam und dementsprechend Querschnittscharakter hatte. Die Mitarbeiterin wird seit 2011 im neuen Service „Populationsaufbau/Erhalt" eingesetzt. Infolge stark zurückgegangener Nachfrage nach Membranspotting wurde dieser Service formell beendet. Allgemein wird für die Zukunft eine noch stärkere Verlagerung der Serviceaktivitäten in Richtung Sequenzierung unter Verwendung herkömmlicher Sanger- als auch NGS-Technologien (ABI 3730, Roche FLX, Illumina HiSeq 2000) erwartet, bei gemeinsamer Nutzung der Geräte durch das PGRC-Serviceteam und durch einzelne Arbeitsgruppen.

2. Wissenschaftlich-technische Organisation:
Die bisherige Organisation des PGRC in sieben methodenorientierte Module konnte den Informationsbedarf im Hause nicht optimal befriedigen und soll daher zum Ende 2011 durch die inzwischen geschaffenen thematischen „task forces" wissenschaftlicher Arbeitsgruppen formell abgelöst werden. Ziel ist die Zusammenführung von Expertise in bestimmten Themenbereichen von arbeitsgruppenübergreifendem Interesse, ein effizienter Informationsfluss inklusive Know-how-Transfer zwischen Wissenschaftlern im Hause, und die Erarbeitung gemeinsamer Strategien für Gerätebeschaffungen, Antragsstellungen, interner und externer Kooperationen etc. Folgende Task Forces existieren zurzeit:

Plant Genome Resources Centre (PGRC)

Coordinator: Dr. Patrick Schweizer

The Plant Genome Resources Centre (PGRC; http://pgrc.ipk-gatersleben.de/) of the IPK provided services in the field of plant genomics to internal users and external cooperation partners in 2010 and 2011, served as platform for scientific exchange and coordinated BarleyGenomeNet (http://www.barleynet.org), an international network of institutions with a main research focus on barley genomics and genetics. The internal structure of the PGRC is currently under re-organisation as outlined below.

1. Service:
Service and support by the PCRC was extended by SNP analysis using the medium-throughput VeraCode system (Illumina Co.) in 2010 and in 2011 by population development and -maintenance for barley, wheat and (if requested) *Arabidopsis thaliana*. These species were nominated by group leaders in 2010. On the other hand, it was decided not to continue TILLING in barley as a PGRC service after the GABI-TILL (BMBF) project came to an end although this was initially considered. Instead, outsourcing of the barley TILLING resource to a commercial service provider is considered. The PGRC technician who had supported GABI-TILL and thus provided TILLING service to internal and external users has been re-integrated into the PGRC core team and is now responsible person for the new population service. Because of a strong decline of requests for membrane spotting this service is being terminated. The same applies to the fragment analysis service on capillary sequencer MegaBACE1000. In general, it can be expected that within the next two years service activities will continue to shift toward sequence-based analyses by Sanger- and especially next-generation sequencing using ABI 3730, Roche FLX and Illumina HiSeq 2000 instruments together with specific research groups.

2. Scientific-technical organisation:
The initial organisation of the PGRC in seven method-oriented research modules did not optimally meet the information needs of IPK scientists and shall therefore be formally replaced by a task-force structure by the end of 2011. These task forces are aimed at bringing together scientific expertise for fields of general interest, to foster the flow of information including know-how transfer between scientific groups at the institute, and to develop common strategies for the acquisition of large instruments, grant proposals, cooperations etc. The following task forces exist to date:

- Next Generation Sequencing (NGS, Coord. N. Stein)
- Association Genetics (Coord. B. Kilian)
- Stress Integration (Coord. P. Schweizer)
- Phenomics (Coord. T. Altmann)
- Metabolite Analysis (Coord. H.-P. Mock).

- Next Generation Sequencing (NGS, Koord. N. Stein)
- Assoziationsgenetik (Koord. B. Kilian)
- Stressintegration (Koord. P. Schweizer)
- Phenomics (Koord. T. Altmann)
- Metabolite Analysis (Koord. H.-P. Mock)

Die Task Forces veranstalteten eine Reihe von Arbeitstreffen und/oder Seminaren, die sich an alle wissenschaftlichen Mitarbeiter oder an Gruppenleiter richteten. Die Schaffung einer weiteren Task Force „Mikroskopie" soll eruiert werden.

3. Nationale und internationale Netzwerke:
Das internationale Netzwerk von Institutionen mit schwerpunktmäßigem Interesse an der Genomforschung der Gerste, BarleyGenomeNet, wird weiterhin vom PGRC-Leiter P. Schweizer koordiniert. Nach rund acht Jahren des Bestehens erweist sich BarleyGenomeNet als fruchtbare Plattform für grundfinanzierte bi- respektive multilaterale Kooperationen mit dem Ziel gemeinsamer Publikation oder der Einreichung koordinierter Projektanträge. Leider wurde ein 2011 zum zweiten Mal eingereichter Antrag zur Förderung eines Marie-Curie-Projektes (ITN, integrated training and research network) des Netzwerkes zur vielfältigen Rolle von Abscisinsäure in der Gerste nicht bewilligt, soll aber 2012 nochmals in verbesserter Form eingereicht werden. Die BarleyGenomeNet-Partner werden am 24./25. November 2011 am James Hutton Institute in Dundee zum nächsten Jahrestreffen zusammenkommen, um unter anderem den ITN-Antrag zu planen und weitere Fördermöglichkeiten zu erörtern.
Weitere für das PGRC bedeutsame Netzwerke wie das Internationale Gerstengenom-Sequenzierungskonsortium (IBSC) und die COST-Aktivität „TritiGen" wurden mit maßgeblicher Beteiligung von PGRC-Mitgliedern weitergeführt.

Patrick Schweizer, November 2011

The task forces have organised a number of workshops and seminars involving either all IPK scientists or group leaders. The formation of an additional task force "Microscopy" should be evaluated in the near future.

3. National and international networks:
The international network of institutions with a major interest in barley genomics and genetics, BarleyGenomeNet, continues to be coordinated by the PGRC leader P. Schweizer. After about eight years of existence, BarleyGenomeNet proved to be a fruitful platform for bi- or multilateral core-funded collaborations aiming at joint publications or generation of proof of concept data that are important for coordinated grant proposals. Unfortunately, a joint proposal for a Marie Curie Research and Training Network (ITN) about the multiple roles of abscisic acid in barley was not successful in 2011 but will be improved and resubmitted in 2012. This will be discussed among other issues at the upcoming annual network meeting taking place at The James Hutton Institute in Dundee in November 2011. Other relevant networks such as the International Barley Sequencing Consortium (IBSC) and the COST action "TritiGen" are being coordinated or supported by PGRC scientists.

For scientific progress achieved in research groups belonging to the PGRC, please read the reports of the corresponding groups.

Patrick Schweizer, November 2011

Die Entwicklung der Bioinformatik am IPK

Koordinator: Prof. Dr. Falk Schreiber

In den Jahren 2010/2011 hat sich die Bioinformatik kontinuierlich zu inzwischen sechs Arbeitsgruppen weiterentwickelt, davon zwei rein drittmittelfinanzierte Nachwuchsgruppen. Diese decken ein breites Spektrum bioinformatischer und systembiologischer Forschung ab, das von Datenbanken und Informationssystemen über Datenanalyse, Modellierung und Simulation bis zur Visualisierung reicht. Die Bioinformatik am IPK ist in vielfältigen interdisziplinären Projekten eng mit der biologischen Forschung am Institut, aber auch mit externen Partnern vernetzt. Für den wissenschaftlichen Fortschritt der Arbeitsgruppen und deren Kooperationen wird auf die Berichte der jeweiligen Gruppen verwiesen.

Durch die Bioinformatikgruppen werden unter anderem Datenbanken, Informationssysteme, und Software-Werkzeuge für die pflanzenbiologische Forschung entwickelt und unterhalten. Beispiele für Datenbanken und Informationssysteme sind das **Genbankinformationssystem** für die Verwaltung und das Management der Muster in der Genbank, die **European Barley-Database** mit über 150.000 Akzessionen europäischer Gerstensammlungen und dreier außereuropäischer Sammlungen sowie Evaluierungsdaten, die **Mansfeld-Datenbank** für kulturpflanzentaxonomische Informationen zu 6.100 weltweit kultivierten Pflanzenarten und **MetaCrop** mit Daten zu metabolischen Pathways diverser Kultur- und Modellpflanzen. Herausragende Bioinformatik-Tools sind VANTED zur Ansicht und Analyse von komplexen biochemischen Datensätzen, besonders von *omics-Daten im Kontext biologischer Netzwerke, **SBGN-ED** zum Erstellen, Ändern, Validieren und Exportieren von Diagrammen entsprechend dem Systems Biology Graphical Notation Standard, **FBASimVis** zur Rekonstruktion stöchiometrischer Modelle, deren Analyse mittels Flux Balance Analysis und der explorativen Visualisierung der Analyseergebnisse, **IAP** zur Verarbeitung der Bilddaten der Hochdurchsatz-Phänotypisierungssysteme am IPK, **Jstacs** für statistische Analysen und Sequenzklassifikation, und **Lailaps**, ein System zur Suche in nicht integrierten Life Science-Datenbanken.

The Development of Bioinformatics at IPK

Coordinator: Prof. Falk Schreiber

In 2010/2011 bioinformatics has continuously developed, encompassing now six bioinformatics research groups including two solely third-party funded junior research groups. They cover a wide spectrum of bioinformatics and systems biology research, which ranges from databases and information systems to data analysis, modelling and simulation, to visualisation. In a diversity of interdisciplinary projects, bioinformatics at the IPK is closely integrated with biological research at the institute, and also with many external partners. With regards to the scientific progress of the individual research groups and their collaborations, see the reports of the respective groups.

As part of their work the bioinformatics groups develop and host databases, information systems and software tools for plant research. Examples for databases and information systems are the **Genebank information system** for the management of accessions in the Genebank, the **European Barley Database** with over 150,000 accessions of European barley collections and three non-European collections as well as evaluation data, the **Mansfeld-Datenbank** for crop plant taxonomical information on 6,100 plant species cultivated worldwide, and **MetaCrop** with data about metabolic pathways of different crop and model plants. Important bioinformatics tools are VANTED for the visualisation and analysis of complex biochemical data sets, especially *omics data in the context of biological networks; **SBGN-ED** for the creation, editing, validation, and export of maps in the Systems Biology Graphical Notation standard; **FBASimVis** for the reconstruction of stoichiometric models, their analysis with Flux Balance Analysis, and the explorative visualisation of analysis results; **IAP** for the processing of image data from IPK high-throughput phenotyping systems; **Jstacs** for statistical analysis and sequence classification; and **Lailaps**, a system for the search in non-integrated life science databases.

Um die Bioinformatik als Einheit zu stärken und über das IPK hinaus sichtbar werden zu lassen, haben die Bioinformatikgruppen neben den eigenen Arbeiten eine Vielzahl gemeinsamer Aktivitäten durchgeführt. Erwähnenswert sind hier das gemeinsam von allen Gruppen durchgeführte Modul Bioinformatik für den AgriGenomics-Studiengang an der Christian-Albrechts-Universität zu Kiel; die (Mit)organisation internationaler Tagungen wie **International Symposium on Integrative Bioinformatics 2010** vom 20. bis 22. März 2010 in Cambridge (UK), **International Symposium on Integrative Bioinformatics 2011** vom 21. bis 23. März 2011 in Wageningen (Niederlande) und des **International Workshop on Systems Biology Graphical Notation** vom 21. bis 23. April 2010 in der Leucorea Wittenberg.

Auch in den nächsten Jahren soll der erfolgreiche Kurs fortgeführt und die Bioinformatik am IPK im Kontext der biologischen Forschung am Institut weiterentwickelt werden. Eine Herausforderung ist dabei einerseits die Stärkung von Bereichen, die durch die Bioinformatik bisher nicht ausreichend abgedeckt sind, andererseits die Verstetigung erfolgreicher Forschungsgebiete beispielsweise in den auslaufenden Nachwuchsgruppen. Zu erwähnen ist auch eine Tagung im nächsten Jahr, die von der Bioinformatik mit organisiert wird und zu der alle Interessierten bereits jetzt herzlich eingeladen sind: das **International Symposium on Integrative Bioinformatics** vom 2. bis 4. April 2012 in Hangzhou (China).

Falk Schreiber, November 2011

To strengthen bioinformatics as a unit and increase its visibility beyond IPK, in addition to their own work, the bioinformatics groups have carried out a large number of joint activities. Worth mentioning here are: the bioinformatics module for the study programme in AgriGenomics at the Christian Albrecht University Kiel; the international conferences **International Symposium on Integrative Bioinformatics 2010** from 20 to 22 March 2010 in Cambridge (UK), **International Symposium on Integrative Bioinformatics 2011** from 21 to 23 March 2011 in Wageningen (The Netherlands), and **International Workshop on Systems Biology Graphical Notation** from 21 to 23 April 2010 at the Leucorea Wittenberg.

Bioinformatics at IPK will continue to grow and develop in the future, reflecting the importance of this field of research to IPK as a whole. The challenge will be on the one hand to continue to expand bioinformatics at IPK into new areas not yet covered, on the other hand to continue to uphold successful research areas, for example, in the junior research groups for which funding is not continuous. All those interested in bioinformatics are warmly invited to an upcoming conference which is co-organised by IPK bioinformatics: the **International Symposium on Integrative Bioinformatics** from 2 to 4 April 2012 in Hangzhou (China).

Falk Schreiber, November 2011

Das Doktorandenprogramm

Sprecherin: Nicole Schmid

Derzeit forschen über 80 Doktoranden am Institut und sind durch das **PhD Student Board (PSB)** organisiert. Das PSB wurde vor ca. sieben Jahren gegründet und ist in einzelne Aufgabenbereiche unterteilt. Hauptaufgabe dieser selbstorganisierten Doktorandenvertretung ist die Durchführung eines promotionsbegleitenden Programms am IPK sowie die Organisation gemeinschaftlich orientierter Veranstaltungen. Seit 2008 verfügt das PSB über ein eigenes Budget, über welches ein vielfältiges Angebot an Seminaren, Exkursionen, Workshops etc. finanziert wird und damit die wissenschaftliche Ausbildung von Nachwuchswissenschaftlern am IPK komplettiert.

In den vergangenen zwei Jahren wurden über 10 Arbeitsseminare zur Vermittlung von Sozial- und Schlüsselkompetenzen angeboten, die sich zumeist reger Beteiligung erfreuten. Um ein möglichst optimales Workshop-Angebot aufstellen zu können, werden die Nachfrage und die Bedürfnisse der Doktoranden jährlich neu ermittelt. Eine anschließende Evaluierung der Veranstaltungen soll sicherstellen, dass Erwartungen und Qualitätsansprüche erfüllt werden. Zudem werden spezielle Anfragen jederzeit mit in das Programm aufgenommen. So konnte 2011 in Kooperation mit Dr. Armin Meister beispielsweise ein Statistikkurs angeboten werden oder, wie in 2010, ein Seminar zur Erlangung eines Zertifikats zur ‚Good Laboratory Practice' (GLP).

In Zusammenarbeit mit der BIO Mitteldeutschland GmbH werden seit letztem Jahr nun regelmäßig Exkursionen in die Industrie angeboten. Damit ist es den Doktoranden möglich, direkt ins Gespräch mit Personalverantwortlichen von Firmen wie Merz Pharmaceuticals, Bioplanta, VITA 34 AG etc. zu kommen und einen Einblick in Firmenabläufe zu erhalten. Zudem sind aber auch die Unternehmen in direkter Nachbarschaft zum IPK für das PSB von Interesse. Einladungen zu Firmenpräsentationen wurden von *SunGene* GmbH und TraitGenetics GmbH gern angenommen und sind auch zukünftig mit weiteren Firmen bereits in Planung. Das so erstellte Seminar- und Exkursionsangebot leistet damit einen wichtigen Beitrag zur Doktorandenausbildung am IPK. Dabei erlauben es insbesondere die Industrieexkursionen, einen Blick über den Tellerrand zu werfen, um auf diesem Wege auch alternative Karrierewege kennen zu lernen.

Des Weiteren hat sich das PSB mit seinen erfolgreichen Einladungen von international bedeutenden Wissenschaftler/-innen mittlerweile als fester Bestandteil des Seminarprogramms am IPK etabliert. Neben sechs eingeladenen Gastrednern, konnte beispielsweise der bekannte Professor Sir David C. Baulcombe von der University of Cambridge dieses Jahr am IPK begrüßt werden. Damit fördert das PSB den Kontakt zwischen Doktoranden und der wissenschaftlichen Gemeinschaft über das IPK hinaus.

The PhD Programme

Speaker: Nicole Schmid

More than 80 PhD students study and work at the IPK and are organised by the **PhD Student Board (PSB)**. The PSB was founded about seven years ago and is structured into different task forces. The main responsibility of this self-organised PhD student representatives is the implementation of the PhD development programme at IPK as well as the organisation of social events. Since 2008, PSB managed its own budget. It is used to finance PhD development programme consisting of diverse events such as seminars, study trips and workshops and thereby completes the education of young scientists at IPK.

In the past two years more than 10 workshops offering social and key competencies have been organised, usually attracting a stable number of participants. In order to provide relevant workshops, the special demands and needs of students are collected via short surveys every year. An evaluation after the completion of the event ensures the implementation meets particular expectations and quality requirements. In addition, further specific requests can be integrated into the programme at any time. For example, this year a statistics seminar was offered in cooperation with Dr. Armin Meister, and a seminar to gain a 'Good Laboratory Practice' (GLP) certificate was held in 2010.

In cooperation with BIO Mitteldeutschland GmbH study trips to larger firms were initiated last year and are now regularly offered. The PhD students have the opportunity to talk directly to human resources managers and get interesting insights into the businesses of companies such as Merz Pharmaceuticals, Bioplanta and VITA 34 AG. Furthermore, companies on-campus are of particular interest and were invited by the PSB. Therefore *SunGene* GmbH and TraitGenetics GmbH gave valuable overviews about their concepts and strategies and it is planned that other companies will be invited in the future. The seminar and education programme makes an important contribution to the PhD qualification at IPK. The study trips to enterprises are especially valuable in enabling the students to get to know alternative career options and to see a broader picture.

Over the past years the PSB has integrated itself into the seminar programme of IPK and hosted prestigious international scientists. In addition to six invited guest speakers, the renowned scientist Professor Sir David C. Baulcombe from Cambridge University was welcomed at IPK. With those seminars PSB promotes the contact between PhD students and the scientific community beyond IPK.

Abb. 52
Die ersten Preisträger des „Beagle Awards": Dr. Manuela Nagel (l.; Ag Ressourcengenetik und Reproduktion), Dr. Nicolai M. Nürk (Mitte; Ag Experimentelle Taxonomie) und Dr. Astrid Junker (r.; Ag Pflanzenbioinformatik; Foto: R. Schnee/IPK Gatersleben).

Fig. 52
The first award winners of the newly established 'Beagle Award': Dr. Manuela Nagel (Resources Genetics and Reproduction group), Dr. Nicolai M. Nürk (Experimental Taxonomy group) and Dr. Astrid Junker (Plant Bioinformatics group). (left to right; Photo: R. Schnee/IPK Gatersleben).

Eine weitere Aktivität des PSB ist die Organisation der **Plant Science Student Conference (PSSC)**, welche 2012 zum achten Mal stattfinden wird. Diese Konferenz wird von Doktoranden für Doktoranden organisiert und findet jährlich im Wechsel mit dem IPB Halle statt. Zwischen 70 und 80 Nachwuchswissenschaftler aus Instituten der Leibniz-Gemeinschaft, der Max-Planck-Gesellschaft und der Julius Kühn-Institute kommen dabei regelmäßig zusammen und haben die Möglichkeit, ihren Promotionskollegen ihre Forschungsarbeiten in Form von Vorträgen und Posterpräsentationen vorzustellen. Herausragende Beiträge werden dabei von einer kompetenten Jury, bestehend aus mindestens fünf etablierten Wissenschaftlern, ausgezeichnet.
Erstmals konnte in diesem Jahr der sogenannte **"Beagle Award"** verliehen werden. Dieser institutsinterne Preis wurde nach mehrjähriger Planung vom PSB am IPK etabliert und hat zum Ziel, sowohl die wissenschaftlichen Leistungen als auch die gemeinschaftlich-sozialen Fähigkeiten und das Engagement von Doktoranden, die am IPK tätig sind, zu würdigen und soll jährlich ausgeschrieben werden. In diesem Jahr wurden Astrid Junker, Manuela Nagel und Nicolai Nürk von der achtköpfigen Jury, die sich aus IPK-Wissenschaftlern, PSB-Mitgliedern und einem nichtwissenschaftlichen IPK-Mitarbeiter zusammensetzte, geehrt.
Als wichtiger Punkt zum Ausbau des promotionsbegleitenden Programms des PSB wird die Einführung einer wissenschaftlichen Seminarreihe betrachtet, in der die Forschungsschwerpunkte des IPK von IPK-Wissenschaftlern an die Doktoranden vermittelt werden. In diesem Zusammenhang wurde bereits zu Beginn letzten Jahres innerhalb des PSBs ein detailliertes Konzept zur Etablierung eines Doktorandenprogramms erarbeitet und intensiv mit Verwaltungs- und Direktoriumsmitgliedern diskutiert. Ziel dieser Anstrengungen ist es, ein Doktorandenprogramm in Form einer umfassend strukturierten **"Graduate School"** aufzubauen, in der das promotionsbegleitende Programm des PSB als obligatorischer Teil der Doktorandenausbildung fest integriert ist.

Nicole Schmid, November 2011

The PSB is also organiser of the **Plant Science Student Conference (PSSC)** which will be held for the 8th time in 2012. This conference is organised by PhD students for PhD students and is taking place at IPK and IPB Halle biannually. Between 70 and 80 young scientists from institutes of the Leibniz Association, the Max Planck Society and the Julius Kühn Institutes can present their research as oral and poster presentations to other PhD students. Outstanding performances are finally awarded prizes by an experienced jury consisting of at least five established scientists.
In 2011 the **'Beagle Award'** was awarded for the first time. This IPK-wide prize was established by the PSB and aims to recognise the scientific achievements and social dedication of PhD Students and will be announced every year. Astrid Junker, Manuela Nagel and Nicolai Nürk received the award after an evaluation by an eight-member jury that consisted of IPK scientists, PSB members and non-scientific IPK staff.

An important step for the improvement of the PhD development programme is the introduction of a seminar series that gives information about the main research topics of the institute to be presented by IPK scientists. In this respect the PSB has developed a detailed concept for the establishment of a course programme at IPK that was discussed thoroughly with responsible persons from the administration and the Board of Directors. The main aim of these intensive efforts is the formation of a comprehensively structured **'Graduate School'** which integrates the programme organised by the PSB as an obligatory part of the PhD qualification at IPK.

Nicole Schmid, November 2011

Kolloquien und Seminare/
Colloquia and Seminars

Gatersleben Lectures

2010

16. Februar 2010
Prof. Dr. C. Jung, Christian-Albrechts-Universität zu Kiel, Institut für Pflanzenbau und Pflanzenzüchtung, Kiel, Germany: Bolting time control in sugar beet and applications in plant breeding.

24. März 2010
Prof. Dr. M. D. McMullen, University of Missouri, Division of Plant Sciences, Columbia, USA: Using genetic diversity to understand phenotypic variation in maize.

29. April 2010
Prof. Dr. M. Yano, QTL Genomics Research Center, National Institute of Agrobiological Sciences, Tsukuba, Japan: Genomics-assisted allele mining and its integration to breeding in rice.

11. Mai 2010
Prof. Dr. G. Coupland, Max-Planck-Institut für Pflanzenzüchtungsforschung, Abt. Entwicklungsbiologie der Pflanzen, Köln, Germany: Seasonal flowering in annual and perennial plants.

17. August 2010
Prof. Dr. U. Bonas, Martin-Luther-Universität Halle-Wittenberg, Institut für Biologie, Abteilung Pflanzengenetik, Halle/S., Germany: How a bacterial pathogen effector manipulates plant transcription.

21. Oktober 2010
Prof. Dr. S. Abel, Leibniz-Institut für Pflanzenbiochemie, Abt. Molekulare Signalverarbeitung, Halle/S., Germany: Phosphate sensing in root development.

16. November 2010
Prof. Dr. W. Martin, Heinrich-Heine-Universität Düsseldorf, Institut für Botanik, Düsseldorf, Germany: Hydrothermal vents and the origin of life, what is the connection?

2. Dezember 2010
Prof. Dr. C. Franklin, University of Birmingham, School of Biological Sciences, Molecular and Cell Biology, Birmingham, UK: Control of inter-homolog recombination in *Arabidopsis* meiosis.

6. Dezember 2010
Prof. Dr. W. B. Frommer, Stanford School of Medicine, Carnegie Institution for Science, Department of Plant Biology, Stanford, USA: FRET sugar sensors uncover a novel class of sugar transporters important for nutrient supply to pathogens.

2011

8. Februar 2011
Prof. Dr. J. Ma, Department of Cellular and Molecular Medicine, St. George´s Hospital Medical, London, UK: Manufacturing recombinant pharmaceuticals in plants – developing a pipeline of products.

14. März 2011
Prof. Dr. Q. Zhang, National Key Laboratory of Crop Genetic Improvement and National Center of Plant Gene Research Huazhong Agricultural University, Wuhan, China: Genetic and molecular characterization of grain size in rice.

3. Mai 2011
Prof. Dr. S. Schuster, Friedrich-Schiller-Universität, Jena, Germany: Biochemical examples of application of elementary-modes analysis to plant metabolism.

17. Mai 2011
Prof. Dr. C.-C. Schön, Lehrstuhl für Pflanzenzüchtung, Technische Universität, München, Germany: Genome-based prediction of testcross values in maize.

4. Juli 2011
Prof. Dr. M. B. Dickman, Texas A & M University, USA: Death be not proud: Modulation of programmed cell death for fungal disease development/stress tolerance in plants.

5. Juli 2011
Prof. Dr. P. Shaw, John Innes Centre, Norwich, UK: Chromatin dynamics and development.

8. Juli 2011
Prof. Dr. T. Fujiwara, Department of Applied Biological Chemistry, Graduate School of Agricultural and Life Sciences, University of Tokyo Yayoi, Japan: Specificity and universality of the relationship between plants and boron: Molecular mechanisms of acclimation to low and high boron conditions.

16. September 2011
Prof. Sir D. C. Baulcombe, University of Cambridge, Department of Plant Sciences, Cambridge, UK: Mobile short RNAs, epigenetics and hybrid phenotypes in plants.

26. September 2011
Prof. Dr. J. Messing, Waksman Institute of Microbiology, Rutgers University, New Jersey, USA: Quality Protein Maize.

11. Oktober 2011
Prof. Dr. P. Christou, Universitat de Lleida, Spain: Multi-gene and multi-pathway engineering for the nutritional improvement of food crops.

15. November 2011
Prof. Dr. R. Bock, Max-Planck-Institut für Molekulare Pflanzenphysiologie, Golm, Germany: Genes gone wild: experimental genome evolution in plants.

6. Dezember 2011
Prof. Dr. U. Paszkowski, University of Lausanne, Switzerland: The art and design of harmony: novel AM-factors from cereals.

Vavilov- und PGRC-Seminare/ Vavilov and PGRC Seminars

2010

9. März 2010
M. Rosenhauer, Hochschule für Technik und Wirtschaft Dresden, Fakultät Landbau/Landespflege, Dresden, Germany: Genetische Untersuchungen des Merkmals Langlebigkeit von Saatgut an der Spezies *Brassica napus* L.

7. April 2010
Dr. N. Tikhenko, Institute St. Petersburg State University, Lab. of Plant Genetics of Biological Research, St. Petersburg, Russia: Postzygotic reproductive isolation systems in plants.

13. April 2010
T. Struckmeyer, Julius Kühn-Institut, Bundesforschungsinstitut für Kulturpflanzen (JKI), Institut für Züchtungsforschung an gartenbaulichen Kulturen und Obst, Quedlinburg, Germany: Petersilie (*Petroselinum crispum*) – Charakterisierung der Variabilität.

11. Mai 2010
E. Mattana, Ph D. Università degli Studi di Cagliari, Centro Conservazione Biodiversità, Cagliari, Italy: Sardinian Germplasm Bank (BG-SAR): conservation strategies and research activities.

12. Mai 2010
Dr. D. T. F. Endresen, Nordic Genetic Resources Centre (NordGen), Biodiversity Informatics, Alnarp, Sweden: Predictive association between trait data and eco-geographic data for barley landraces (Trait mining with eco-geographic data for identification of trait properties useful for improvement of food crops).

20. Mai 2010
Dr. Y. Shavrukov, University of Adelaide, Australian Centre for Plant Functional Genomics, Adelaide, Australia: Nax3 – a novel gene for sodium exclusion in barley. Mapping and identification: Mystery and reality.

26. Mai 2010
Dr. M. Pelc, Warsaw University of Life Sciences, Department of Vegetable and Medicinal Plants, Warsaw, Poland: Medicinal and aromatic plants in Poland and approaches to preserve their germplasm.

7. Juli 2010
J. Walter, Helmholtz-Zentrum für Umweltforschung GmbH – UFZ, Department Naturschutzforschung, Leipzig, Germany: Do plants remember drought? Evidence for drought-memory in grasses.

11. August 2010
Dr. K. Zaynali Nezhad, Leibniz-Institut für Pflanzengenetik und Kulturpflanzenforschung (IPK) Gatersleben, Abteilung Genbank, Gatersleben, Germany: Genetic linkage map construction and identification of quantitative trait loci (QTLs) determining post-anthesis drought tolerance in bread wheat.

15. September 2010
Dr. P. Römer, GHG Saaten GmbH, Aschersleben, Germany: Evaluierung von verschiedenen Herkünften sowie von Zuchtmaterial von Basilikum (*Ocimum basilicum*) im Hinblick auf ihre Kältetoleranz.

20. Oktober 2010
Prof. Dr. F. Corbineau, University Pierre et Marie Curie, Faculty of Medicine, Paris, France: Seed deterioration and storage: Basic and applied aspects.

27. Oktober 2010
Dr. S. P.C. Groot, Plant Research International B.V., Wageningen Seed Centre, Wageningen, The Netherlands: The effect of oxygen on seed ageing.

3. November 2010
Prof. M. Stein, Seed Bank, Evogene Ltd, Rehovot, Israel: Introduction to Evogene and seed bank activity.

1. Dezember 2010
Dr. Johannes Ravn Jørgensen, Aarhus University, Faculty of Agricultural Sciences, Department of Genetics and Biotechnology, Slagelse, Denmark: Use of non-destructive technologies to determine seed quality.

2011

9. Februar 2011
Dr. E. Maul, Julius Kühn-Institut (JKI) Bundesforschungsinstitut für Kulturpflanzen, Institut für Rebenzüchtung Geilweilerhof, Siebeldingen, Germany: Die Domestikation der Rebe im Zeitraffer.

23. März 2011
T. Jinjikhadze, Ilia State University, National Botanical Garden of Georgia, Institute of Botany, Tbilisi, Georgia: Creation and use of the national inventory of wheat wild relatives (*Aegilops* L.).

31. März 2011
Dr. habil. H.K. Parzies, Universiät Hohenheim, Institut für Pflanzenzüchtung, Saatgutforschung und Populationsgenetik, Stuttgart, Germany: Marker assisted recurrent selection for increased outcrossing rates in barley and sorghum.

27. April 2011
A. Breuing, Leibniz-Universität Hannover, Institut für Zierpflanzen- und Gehölzwissenschaften, Hannover, Germany: Einschätzung der Kosteneffektivität verschiedener Strategien der Langzeiterhaltung von Knoblauch (*Allium sativum* L.) in der Genbank Gatersleben.

4. Mai 2011
Dr. S. Mira, Universidad Politecnica de Madrid, Departamento de Biologia Vegetal E.U.I.T. Agricol, Madrid, Spain: Seed conservation: physiological aspects and volatile production.

11. Mai 2011
Dr. W. Spielmeyer, CSIRO Plant Industries, Canberra, Australia: Durable rust resistance in wheat, are we there yet?

23. Juni 2011
Dipl.-Biol. C. Scheriau, Ruprecht-Karls-Universität Heidelberg, Fakultät für Biowissenschaften, COS, Abteilung Biodiversität und Pflanzensystematik, Heidelberg, Germany: The origin, centre of variation and evolutionary history of *Hypericum perforatum* L.

4. Juli 2011
Dr. Y. Turuspekov, Institute of Plant Biology and Biotechnology, Almaty, Kazakhstan: Barley research in Kazakhstan.

15. Juli 2011
Dr. I. Kranner, Royal Botanical Gardens, Kew, Millenium Seedbank Partnership, Richmond, UK: Was ist Stress? Konzepte und Beispiele für invasive und nicht-invasive Diagnostik von Samenqualität und -stress.

24. August 2011
Dr. A. Westphal, Julius Kühn-Institut (JKI) Bundesforschungsanstalt für Kulturpflanzen, Institut für Pflanzenschutz in Ackerbau und Grünland, Münster, Germany: Damage potential of cyst nematodes on field crops.

14. September 2011
Dr. J. Buitink, INRA, Department of Molecular Seed Physiology, Angers, France: Genetic analysis of seed-soluble oligosaccharides in relation to seed vigour in *Medicago truncatula*.

19. Oktober 2011
Dr. M. Havrlentova, CVRV, Plant Production Research Centre (PPRC), Piestany, Slovak Republic: Cereal β-D-glucan – a miracle or a reality?

23. November 2011
Dr. M. Muminova, Tashkent Chemical-Technological Institute, Tashkent, Uzbekistan: Antioxidants in and cold tolerance of *in vitro* cultures for cryopreservation.

30. November 2011
C.M. Richards, PhD, National Center for Genetic Resources Preservation, Fort Collins, CO, USA: Eco-geographic differentiation in dwarf sunflower (*Helianthus pumilus*).

30. November 2011
I. Thormann, Bioversity International, *Ex situ* conservation and use project, Maccarese, Rome, Italy: Bioversity International projects to conserve and use agrobiodiversity.

7. Dezember 2011
Dr. I. Ferraz, The National Institute of Amazonian Research, Manaus, Brazil: Tropische Baumsamen und die Erfahrungen des brasilianischen Samennetzwerks aus dem Amazonasgebiet.

14. Dezember
R. Joosen, Wageningen University, Department of Plant Physiology, Wageningen, The Netherlands: High-throughput germination analysis to determine the genetic landscape of seed performance.

Vavilov-Vortragsabende/Vavilov Lectures

2010

20. April 2010
N. Nürk, Leibniz-Institut für Pflanzengenetik und Kulturpflanzenforschung (IPK) Gatersleben, Abteilung Genbank, Gatersleben, Germany: Im Regen, im August, in Japan – Impressionen einer Exkursion.

2011

20. April 2010
E. Willner, Leibniz-Institut für Pflanzengenetik und Kulturpflanzenforschung (IPK) Außenstelle Nord, Abteilung Genbank, Malchow/Poel, Germany: Neuseeland – Eindrücke von einer Wander- und Studienreise.

19. Juli 2011
Dr. U. Lohwasser, Leibniz-Institut für Pflanzengenetik und Kulturpflanzenforschung (IPK) Gatersleben, Abteilung Genbank, Gatersleben, Germany: Jordanien – Land der Nabatäer.

Genetische Seminare/Genetics Seminars

2010

26. Januar 2010
D. Wiechers, Leibniz-Universität Hannover, Hannover, Germany: Modelling the influence of canopy structure on light distribution and productivity of cucumber.

1. Februar 2010
Dr. J. Kranigk, Bergdata Biometrics GmbH, Bonn, Germany: Analysis of natural geometric structures – examples and applications.

9. Februar 2010
Dr. B. Steiner, Universität für Bodenkultur Wien, Department IFA-Tulln, Tulln, Austria: Gene expression analysis of near isogenic wheat lines differing in two major resistance QTL after *Fusarium graminearum* inoculation.

17. März 2010
Dr. Y. Markaki, Ludwig-Maximilians-Universität München, Fakultät für Biologie, Ag Humangenetik, München, Germany: Histone H3 threonine 3 phosphorylation is part of an editable histone modification pattern that marks and configures mitotic chromatin.

12. April 2010
Prof. Dr. C. Cremer, Kirchhoff-Institut für Physik, Heidelberg, Germany: Lightoptical imaging of cellular structures at molecular resolution.

20. April 2010
Dr. U. Bechtold, University of Essex, Department of Biological Sciences, Colchester, UK: Over-expression of *Arabidopsis* Heat Shock Transcription Factor Alb increases drought tolerance, water productivity and basal disease resistance.

3. Mai 2010
O. Kirioukhova, PhD, University of Zurich, Institute of Plant Biology, Department of Plant Developmental Genetics, Zurich, Switzerland: A novel *Arabidopsis* orthologue of Inner Centromere Protein is critical for reproductive development.

31. Mai 2010
Dr. H. Vogel, Max-Planck-Institut für Chemische Ökologie, Abteilung Entomologie, Jena, Germany: Insect defenses in chemical coevolution.

14. Juni 2010
S. Andorf, Leibniz-Institut für Nutztierbiologie, Genetik und Biometrie, Ag Biomathematik und Bioinformatik, Dummerstorf, Germany: Integrating a molecular network hypothesis and QTL results for heterosis in *Arabidopsis thaliana*.

18. Juni 2010
B. Yang, PhD, Beijing Genomics Institute (BGI), Shenzhen, China: Harvest the fruits of genomics.

22. Juni 2010
K. Dehesh, University of California, College of Biological Sciences, Plant Biology Department, Davis, USA: Molecular mechanisms regulating stress signalling networks in plants.

5. August 2010
Dr. M. Wissuwa, Japan International Research Center for Agricultural Sciences (JIRCAS), Tsukuba, Japan: Abiotic stresses in rice and genetic factors contributing to tolerance.

20. September 2010
Dr. N. Ohmido, Kobe University, Faculty of Human Development, Graduate School of Human Development and Environment, Kobe, Japan: Chromosome analysis based on the synteny of legume plants.

23. September 2010
Prof. P. S. Soltis, University of Florida, Laboratory of Molecular Systematics and Evolutionary Genetics, Gainesville, USA: Polyploidy and plant evolution.

22. Oktober 2010
Dr. K. Vijverberg, Radboud University Nijmegen, Institute for Water and Wetland Research (IWWR), Department of Plant Genetics, Nijmegen, The Netherlands: Genetic fine-mapping of DIPLOSPOROUS in *Taraxacum* indicates a duplicated DIP-gene.

25. November 2010
Dr. D. Dechyeva, Technische Universität Dresden, Lehrstuhl für Zell- und Molekularbiologie der Pflanzen, Dresden, Germany: Integration of genetic linkage and chromosomal maps of sugar beet by high-resolution molecular cytogenetics.

8. Dezember 2010
Dr. M. Trujillo, Julius-Maximillians-Universität Würzburg, Julius-von-Sachs-Institut für Biowissenschaften, Lehrstuhl für Pharmazeutische Biologie, Würzburg, Germany: Plant U-box type E3-ubiquitin ligases as regulators of plant immunity.

2011

25. Januar 2011
Dr. A.-C. Cosendai, Universität Wien, Fakultät für Lebenswissenschaften, Abteilung Botanische Systematik und Evolutionsforschung, Wien, Austria: What influences geographical parthenogenesis patterns in *Ranunculus kuepferi*: apomixis, genetic diversity and/or evolution?

22. Februar 2011
Dr. R. Ivanov, Universität des Saarlandes, Naturwissenschaftlich-Technische Fakultät III, Abteilung für Molekulare Pflanzenbiologie und Botanik, Saarbrücken, Germany: Insights into the role of protein dynamics in *Arabidopsis* iron uptake.

25. Februar 2011
Prof. Dr. M. Lenhard, Universität Potsdam, Institut für Biochemie und Biologie, Arbeitsgruppe Genetik, Potsdam, Germany: Genetic control and evolutionary modification of plant organ size.

1. März 2011
Dr. B.-J. Shi, University of Adelaide, Australian Centre for Plant Functional Genomics, Adelaide, Australia: miRNA profiling in barley.

8. März 2011
apl. Prof. Dr. J. C. Reif, Universität Hohenheim, Landesanstalten und Versuchsstationen, Landessaatzuchtanstalt, Stuttgart, Germany: Modern biometrical models for QTL mapping of main and epistatic effects.

10. März 2011
Dr. Ir. B. van der Zaal, Leiden University, Institute of Biology, Leiden, The Netherlands: Zinc finger-based DNA binding proteins as tools for plant molecular genetics.

1. April 2011
Prof. Dr. S. Renner, Ludwig-Maximilians-Universität München, Fakultät für Biologie, Abteilung für Systematische Botanik und Mykologie, München, Germany: Sex Chromosomes in Land Plants.

12. April 2011
Prof. Dr. C. Peterhänsel, Leibniz-Universität Hannover, Institut für Botanik: Photorespiration redesigned, Hannover, Germany: Synthetic bypass reactions and what they tell us about evolution of the pathway.

14. April 2011
Prof. Dr. T. Börner, Humboldt-Universität zu Berlin, Institut für Biologie, Arbeitsgruppe Genetik, Berlin, Germany: Small genome and complex machinery: transcription of chloroplast genes.

19. April 2011
Dr. D. van Damme, Ghent University, VIB Department of Plant Systems Biology, Ghent, Belgium: Aurora kinase 1 and 2 are required for correct cell division plane orientation during formative divisions in *Arabidopsis*.

4. Mai 2011
PD Dr. J. Boch, Martin-Luther-Universität Halle-Wittenberg, Institut für Biologie, Abteilung Genetik, Halle/S., Germany: TAL effectors from *Xanthomonas* – a novel DNA-binding domain with programmable specificity.

30. Mai 2011
Dr. J. Parker, National Research Council Canada, Plant Biotechnology Institute, Saskatoon, Saskatchewan, Canada: The evolution of farming, plant breeding, and biotechnology – the next 30 years.

1. Juni 2011
Dr. P. J. van Dijk, Keygene N.V., Wageningen, The Netherlands: Molecular breeding to accelerate improvement of the Russian dandelion, a potential rubber crop.

5. August 2011
Prof. Dr. R. K. Varshney, International Crops Research Institute for the Semi-Arid Tropics, Patancheru, Hyderabad, India: Harnessing the potential of genomics and germplasm diversity for enhancing the legume productivity in Africa and Asia.

18. August 2011
Dr. M. Stam, University of Amsterdam, Nuclear Organisation Group, Amsterdam, The Netherlands: Gene regulation by epigenetics and chromosomal interactions: paramutation in maize.

25. August 2011
Prof. Dr. M. Guerra, Universidade Federal de Pernambuco, Departamento de Botânica, Recife, Brazil: Are chromosome banding methods still useful nowadays?

18. Oktober 2011
D. Orzaez, University of Valencia, Instituto de Biología Molecular y Celular de Plantas, Valencia, Spain: GoldenBraid: An iterative cloning system for standardized multigene assembly in plants.

30. November 2011
Prof. Dr. W. Traut, Universität Lübeck, Institut für Biologie, Lübeck, Germany: Evolution of sex chromosomes.

24. November 2011
Prof. S. Abrams, National Research Council Canada, Plant Biotechnology Institute, Saskatoon, Saskatchewan, Canada: Plant hormone research toward crop improvement.

8. Dezember 2011
Dr. A. Manetto, baseclick GmbH, Tutzing, Germany: Click chemistry – a novel technology for efficient labeling of DNA and protein.

Zellbiologische Seminare/Cell Biology Seminars

2010

15. Januar 2010
Prof. Dr. V. Passoth**,** Swedish University of Agricultural Sciences, Department of Microbiology, Uppsala, Sweden: Non-conventional yeasts for bioethanol production and beyond.

27. Januar 2010
Dr. L. Gugsa, Ethiopian Institute of Agricultural Research, EARO Holetta Research Centre, Holetta, Ethiopia: Biotechnology in the traditional Ethiopian cereal tef (*Eragrostis tef*).

2. Februar 2010
Prof. Dr. C. Stöhr, Ernst-Moritz-Arndt-Universität Greifswald, Institut für Botanik & Landschaftsökologie, Greifswald, Germany: Root specific plasma membrane proteins involved in nitrogen assimilation and metabolism.

4. Juni 2010
Dr. J. Hüge, Dr. J. Kopka, Max-Planck-Institut für Molekulare Pflanzenphysiologie, Angewandte Metabolom-Analyse/Wurzelmetabolismus, Golm, Germany: Metabolic profiling of cyanobacteria with special emphasis towards inorganic carbon limitation of *Synechocystis* sp. PCC 6803.

10. Juni 2010
Prof. J. Degenhardt, Martin-Luther-Universität Halle-Wittenberg, Institut für Pharmazie, Abteilung Pharmazeutische Biotechnologie, Halle/S., Germany: The roles of volatile terpenes in direct and indirect defenses of plants.

15. September 2010
Prof. Dr. R. Scheibe, Universität Osnabrück, Fakultät für Biologie und Chemie, Botanischer Garten, Osnabrück, Germany: Role of malate valves for redox-homeostasis in light and dark.

29. September 2010
Dr. A. Svatos, Max-Planck-Institut für Chemische Ökologie, Mass Spectrometry/Proteomics, Jena, Germany: Looking through mass spectrometric magnifying glass: distribution of metabolites in natural samples.

20. Oktober 2010
Dr. V. Ordenes, Center for Advanced Studies on Arid Zones (CEAZA), La Serena, Chile: BioaCu Initiative: From molecular function to clean production.

27. Oktober 2010
Dr. C. Neuvéglise, AgroParisTech/INRA, Department of Life Sciences and Health, Paris, France: Exploratory genomics of oleaginous yeasts.

27. Oktober 2010
Prof. Dr. C. Gaillardin, AgroParisTech/INRA, Department of Life Sciences and Health, Paris, France: Redirecting lipid metabolism in the oleaginous yeast *Yarrowia lipolytica***.**

18. November 2010
Dr. C. Hermans, Université Libre de Bruxelles, Faculté des Sciences, Brussels, Belgium: Root morphological adaptation to nitrate availability in the model species *Arabidopsis thaliana*.

6. Dezember 2010
Dr. G. Sahni, Institute of Microbial Technology, Chadigarh, India: Development of novel clot buster enzymes.

14. Dezember 2010
Dr. S. Tenzer, Johannes-Gutenberg-Universität Mainz, Universitätsmedizin, Institut für Immunologie, Mainz, Germany: Optimizing sample preparation and software for label-free quantitative proteomics.

14. Dezember 2010
Prof. Dr. H. Deising, Martin-Luther-Universität Halle-Wittenberg, Institut für Agrar- und Ernährungswissenschaften, Abteilung Pflanzenwissenschaften, Halle/S., Germany: Infection strategy of the maize pathogen *Colletotrichum graminicola*.

2011

5. Januar 2011
Dr. M. Pourkheirandish, National Institute of Agrobiological Sciences, Plant Genome Research Unit, Tsukuba Ibaraki, Japan: Domestication related gene in barley.

22. März 2011
S. Lingam, Universität Saarbrücken, Institut für Botanik, Saarbrücken, Germany: Expression and stability of the transcription factor FIT – Crosstalk between iron uptake, ethylene response and nitric oxide signalling.

9. Mai 2011
Prof. Dr. L. Anderson, University of Illinois at Chicago, Department of Biological Sciences, Chicago, USA: Enzyme-enzyme interaction in the plant cloroplast.

31. Mai 2011
Prof. Dr. S. Schmidt, The University of Queensland, Faculty of Science, School of Biological Sciences, Brisbane, Australia: Nitrogen stories from ecosystems to molecules.

23. Juni 2011
Dr. F. Barriere, Université de Rennes 1, Institut des Sciences Chimiques de Rennes, France: Enzymes and microbes as catalysts in fuel cells.

27. Juli 2011
Dr. M. Wissuwa, Japan International Center for Agricultural Sciences, Tsukuba, Japan: Phosphorus and Zinc efficiency in rice: From QTLs to tolerance mechanisms and associated gene.

22. August 2011
Dr. K. Baronian, University of Canterbury, School of Biological Sciences, Microbiology, Christchurch, New Zealand: The *Arxula* microbial fuel cell; can it match bacterial microbial fuel performance.

6. September 2011
Prof. Dr. S. Baginsky, Martin-Luther-Universität Halle-Wittenberg, Institut für Biochemie und Biotechnologie, Abteilung Pflanzenbiochemie, Halle/S., Germany: Functional proteomics: A cornerstone in plant systems biology.

2. November 2011
Dr. T. Boller, University of Basel, Institute of Botany, Basel, Switzerland: Pattern recognition receptors in plant innate immunity and some surprises with mycorrhizal fungi.

19. Dezember 2011
Dr. V. Ordenes Ortiz, Sciences & Biotechnology, Chile: Yeast-based technologies for biomining and bioremediation.

Waterman-Seminare/Waterman Seminars

2010

23. Februar 2010
D. Albrecht, Leibniz-Institut für Naturstoff-Forschung und Infektionsbiologie e.V. - Hans-Knöll-Institut (HKI) Jena, Abteilungen Systembiologie/Bioinformatik, Jena, Germany: OmniFung – Data Warehouse for integrating fungal omics data.

13. April 2010
Dr. I. A. Paponov, Albert-Ludwigs-Universität Freiburg, Fakultät für Biologie/Institut für Biologie II, Freiburg, Germany: Bioinformatics as a tool to reveal the mechanism of auxin action.

12. Mai 2010
Dr. D. T. F. Endresen, Nordic Genetic Resources Centre (NordGen), Biodiversity Informatics, Alnarp, Sweden: Predictive association between trait data and eco-geographic data for barley landraces (Trait mining with eco-geographic data for identification of trait properties useful for improvement of food crops).

3. Juni 2010
Dipl.-Inf. R. Henkel, Graduiertenkolleg dIEM oSIRIS, Universität Rostock, Fakultät für Informatik und Elektrotechnik (IEF), Institut für Informatik, Datenbank- und Informationssysteme, Rostock, Germany: Information retrieval for computational biological models.

11. August 2010
A. S. Ghassemi Hosseini, Technische Universität Darmstadt, Fraunhofer-Institut für Graphische Datenverarbeitung IGD, Darmstadt, Germany: Bone mineral density (BMD) assessment with dual energy CT.

3. September 2010
Prof. I. Small, University of Western Australia, ARC Centre of Excellence, Plant Energy Biology, Crawley, Australia: Perfectly prepared RNA: getting transcripts ready for translation.

23. September 2010
Dr. J. Hollunder, Ghent University, VIB Department of Plant Systems Biology, Ghent, Belgium: Module discovery – getting the 'gold' out of your data.

23. November 2010
M. Hotze, Friedrich-Schiller-Universität Jena, Fakultät für Mathematik und Informatik, Lehrstuhl Bioinformatik, Jena, Germany: *In silico* sequence optimization of synthetic genes and assignment of the expression levels using transcription analysis in *Candida albicans.*

2011

13. Januar 2011
Dr. M. Strickert, Universität Siegen, Institut für Bildinformatik, Siegen, Germany: Partial generalized correlation and matrix correlation mapping for high-dimensional data and multispectral images.

9. Februar 2011
Dr. M. van Iersel, Maastricht University, BiGCaT Bioinformatics and Systems Biology Research Group, Maastricht, The Netherlands: Data integration with biological pathways.

11. Februar 2011
Dr. A. C. Villéger, University of Manchester, School of Computer Science, Manchester, United Kingdom: Perspectives on the Visualisation of Biological Systems: From biochemical models to systems biology maps, and back.

23. März 2011
Dr. A. Beyer, Technische Universität Dresden, Biotechnologisches Zentrum (BIOTEC), Dresden, Germany: Disentangling genetic networks controlling complex traits.

26. Mai 2011
Dr. S. Arvidsson, Max-Planck-Institut für Molekulare Pflanzenphysiologie, Arbeitsgruppe Bioinformatik, Potsdam-Golm, Germany: Phenotyping *Arabidopsis thaliana* with the LemnaTec Scanalyzer HTS system.

27. Mai 2011
Prof. Dr.-Ing. R. Dachselt, Otto-von-Guericke-Universität Magdeburg, Fakultät für Informatik, Institut für Simulation und Graphik, Magdeburg, Germany: Natural ways of interacting with information spaces.

27. Mai 2011
Prof. Dr.-Ing. A. Nürnberger, Otto-von-Guericke-Universität Magdeburg, Fakultät für Informatik, Institut für Technische und Betriebliche Informationssysteme (ITI), Magdeburg, Germany: Context-based information exploration.

1. Juli 2011
Dr.-Ing. S. Oeltze, Otto-von-Guericke-Universität Magdeburg, Fakultät für Informatik, Institut für Simulation und Graphik, Magdeburg, Germany: Interactive, graph-based visual analysis of protein colocalization studies in toponomics.

7. Juli 2011
Dr. A. W. Schreiber, The University of Adelaide, Australian Centre for Plant Functional Genomics (ACPFG), Bioinformatics Group, Adelaide, Australia: Assembling the transcriptome of bread wheat.

8. Juli 2011
Prof. Dr. B. Meyer, Monash University, Faculty of Information Technology, Centre for Research in Intelligent Systems (CRIS), Clayton, Australia: Mavericks required – understanding collective decision making through diffusion modelling.

12. September 2011
A.-L. Lamprecht, Technische Universität Dortmund, Fakultät für Informatik, Dortmund, Germany: Semantics-supported design of bioinformatics workflows in Bio-jETI.

7. November 2011
J. Einloft, Johann-Wolfgang-Goethe-Universität Frankfurt am Main, Institut für Molekulare Biowissenschaften, Abteilung für Molekulare Zellbiologie der Pflanzen, Frankfurt am Main, Germany: MonaLisa - visualization of Petri nets and more.

Vorträge und Poster/ Lectures and Posters

Eingeladene Vorträge auf internationalen Tagungen (Auswahl)/Invited Lectures at International Conferences (Selection)

2010

V1. Agarwal, R., M. Melzer & J.K. Sainis (vorgetragen von Agarwal, R.): High Pressure Freezing of cyanobacteria for immunolocalisation studies. – International Conference on Advances in Electron Microscopy and Related Techniques & XXXI Annual Meeting of EMSI (EMSI-2010), Mumbai/India, 08.-10.03.2010.

V2. Altmann, T.: Analysis of *Arabidopsis* natural genetic variation and heterosis in biomass accumulation and metabolism. – 10th Korean-German Joint Symposium, Jinju/Korea, 27.-28.09.2010.

V3. Börner, A.: High quality long term conservation, reproduction and utilisation of plant genetic resources at the German *ex situ* genebank. – 2nd Workshop "Seed quality in genetic resources conservation of cultivated plants", Warsaw/Poland, 25.-26.05.2010.

V4. Florschütz, K., A. Schröter, M. Körner, S. Schmieder, F. Sonntag, U. Klotzbach & G. Kunze (vorgetragen von Florschütz, K.): Detection of phytopathogenic RNA-viruses. – 16th International Conference on Renewable Resources and Plant Biotechnology, NAROSSA®2010, Magdeburg, 07.-08.06.2010.

V5. Graner, A.: Exploiting the diversity of crop plants: present state and future challenges. – 2nd International Symposium on Genomics of Plant Genetic Resources, Bologna/Italy, 24.-27.04.2010.

V6. Graner, A.: Toward genomics-driven breeding of barley (*Hordeum vulgare*): challenges and opportunities. – 5th EPSO Conference "Plants for Life", Olos/Finland, 29.08.-02.09.2010.

V7. Graner, A.: Plant Genetic Resources: the challenge of valorization. – 54th Annual Congress of the Italian Society of Agricultural Genetics (SIGA), Matera/Italy, 27.-30.09.2010.

V8. Houben, A.: Mechanisms of uniparental genome elimination in wide hybrids. – SEB (Society for Experimental Biology) Annual Main Meeting, Prague/Czech Republic, 30.06.-03.07.2010.

V9. Houben, A.: Histone phosphorylation – a dynamic affair. – 7th Tri-National Arabidopsis Meeting (TNAM 2010), Salzburg/Austria, 15.-18.09.2010.

V10. Houben, A.: Mechanisms of uniparental chromosome elimination. – Symposium EPS theme 4 "Genome Plasticity", University of Wageningen, Wageningen/The Netherlands, 10.12.2010.

V11. Keller, E.R.J., A. Senula, C. Zanke, M. Grübe & A. Kaczmarczyk (vorgetragen von Keller, E. R. J.): Cryopreservation and *in vitro* culture – state of the art as conservation strategy for genebanks. – International Horticulture Congress IHC, Symposium on New Tools for Plant Genetic Resources, Lisbon/Portugal, 22.-29.08.2010.

V12. Kilian, B., S.S. Jakob, H. Özkan, S. Shaaf, F.A. Konovalov, R.K. Pasam, R. Sharma, S. Hübner, F. Salamini, A. Graner, M. von Korff & G. Coupland (vorgetragen von Kilian, B.): Comparing genetic diversity within a crop and its wild progenitor: a case study for barley. – ECPGR Symposium "Towards the Establishment of Genetic Reserves for Crop Wild Relatives and Landraces in Europe", Funchal/Madeira, 13.-16.09.2010.

V13. Krach, C. & B. H. Junker (vorgetragen von Krach, C.): Systems biology approaches to crop plant metabolism. – Brazil-Deutschland Systems Biology Meeting, Ouro Preto/Brazil, 25.-29.04.2010.

V14. Kumlehn, J.: Genetic engineering in cereals – methods and applications. – Symposium and Training Course on Climate Change – Challenge for Plant Breeding and the Biotech Response, Martonvásár/Hungary, 12.-16.04.2010.

V15. Kumlehn, J., T. Guse, C. Marthe, E. Grützemann, C. Bollmann & G. Hensel (vorgetragen von Kumlehn, J.): Haploid technology and genetic engineering in rye. – EUCARPIA - International Symposium on Rye Breeding & Genetics, Minsk/Belarus, 29.06.-02.07.2010.

V16. Melzer, M. & D. Daghma (vorgetragen von Melzer, M.): High pressure freezing and microwave-assisted tissue processing for transmission electron microscopy in plant research. – International Conference on Advances in Electron Microscopy and Related Techniques & XXXI Annual Meeting of EMSI (EMSI-2010), Mumbai/India, 08.-10.03.2010.

V17. Meyer, R.C., D. Riewe, K. Weigelt, B. Ebert, R. Schmidt, J. Lisec, M. Steinfath & T. Altmann (vorgetragen von Meyer, R.C.): Genetic and molecular analysis of early stage heterosis for growth related traits in the model species *Arabidopsis thaliana*. – EUCARPIA Cereal Section Meeting, Cambridge/UK, 06.-08.04.2010.

V18. Meyer, R.C., B. Ebert, B. Kusterer, J. Lisec, D. Riewe, R. Schmidt, M. Steinfath, K. Weigelt, A.E. Melchinger, J. Selbig, L. Willmitzer & T. Altmann (vorgetragen von Altmann, T.): Molecular and genetic analysis of biomass heterosis in *Arabidopsis thaliana*. – 21st International Conference on Arabidopsis Research, Yokohama/Japan, 06.-10.06.2010.

V19. Meyer, R.C., B. Ebert, B. Kusterer, J. Lisec, D. Riewe, R. Schmidt, M. Steinfath, K. Weigelt, A.E. Melchinger, J. Selbig, L. Willmitzer & T. Altmann (vorgetragen von Altmann, T.): Molecular and genetic analysis of biomass and metabolite heterosis in *Arabidopsis thaliana*. – Brassica2010,17th Crucifer Genetics Workshop, Saskatoon/Canada, 05.-09.09.2010.

V20. Nagel, M.: Genetics and physiology of seed longevity. – 2nd Workshop "Seed quality in genetic resources conservation of cultivated plants", Warsaw/Poland, 25.-26.05.2010.

V21. Rajanikant, C., M. Melzer & J.K. Sainis (vorgetragen von Rajanikant, C.): Visualizing DNA and DNA protein interactions of rice recombinase using TEM. – International Conference on Advances in Electron Microscopy and Related Techniques & XXXI Annual Meeting of EMSI (EMSI-2010), Mumbai/India, 08.-10.03.2010.

V22. Schubert, I.: DNA damage and its chromosomal endpoints in plants. – Plant and Animal Genome XVIII. Conference, San Diego/USA, 09.-13.01.2010.

V23. Schubert, I.: Interphase chromosome arrangement is dynamic and important for homologous recombination repair. – 2nd International Conference on Plant DNA Repair and Recombination 2010, Asilomar Conference Center, Pacific Grove, California/USA, 02.-05.03.2010.

V24. Schweizer, P.: Converging evidence for genes of basal defense in barley. – 2nd International Symposium on Genomics of Plant Genetic Resources, Bologna/Italy, 24.-27.04.2010.

V25. Schweizer, P.: Genes and loci for quantitative disease resistance in barley. – 4th International Workshop Rauischholzhausen, Schloss Rauischholzhausen, Gießen, 01.10.2010.

V26. Stein, N.: Physical mapping and sequencing of the barley genome: IBSC and the GABI program. – Plant and Animal Genome XVIII. Conference, San Diego/USA, 09.-13.01.2010.

V27. Stein, N.: Barley genome: maps & sequence. – EUCARPIA Cereal Section Meeting, Cambridge/UK, 06.-08.04.2010.

V28. Stein, N.: How to sequence a 5 Gigabase genome – a case study of barley (*Hordeum vulgare*). – 1st EMEA GS FLX User Meeting, Athens/Greece, 15.-17.06.2010.

V29. Steuernagel, B.: Utilizing next generation sequencing to analyze the complex genome of barley. – Bio IT World Europe Conference & EXPO 2010, Hannover, 05.-07.10.2010.

V30. von Wirén, N.: Morphological responses of *Arabidopsis* roots to localized iron supply. – 15th International Symposium on Iron Nutrition and Interactions in Plants, Budapest/Hungary, 26.-30.06.2010.

V31. von Wirén, N.: Identification of genes and mechanisms involved in nutrient acquisition and homeostasis. – XVII Conference of the Federation of European Societies of Plant Biology (FESPB 2010), Valencia/Spain, 04.-09.07.2010.

V32. von Wirén, N.: Localized ammonium supply increases lateral root branching. – 1st International Symposium on the Nitrogen Nutrition of Plants (Nitrogen2010), Inuyama International Sightseeing Center "FREUDE", Aichi/Japan, 26.-30.07.2010.

V33. Wobus, A.M.: Pancreatic differentiation of mouse embryonic stem cells and the potential of Sox17-positive cells. – EMBO Workshop "Disease, development and stem cells in the pancreas", Stockholm/Sweden, 14.-16.06.2010.

V34. Wobus, A.M.: Stem cell research in Germany with specific consideration of human embryonic stem cells. – Conference "Differing routes towards stem cell research: Germany and Italy", University of Trento/Italy, 21.-22.09.2010.

2011

V1. Altmann, T.: Molecular and genetic analysis of biomass- and metabolite-heterosis in *Arabidopsis* and maize. – European Plant Breeding Academy, Gatersleben, 20.06.2011.

V2. Altmann, T.: Molecular and genetic analysis of biomass- and metabolite-heterosis in *Arabidopsis* and maize. – Botanikertagung 2011 "Diversity makes the Difference", Berlin, 18.-23.09.2011.

V3. Altmann, T.: Molecular genetics of natural variation in plant growth and metabolism. – Banbury Meeting "Genotype to phenotype: Deriving biological knowledge from large genomic datasets", Cold Spring Harbor Laboratory, New York/USA, 16.-19.10.2011.

V4. Altmann, T.: Molecular and genetic analysis of biomass- and metabolite-heterosis in *Arabidopsis*. – Meeting "Epigenetics and Heterosis", Black Mountain (Brisbane)/Australia 04.-07.12.2011.

V5. Borisjuk, L.: Integration of MRI and metabolic modelling to study spatial arrangement of storage in developing seed. – BIT's 1st Annual World Congress of Agricultural Biotechnology (WCAB-2011), Changchun/China, 28.-30.10.2011.

V6. Börner, A.: Plant genetic resources – molecular tools for characterization and utilization. Genomics of genebanks workshop. – Plant and Animal Genome XIX. Conference, San Diego/USA, 15.-19.01.2011.

V7. Börner, A.: Plant genetic resources for food and agriculture (PGRFA) – conservation and utilisation. – Symposium on Genomics and Biodiversity, Hyderabad/India, 23.-25.02.2011.

V8. Börner, A., E.K. Khlestkina, S. Chebotar, M. Nagel, M.A. Rehman Arif, K. Neumann, B. Kobiljski, U. Lohwasser & M S Röder (vorgetragen von Börner, A.): Maintenance and exploitation of genetic resources for future plant breeding. – Agrisafe Final Conference "Climate Change: Challenge for Training of Applied Plant Scientists", Budapest/Hungary, 21.-23.03.2011.

V9. Conrad, U.: Production of vaccines and therapeutic antibodies for veterinary applications in transgenic plants: an overview. – International Conference "Plant Transformation Technologies II", Vienna/Austria, 19.-22.02.2011.

V10. Florschütz, K.: On-Chip-Nachweis von phytopathogenen RNA-Viren und miRNA mittels Oberflächenplasmonenresonanz. – fms-Sondersession 2011 "Sensorforschung für Medizin und Technik", Nürnberg, 09.06.2011.

V11. Fuchs, J., I. Lermontova, V. Schubert, A. Pecinka, M.A. Lysak, G. Jovtchev & I Schubert (vorgetragen von Fuchs, J.): Flow-sorted nuclei are valuable subjects to investigate structural and functional aspects of nuclear architecture in plants. – 6th Conference on Analytical Cytometry, Prague/Czech Republic, 08.-11.10.2011.

V12. Gils, M.: Pollination control systems for hybrid wheat breeding. – International Conference "Plants & People", Universität Potsdam, 06.09.2011.

V13. Graner, A.: Challenges and opportunities regarding the genomics-driven exploitation of genetic diversity in barley. – 15th Annual ADNAT Convention, International Symposium on Genomics and Biodiversity, Hyderabad/India, 23.-25.02.2011.

V14. Graner, A.: Disentangling the barley genome – a community effort. – North American Barley Researchers Workshop, Corvallis/USA, 06.-08.06.2011.

V15. Graner, A.: Sequence based utilization of plant genetic resources of barley: opportunities and constraints. – Indo-German Symposium on Plant Biology, Indian National Science Academy (INSA), New Delhi/India, 18.-20.10.2011.

V16. Graner, A.: Genomics assisted valorization of plant genetic resources of barley: Opportunities and constraints. – 25th Colloquium "Crop Plants: Biodiversity & Genomics" of the Research Center of Biotechnology and Plant Breeding, Universität Hohenheim, 16.-17.11.2011.

V17. Hartmann, A., T. Czauderna, R. Hoffmann, C. Klukas, T. Altmann & F. Schreiber (vorgetragen von Stein, N.): High-throughput phenotyping in barley – the IPK plant phenomics facilities. – Plant and Animal Genome XIX. Conference, San Diego/USA, 15.-19.01.2011.

V18. Hensel, G., A. Himmelbach, D. Nowara, C. Kastner, J. Riechen, D. Douchkov, P. Schweizer & J. Kumlehn (vorgetragen von Hensel, G.): A toolbox for the study of plant-pathogen interactions in cereals. – AgriGenomics Congress, Hamburg, 30.06.-01.07.2011.

V19. Jakob, S.S., C. Heibl, D. Rödder & F. R. Blattner (vorgetragen von Jakob, S.S.): Population demography influences climatic niche evolution: evidence from diploid American *Hordeum* species (Poaceae). – BioSystematics, Berlin, 21.-27.02.2011.

V20. Junker, B.H.: Quantification of intracellular metabolic fluxes in developing plant seeds. – Workshop "Systems Biology: Between Science and Application", Frankfurt am Main, 18.-19.01.2011.

V21. Junker, B.H.: Central metabolic fluxes in seeds of the legume plant family. – JCB Workshop "Nucleotides – Networks – Novelties. Understanding Evolution Beyond Darwin and Haeckel", Jena, 28.-29.03.2011.

V22. Junker, B.H.: Metabolic flux analysis in plant seeds – at the interface between metabolomics and systems biology. – Workshop "Trends in Metabolomics – Analytics and Applications", Frankfurt am Main, 19.-20.05.2011.

V23. Junker, B.H.: Quantification and simulation of intracellular metabolic fluxes in plants. – International Fall Meeting of the German Society for Biochemistry and Molecular Biology "Molecular Life Sciences", Frankfurt am Main, 25.-28.09.2011.

V24. Junker, B.H.: Towards high-throughput metabolic flux analysis in seeds of crop plants. – 7th Workshop "Molecular Interactions", Berlin, 05.-07.10.2011.

V25. Keller, E.R.J., A. Senula, C. Zanke & M. Grübe (vorgetragen von Keller, E.R.J.): Genebank management of three crops, potato, garlic and mint, and integration of cryopreservation in a complex collection. – International Conference on Cryopreservation of Horticultural Crops in China, Northwest A & F University, Yangling, Shaanxi, China, 28.-30.06.2011.

V26. Keller, E.R.J., B. Panis & F. Engelmann (vorgetragen von Keller, E.R.J.): *In vitro* storage and cryopreservation as substantial complements in concerted actions to better maintain and use crop germplasm. – 7th International Symposium on *In Vitro* Culture and Horticultural Breeding, Biotechnological Advances in *In Vitro* Horticultural Breeding, Ghent/Belgium, 18.-22.09.2011.

V27. Klukas, C.: Integrated visualization and analysis of *omics data, networks and images. – Institute of Cytology and Genetics SB RAS, Novosibirsk/Russia, 19.04.2011.

V28. Knüpffer, H.: Rye genetic resources in the world's genebanks. – International Conference "More Attention to Rye", Tartu/Estonia, 06.-08.10.2011.

V29. Kunze, G.: On-Chip-Nachweis von phytopathogenen RNA-Viren mittels Oberflächenplasmonresonanz. – Sitzung des fms/ProcessNet-Gemeinschafts-Ausschusses "Sensoren und Sensorsysteme", Frankfurt am Main, 27.01.2011.

V30. Kunze, G.: *Arxula adeninivorans* – a valuable tool for characterization of metabolic pathways in eukaryotes, producer of recombinant proteins and microbial compound for biosensors. – Institute of Cell Biology, NAS of Ukraine, Department of Molecular Genetics and Biotechnology, Lviv/Ukraine, 15.02.2011.

V31. Kunze, G.: *Arxula adeninivorans* – a valuable tool for basic research and biotechnological application. – YNC 2011. 1st International Symposium on Nonconventional Yeast in Postgenomic Era, Lviv/Ukraine, 11.-14.09.2011.

V32. Lippmann, R., K. Witzel, S. Kaspar, A. Matros & H. P. Mock (vorgetragen von Mock, H.-P.): Plant proteomics to support breeding and biotechnological applications. – 3rd International Symposium "Frontiers in Agriculture Proteome Research", Tsukuba/Japan, 08.-10.11.2011.

V33. Matros, A.: Application of MALDI-MS imaging for spatial protein and metabolite profiling during barley grain development. – Bruker Imaging Meeting, Bremen, 27.01.2011.

V34. Mock, H.-P.: Advanced techniques in mass spectrometry and their potential to provide novel insights into plant seed biology. – 6th European Symposium on Enzymes in Grain Processing, Carlsberg Research Center, Copenhagen/Denmark, 28.-30.11.2011.

V35. Peukert, M., S. Kaspar, A. Matros & H.-P. Mock (vorgetragen von Mock, H.-P.): Studying barley seed development by spatially resolved mass spectrometrical analysis. – 3rd International Symposium "Frontiers in Agriculture Proteome Research", Tsukuba/Japan, 08.-10.11.2011.

V36. Rolletschek, H.: Seed-specific elevation of non-symbiotic hemoglobin AtHb1: beneficial effects and underlying molecular networks in *Arabidopsis thaliana*. – International Conference for Plant Mitochondrial Biology 2011 (ICPMB), Hohenroda, 14.-19.05.2011.

V37. Rolletschek, H.: Systems biology as tool for modeling and improvement of crop seeds. – BIT's 1st Annual World Congress of Agricultural Biotechnology (WCAB-2011), Changchun/China, 28.-30.10.2011.

V38. Schnurbusch, T.: The developmental and genetic analysis of pre-flowering phases in barley and wheat. – Plant and Animal Genome XIX. Conference, Workshop "Genomics of Plant Development and Signal Networks", San Diego/USA, 15.-19.01.2011.

V39. Schubert, I.: Recombination repair and mechanics of chromosome and karyotype evolution. – Plant and Animal Genome XIX. Conference, San Diego/USA, 15.-19.01.2011.

V40. Schubert, I.: Interpretation of karyotype evolution should consider chromosome structural constraints. – XL Congreso Argentino de Genética, III Simposio Latinoamericano de Citogenética y Evolución I Jornadas Regionales SAGNEA, Corrientes/Argentina, 18.-21.10.2011.

V41. Schubert, V., A. Berr, A. Meister & I Schubert (vorgetragen von Schubert, V.): Interphase chromatin organization in *Arabidopsis*. – 18th International Chromosome Conference, University Place, Manchester/UK, 29.08.-02.09.2011.

V42. Schweizer, P.: Genes and loci for quantitative disease resistance in barley. – 1st Congress of Cereal Biotechnology and Breeding, Szeged/Hungary, 24.-27.05.2011.

V43. Schweizer, P.: Race-nonspecific powdery mildew resistance in barley: One trait – many genes. – Annual Meeting of the Chinese Society for Plant Pathology, Yichang/China, 18.-24.08.2011.

V44. Schweizer, P.: Quantitative powdery mildew resistance in barley: One trait – many genes. – *Botrytis/Sclerotinia* Post-Genome Workshop, Lyon/France, 15.-17.09.2011.

V45. Schweizer, P.: Nichtwirtsresistenz – ein gangbarer Weg zu dauerhafter Pathogenresistenz in Getreide? – Resistenztagung Fulda 2011 der GPZ, Fulda, 05.-06.12.2011.

V46. Stein, N., R. Zhou, T. Schmutzer, B. Steuernagel, U. Scholz, M.M. Martis, M. Seidel, K. Mayer, H. Simkova, J. Dolezel, G. Haseneyer, E. Bauer, P. Hedley, H. Liu & R. Waugh (vorgetragen von Stein, N.): Triticeae synteny revisited by barley chromosomal genomics. – Plant and Animal Genome XIX. Conference, San Diego/USA, 15.-19.01.2011.

V47. Stein, N.: The impact of NGS technology on sequencing the 5.1 gigabase barley genome. – Next Generation Sequencing Day, Modena/Italy, 22.02.2011.

V48. Stein, N.: The International Barley Sequencing Consortium – when will the barley genome sequence be available? – 9th Plant Genomics European Meeting (Plant GEM), Istanbul/Turkey, 04.-07.05.2011.

V49. Stein, N.: The barley genome – from virtual gene order to a genetically anchored physical map. – 21st International Triticeae Mapping Initiative (ITMI) Workshop, Mexico City/Mexico, 05.-09.09.2011.

V50. von Wirén, N.: Local Fe supply alters AUX-1 dependent auxin accumulation and stimulates lateral root elongation in *Arabidopsis* plants. – Botanikertagung 2011 "Diversity makes the Difference", Berlin, 18.-23.09.2011.

Vorträge/Lectures

2010

V1. Altmann, T.: WP1; Leaf Growth Phenotyping @MPI-MP/UP. – "AGRON-OMICS" Meeting, Bern, Konolfingen/Switzerland, 03.-05.02.2010.

V2. Altmann, T.: Introduction: plant phenotyping at IPK. – Workshop "Phenotyping and beyond", Jülich, 18.-19.02.2010.

V3. Altmann, T.: Analysis of plant growth/biomass accumulation and metabolism in *Arabidopsis* and maize. – Workshop "Phenotyping and beyond", Jülich, 18.-19.02.2010.

V4. Altmann, T.: Analysis of *Arabidopsis* natural genetic variation and heterosis in biomass accumulation and metabolism. – CropDesign, Ghent/Belgium, 04.05.2010.

V5. Altmann, T.: Analysis of *Arabidopsis* natural genetic variation and heterosis in biomass accumulation and metabolism. – Antrittsvorlesung, Martin-Luther-Universität Halle-Wittenberg, Halle/S., 01.06.2010.

V6. Altmann, T.: Analysis of *Arabidopsis* natural genetic variation and heterosis in biomass accumulation and metabolism. – CSHL – Pioneer/DuPont Plant Development and Phenomics Meeting, Banbury Center, Lloyd Harbor, New York/USA, 20.-21.09.2010.

V7. Altmann, T.: Moderne Methoden der Pflanzenforschung und -züchtung. – Dialogreihe „Innovationsfeld Pflanze", Magdeburg, 14.10.2010.

V8. Altmann, T.: Die Suche nach dem Gold der Genbanken – Neue Möglichkeiten der Erschließung und Nutzung genetischer Vielfalt. – GFP-Jahrestagung, Magdeburg, 03.-04.11.2010.

V9. Amiteye, S. & T. F. Sharbel (vorgetragen von Amiteye, S.): Do microRNAs cause a loss of sex in *Boechera*? – 9th IMPRS Symposium, Dornburg, 15.02.2010.

V10. Amiteye, S. & T. F. Sharbel (vorgetragen von Amiteye, S.): Do microRNAs cause a loss of sex in *Boechera*? – 6th Plant Science Student Conference, IPK, Gatersleben, 15.-18.06.2010.

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V15. Bäumlein, H.: An apospory-locus in *Hypericum*. – Universität Regensburg, 03.02.2010.

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V19. Börner, A.: Pflanzengenetische Ressourcen – Ausgangsmaterial zur Züchtung auf abiotische Stresstoleranz bei Getreide. – Pflanzengenetisches Kolloquium, Georg-August-Universität Göttingen, 14.01.2010.

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V21. Börner, A. & M. Nagel (vorgetragen von Börner, A.): Die internationale Bank für Pflanzensamen auf Spitzbergen – Lagerung für die Ewigkeit? – Aachener Gesellschaft für Gartenkultur, Aachen, 25.03.2010.

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V23. Börner, A.: 60 Jahre Evaluierung von Genbankmaterial – unüberschaubares Datenmeer oder nutzbare Ressource. – GPZ-Tagung Geschichte der Pflanzenzüchtung, Drübeck, 06.-07.05.2010.

V24. Börner, A.: Molekulargenetische Ansätze zur Erhaltung und Nutzbarmachung pflanzengenetischer Ressourcen. – Pflanzenzüchtung-Kolloquium, Martin-Luther-Universität Halle-Wittenberg, Halle/S., 21.05.2010.

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V26. Börner, A., K. Neumann, S. Koller & M.S. Röder (vorgetragen von Börner, A.): Assoziationsgenetische Studien in Weizen. – GFP Sommertagung Getreide, IPK, Gatersleben, 09.-10.06.2010.

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V28. Börner, A.: Seed longevity – the focal point of *ex situ* genebank collections. – Institutstag IPK, Gatersleben, 04.-05.10.2010.

V29. Börner, A.: Pflanzengenetische Ressourcen – Kleingärten in ihrer Bedeutung zur Erhaltung der Artenvielfalt. – 14. Forum Stadtgrün, Dresden, 25.11.2010.

V30. Brassac, J. & F. R. Blattner (vorgetragen von Brassac, J.): Analysis of phylogenetic relationships of *Hordeum* (Poaceae) polyploids. – 6th Plant Science Student Conference, IPK, Gatersleben, 15.-18.06.2010.

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V34. Czauderna, T.: SBGN-ED: editing, validating and translating of SBGN maps. – Workshop SBGN-5.5, Wittenberg, 21.-23.04.2010.

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V37. Czauderna, T. & A. Hartmann: Modelling, visualisation and data handling for Optimas. – Project Meeting Optimas, Düsseldorf, 15.10.2010.

V38. Daghma, D. & M. Melzer (vorgetragen von Daghma, D.): Embryogenesis of barley pollen – from live cell imaging to ultrastructural analysis. – 6th Plant Science Student Conference, IPK, Gatersleben, 15.-18.06.2010.

V39. Dehmer, K.J.: Research activities on the IPK forage collections. – 10th ECPGR Forages Working Group Meeting, Malchow (Poel), 28.-29.04.2010.

V40. Dehmer, K.J.: Die Groß Lüsewitzer Kartoffel-Sortimente (GLKS) als Teilsammlung der IPK-Genbank. – Besichtigung des Kartoffelstandorts Groß Lüsewitz durch Mitarbeiter einer Thüringer Kartoffelvertriebsgesellschaft; Groß Lüsewitz, IPK Gatersleben, 18.06.2010.

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V42. Dehmer, K.J.: Analyse und Nutzung genetischer Ressourcen zur Erstellung neuer Diversität in Futter- und Rasengräsern. – BLE-Innovationstage, Berlin, 06.-07.10.2010.

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V45. Entzian, A.: LemnaTec database architecture and image analysis. – Bayer CropScience, Frankfurt am Main, 07.12.2010.

V46. Finke, A.: Genetic and molecular analysis of RNA-directed transcriptional gene silencing (RdTGS) in *Arabidopsis thaliana*. – 23.Tagung "Molekularbiologie der Pflanzen", Dabringhausen, 23.-26.02.2010.

V47. Florschütz, K., A. Schröter, M. Körner, S. Schmieder, F. Sonntag, K. Vetter, R. Watzke & G. Kunze (vorgetragen von Florschütz, K.): Auf den Spuren von Pilzen und Viren mittels SPR und Plattenassay. – Technische Systeme für die Lebenswissenschaften. – 15. Heiligenstädter Kolloquium, Heiligenstadt, 27.-29.09.2010.

V48. Franke, M., C. Krach, H. Poskar & B. H. Junker (vorgetragen von Franke, M.): Metabolic flux analysis in *Medicago truncatula*. – 6th Plant Science Student Conference, IPK, Gatersleben, 15.-18.06.2010.

V49. Friedel, S.: Searching for pattens in nucleotide sequences. – Robert-Koch-Institut, Berlin, 20.10.2010.

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V51. Fritsch, R.M.: The genus *Allium* L. – how to classify an extreme diversity. – Colloquium of the Department of Plant Systematics, Botanical Institute of the Armenian National Academy of Sciences, Jerewan/Armenia, 31.05.2010.

V52. Fritsch, R.M.: Iran – terra incognita Alliorum? – Colloquium of the Department of Plant Systematics, Botanical Institute of the Armenian National Academy of Sciences, Jerewan/ Armenia, 31.05.2010.

V53. Fuchs, J.: Analyse pflanzlicher Genome mit Hilfe der Durchflusszytometrie. – Gastkolloquium, Leibniz-Institut für Gemüse- und Zierpflanzenbau, Großbeeren & Erfurt, 18.11.2010.

V54. Gerlach, T., J. Knaust, C. Kaiser, M. Giersberg, K. Sędzielewska, M. Körner, K. Florschütz, S. Uhlig, K. Simon, K. Kunath & G. Kunze (vorgetragen von Gerlach, T.): Development of a biosensor based on the yeast *Arxula adeninivorans* for the detection of androgenic activities in environmental samples. – 6th Plant Science Student Conference, IPK, Gatersleben, 15.-18.06.2010.

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V58. GILS, M.: Der Klimawandel als Herausforderung für die Züchtung. – Besuch H. Brehmer, IPK, Gatersleben, 06.12.2010.

V59. Goedeke, S., G. Hensel, C. Kaydamov, J. Macek, T. Rutten, I. Saalbach & J. Kumlehn (vorgetragen von Goedeke, S.): Production of recombinant protein in transgenic barley grains. – COST FAO804 Workshop "Molecular farming: plants as a production platform for high value proteins", Wageningen/The Netherlands, 25.-26.01.2010.

V60. Graner, A.: Bewahren und Verändern: Forschungsarbeiten zur Nutzbarmachung pflanzlicher Biodiversität am IPK Gatersleben. – Museum für Naturkunde, Magdeburg, 22.04.2010.

V61. Graner, A.: The Leibniz Institute of Plant Genetics and Crop Plant Research (IPK). – 10th ECPGR Forages Working Group Meeting, Malchow (Poel), 28.-29.04.2010.

V62. Graner, A.: Saatgut und pflanzliche Leistung: Forschungsansätze zur züchterischen Verbesserung von Kulturpflanzen. – Tagung „Megatrend Agrarrohstoffe", K+S Kali GmbH, Kassel, 10.06.2010.

V63. Graner, A.: Von der Natur zur Kultur: Nutzpflanzen als Lebensgrundlage des Menschen. Veranstaltungsreihe „Melanchthons Erben". – Kreisvolkshochschule Harz, Quedlinburg, 17.06.2010.

V64. Graner, A.: Grüne Gentechnik: Anmerkungen aus der Wissenschaft. – Fraktionstagung DIE LINKE im Landtag von Sachsen-Anhalt, Halle/S., 19.10.2010.

V65. Graner, A.: Nutzung genetischer Vielfalt: Herausforderungen und Perspektiven. – Fachtagung des Dachverband Agrarforschung (DAF), Braunschweig, 20.-21.10.2010.

V66. Graner, A.: Utilization of Plant Genetic Resources: a research and technology perspective. – 1st International Expo Forum "Food Security and Agro-Biodiversity", Milano/Italy, 18.-19.11.2010.

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cum turgidum L. var. *durum*) to recent Eastern African isolate of stem rust, *Puccinia graminis* f. sp. *tritici*, Ug99. – 6th Plant Science Student Conference, IPK, Gatersleben, 15.-18.06.2010.

V70. Hajirezaei, M.-R.: Improvement of biomass production: resources, opportunities and constraints. – 16th International Conference on Renewable Resources and Plant Biotechnology, NAROSSA®2010, Magdeburg, 07.-08.06.2010.

V71. Hanemann, A., N. Weichert, H. Simkova, J. Dolezel & M. S. Röder (vorgetragen von Röder M. S.): Exploiting the genomic sequences of rice and *Brachypodium* for delimiting a grain size QTL in wheat. – 2nd International Symposium on Genomics of Plant Genetic Resources, Bologna/Italy, 24.-27.04.2010.

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V76. Houben, A.: Biology of B chromosomes. – University of Zurich, Zurich/Switzerland, 23.02.2010.

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V81. Houben, A.: Centromere-mediated instability in wide hybrids. – Institutstag IPK, Gatersleben, 04.-05.10.2010.

V82. Jacob, S.S.: "Almost a form of schizophrenia": Wie Populationsdemographie Veränderungen der ökologischen Nische beeinflusst – am Beispiel diploider amerikanischer Gersten. – Senckenberg-Museum, Görlitz, 06.03.2010.

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V85. Johnston, A.J.: Retinoblastoma in cell differentiation. – Universität Regensburg, 03.02.2010.

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V88. Johnston, A.J. & O. Kirioukhova (vorgetragen von Johnston, A. J.): RKD in plant evolution. – National Institute for Basic Biology, Okazaki/Japan, 01.12.2010.

V89. Jovtchev, G., J. Fuchs & I. Schubert (vorgetragen von Jovtchev, G.): Distinct methylation marks characterize the sex chromatin in *Rumex acetosa*. – Laboratory of Plant Developmental Genetics Institute of Biophysics, Czech Academy of Sciences, Brno/Czech Republic, 26.-30.07.2010.

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V91. Junker, B.H.: Systems approaches to *Medicago truncatula* seed metabolism. – Joint 5th International Food Legumes Research Conference & 7th European Conference on Grain Legumes, Antalya/Turkey, 26.-30.04.2010.

V92. Kapusi, E., C.H. Teo, L. Ma, G. Hensel, I. Schubert, M.F. Mette & J. Kumlehn (vorgetragen von Kapusi, E.): Engineered minichromosomes as vectors in barley. – Gemeinsame Tagung des Arbeitskreises Deutsche In Vitro Kulturen (ADIVK) und der Gesellschaft für Pflanzenbiotechnologie e.V. „Pflanzenbiotechnologie in Deutschland – wo stehen wir?", Hannover, 13.-15.09.2010.

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V95. Keller, E.R.J. & A. Senula (vorgetragen von Keller E. R. J.): Pollen cryopreservation as a tool for genebank maintenance of germplasm. – COST Action 871, 4th Meeting of WG 1, Fundamental Aspects of Plant Cryopreservation, Cryoprotection and Genetic Stability, Poznan/Poland, 29.-30.04.2010.

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V99. Klukas, C.: Auswertung und Visualisierung von Hochdurchsatzdaten mittels VANTED. – Kolloquium der Roux-Forschergruppe, Medizinische Fakultät der Martin-Luther-Universität Halle-Wittenberg, Halle/S., 28.01.2010.

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V110. Kohl, S.: Senescence-induced N remobilisation and seed filling in barley. – Arbeitstreffen DFG-Forschergruppe FOR 948 „Seneszenz", Hohenlieth, 06.05.2010.

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V120. Lange, M.: The LAILAPS search engine: a feature model for relevance ranking in life science databases. – 6th International Symposium on Integrative Bioinformatics 2010, Cambridge/UK, 22.-24.03.2010.

V121. Lange, M.: Databases and information systems in Bioinformatics: from information retrieval to search engines. – International Summer School on Integrative Biological Pathway Analysis and Simulation, Universität Bielefeld, 20.05.2010.

V122. Leonova, I.N., E.B. Budashkina, N.P. Kalinina, M.S. Röder, E.S. Skolotneva, A. Börner & E. A. Salina (vorgetragen von Le-

onova, I. N.): *T. aestivum* × *T. timopheevii* introgression lines as a source of pathogen resistance genes. – 8th International Wheat Conference, St. Petersburg/Russia, 01.-04.06.2010.

V123. Lippmann, R., A. Matros, J. Kumlehn & H.-P. Mock (vorgetragen von Lippmann, R.): Identification of potential feeder substances promote pollen embryogenesis (POEM) from the secretome of pistils. – 6th Plant Science Student Conference, IPK, Gatersleben, 15.-18.06.2010.

V124. Lohwasser, U., M. Nagel & A. Börner (vorgetragen von Lohwasser, U.): Untersuchungen zur Langlebigkeit und Langzeitlagerung von Saatgut. – 20. Bernburger Winterseminar für Arznei- und Gewürzpflanzen, Bernburg, 23.02.2010.

V125. Lohwasser, U. & A. Börner (vorgetragen von Lohwasser, U.): Saatgutqualität im Wandel der Zeit – Von der Domestikation zum Qualitätsmanagement. – Arbeitstagung der Arbeitsgemeinschaft Saatgut- und Sortenwesen der GPZ und GPW, IPK, Gatersleben, 24.-25.02.2010.

V126. Lohwasser, U.: Saatgutqualität im Wandel der Zeit – Von der Domestikation zum Qualitätsmanagement. – Saatbautagung 2010 des Saatbauverbandes Sachsen-Anhalt, Bernburg-Strenzfeld, 10.03.2010.

V127. Lohwasser, U. & A. Börner (vorgetragen von Lohwasser, U.): Die bundesdeutsche *ex situ*-Genbank in Gatersleben, Erhalt pflanzengenetischer Ressourcen. – Weihenstephaner Symposium zur Gartendenkmalpflege, Freising-Weihenstephan, 25.06.2010.

V128. Lohwasser, U., T. Bruchmüller, H. Budahn, H. Krüger, D. Ulrich, A. Börner & F. Marthe (vorgetragen von Lohwasser, U.): Ergebnisse eines Genpoolscreenings bei Petersilie (*Petroselinum crispum* (Mill.) Nyman) hinsichtlich wirtschaftlich bedeutsamer Merkmale. – Tagung der GPZ-AG Gemüse und Arznei- und Gewürzpflanzen und der GFP Abteilung Gemüse, Heil- und Gewürzpflanzen, Erfurt, 07.-08.09.2010.

V129. Lohwasser, U.: "Leafy Vegetables" – ein europäisches Projekt zur verbesserten Nutzbarmachung verschiedener Blattgemüsearten. – GFP-Jahrestagung, Abteilung Gemüse, Heil- und Gewürzpflanzen, Bonn, 02.-04.11.2010.

V130. Lohwasser, U.: Leafy vegetables, stimulating use – characterisation and regeneration. – Leafy Vegetable Meeting, Avignon/France, 16.-17.11.2010.

V131. Matros, A., S. Kaspar, U. Seiffert, W. Weschke & H.-P. Mock (vorgetragen von Matros, A.): Elucidation of temporal and spatial protein patterns in developing barley grains by multiplexed LC-MS and MALDI-imaging MS approaches. – 43. Jahrestagung der Deutschen Gesellschaft für Massenspektrometrie (DGMS), Halle/S., 07.-10.03.2010.

V132. Matros, A.: LC-based protein analysis of barley grain development. – German Proteomics Summit, Freising-Weihenstephan, 06.05.2010.

V133. Matros, A.: Proteomic approaches for analysis of barley grain development. – Massenspektrometrie Forum Hannover, Hannover, 15.06.2010.

V134. Matthies, I., S. Weise & M.S. Röder (vorgetragen von Matthies, I.): Association mapping in barley – a genome wide and candidate gene approach. – Conference "Green Plant Breeding Technologies", Vienna/Austria, 02.-05.02.2010.

V135. Matthies, I., M.S. Röder, R.K. Pasam, B. Kilian & A. Graner (vorgetragen von Röder, M.S.): Assoziationsgenetik bei Gerste. – GFP Sommertagung Getreide, IPK, Gatersleben, 09.-10.06.2010.

V136. Mau, M. & T. F. Sharbel (vorgetragen von Mau, M.): Unreduced pollen formation in *Boechera* – a transcriptomic study. – 6th Plant Science Student Conference, IPK, Gatersleben, 15.-18.06.2010.

V137. Mehlhorn, H.: The DBE2 information system. – SEA Project Meeting, IPK, Gatersleben, 21.-22.01.2010.

V138. Mehlhorn, H.: The DBE2 information system. – Task Force Metabolite Profiling, IPK, Gatersleben, 26.02.2010.

V139. Mehlhorn, H.: Ontologies – arrangements of beings. – 6th Plant Science Student Conference, IPK, Gatersleben, 15.-18.06.2010.

V140. Melzer, M.: Recent developments in modern microscopy: Methods and application. – Bhabha Atomic Research Centre, Mumbai/India, 19.03.2010.

V141. Melzer, M.: Recent developments in modern microscopy: Methods and application. – TATA Institute of Fundamental Research (TIFR), Mumbai/India, 24.03.2010.

V142. Mette, M.F.: RNA-directed DNA methylation in plants. – European Networking Summer School (ENSS) Plant Epigenetics 2010, IPK, Gatersleben, 20.-24.09.2010.

V143. Mette, M.F.: RNA-directed RNA polymerases involved in transcript level-mediated post-transcriptional gene silencing in *Arabidopsis thaliana*. – Institutstag IPK, Gatersleben, 04.-05.10.2010.

V144. Meyer, R.C., B. Ebert, T. Gärtner, B. Kusterer, J. Lisec, D. Riewe, R. Schmidt, M. Steinfath, K. Weigelt, A.E. Melchinger, J. Selbig, L. Willmitzer & T. Altmann (vorgetragen von Altmann, T.): Molecular and genetic analysis of biomass and metabolite heterosis in *Arabidopsis thaliana*. – Genomics-based breeding, Justus-Liebig-Universität, Gießen, 26.-28.10.2010.

V145. Miedaner, T., M. Loeffler, P. Risser, L. Hartl, G. Strittmatter, M. Ouzunova, B. Holtschulte, B. Kessel, V. Korzun, E. Ebmeyer, P. Karlovsky, I. Feussner, S. Nutz, P. Schweizer, J. Kumlehn, D. Mueller, D.J. Stahl, F. Felsenstein, S. Praud, M. Trottet, S.G. Atienza Penas, M.J. Giménez & B. Keller (vorgetragen von Miedaner, T.): Securing a sustainable production of feed and food – a functional genomic-guided strategy for improving biotic stress tolerance in cereals. – 10th GABI Status Seminar, Potsdam, 09.-11.03.2010.

V146. Mock, H.-P.: Proteomics to evaluate genetic resources for stress defence responses. – Charles University, Prague/Czech Republic, 13.04.2010.

V147. Mock, H.-P.: Proteomics to evaluate genetic resources for stress defence responses. – University of Silesia, Katowice/Poland, 23.06.2010.

V148. Mock, H.-P.: Proteomics to evaluate genetic resources for stress defence responses. – Frontier in Agriculture Proteome Research, National Institute of Crop Science, Tsukuba/Japan, 18.11.2010.

V149. Muth, J., T. Altmann, E. Bauer, S. Frerichmann, H.-J. Harloff, C. Jung, V. Korzun, T. Kraft, J. Kumlehn, G. Leckband, M. Ouzunova, D. Prüfer, N. Stein, D. Stelling, E. Tacke & B. Weisshaar (vorgetragen von Muth, J.): GABI-TILL: Expansion and use of the GABI-TILLING platform for crop gene function analysis. – 10th GABI Status Seminar, Potsdam, 09.-11.03.2010.

V150. Nagel, M., I. Kranner & A. Börner (vorgetragen von Nagel, M.): Langlebigkeit von Getreidesamen – Physiologie und Genetik. – Arbeitstagung der Arbeitsgemeinschaft Saatgut- und Sortenwesen der GPZ und GPW, IPK, Gatersleben, 24.-25.02.2010.

V151. Nagel, M., I. Kranner & A. Börner (vorgetragen von Nagel, M.): Parameters related to seed longevity in cereal seeds. – Departmental Science and Conservation Seminar Series, Millennium Seed Bank Project, Wakehurst Place, West Sussex/UK, 17.03.2010.

V152. Nagel, M.: The longevity of crop seeds stored under ambient conditions. – Research Meeting, Millennium Seedbank, KEW Botanical Gardens/Wakehurst Place, West Sussex/UK, 09.05.2010.

V153. Nagel, M.: The genetic architecture of maize flowering time. – New Areas in Plant Breeding, PAG (Promotionsstudiengang Agrar): Modul – Vertiefung des Fachwissens, Georg-August-Universität, Göttingen, 09.07.2010.

V154. Nagel, M., I. Kranner & A. Börner (vorgetragen von Nagel, M.): Seed conservation in *ex situ* gene banks; genetical and physiological backgrounds for viability loss in wheat and barley after storage. – 29th Congress of the International Seed Testing Association (ISTA), Köln 2010, 15.-18.06.2010.

V155. Neumann, K.: Assoziationskartierung von Trockentoleranz in Gerste. – Oberseminar Pflanzenzüchtung, Martin-Luther-Universität Halle-Wittenberg, Halle/S., 08.07.2010.

V156. Nürk, N.M.: Tracing the impact of the Andean uplift – Evolutionary history of *Hypericum* in South America: biogeography, character evolution, niche shifts and age estimations. – DFG Nachwuchsakademie „Systematik der Pflanzen und Pilze", Senckenberg-Naturmuseum, Frankfurt am Main, 25.09.2010.

V157. Nürk, N.M., S. Madriñán, M. Carine, M. Chase & F. R. Blattner (vorgetragen von Nürk, N. M.): Molecular phylogeny and historical biogeography of *Hypericum*. – 3rd Annual Hypericum Meeting, University of Padua, Padua/Italy, 29.10.2010.

V158. Nürk, N.M., S. Uribe-Convers, D. Tank & F. R. Blattner (vorgetragen von Nürk, N. M.): Out of the tropics? Parametric model based biogeography reconstructions in the temperate genus of St. John's wort (*Hypericum*). – PuRGe Seminar, University of Idaho & University of Washington, Moscow/USA, 19.11.2010.

V159. Oppermann, M.: Das Genbankinformationssystem GBIS. Ein Überblick. – Arbeitstagung der Arbeitsgemeinschaft Saatgut- und Sortenwesen der GPZ und GPW, IPK, Gatersleben, 24.-25.02.2010.

V160. Oppermann, M.: Suggestions: handling of C&E data in the European context. – 10th ECPGR Forages Working Group Meeting, Malchow (Poel), 27.-29.04.2010.

V161. Oppermann, M.: General aspects of Genebank Information Systems, – InWent-Refresher-Kurs, IPK Gatersleben, 18.05.2010.

V162. Ouzunova, M., T. Presterl, P. Westhoff, K. Ernst, E. Pestsova, T. Altmann, R.C. Meyer, M. Ernst, A.E. Melchinger, J.M. Montes, J. Selbig, M. Stitt, R. Sulpice, A. Czedik-Eysenberg & L. Willmitzer (vorgetragen von Altmann, T.): Biomass production in maize – genomics guided breeding of energy maize and a systems-oriented analysis. – 10th GABI Status Seminar, Potsdam, 09.-11.03.2010.

V163. Paliwal, R., A.K. Joshi, U. Kumar & M. S. Röder (vorgetragen von Paliwal, R.): M-QTL and epistasis contribute to terminal heat tolerance in hexaploid wheat (*T. aestivum* L.). – 6th Plant Science Student Conference, IPK, Gatersleben, 15.-18.06.2010.

V164. Pellino, M. & T. F. Sharbel (vorgetragen von Pellino, M.): Effects of hybridization on expression of apomixis in *Ranunculus auricomus*. – EU COST Apomixis Workshop, Wageningen/The Netherlands, 05.07.2010.

V165. Plasun, K., M. Müller, M. Melzer, B. Melzer, T. Altmann & J. Kumlehn (vorgetragen von Plasun, K.): Haploid technology in the major experimental model plants *Arabidopsis thaliana* and *Brachypodium distachyon*: An initial approach. – 6th Plant Science Student Conference, IPK, Gatersleben, 15.-18.06.2010.

V166. Posgar, H. & B. H. Junker (vorgetragen von Posgar, H.): Metabolic flux analysis. – Dechema Summer School "Quantitative Biology – From Cell to Process", Bad Herrenalb, 26.-30.07.2010.

V167. Poursarebani, N., R. Ariyadasa, D. Schulte, R. Zhou, B. Steuernagel, M.M. Martis, K. Mayer, A. Graner & N. Stein (vorgetragen von Poursarebani, N.): Genetic anchoring of the physical map of barley (*Hordeum vulgare* L.) using a virtual gene map order of the barley genome. – 6th Plant Science Student Conference, IPK, Gatersleben, 15.-18.06.2010.

V168. Puente Molins, M., J.M. Corral, O.M. Aliyu, J.L. Maron & T. F. Sharbel (vorgetragen von Puente Molins, M.): Hybridization and its role in the reproduction of *Hypericum perforatum*. – Botany 2010, Providence, Rhode Island/USA, 02.-06.08.2010.

V169. Rehman Arif, M.A., U. Lohwasser & A. Börner (vorgetragen von Rehman Arif, M. A.): Seed longevity in wheat (*Triticum aestivum* L.) – Genetics and beyond. – Arbeitstagung der Arbeitsgemeinschaft Saatgut- und Sortenwesen der GPZ und GPW, IPK, Gatersleben, 24.-25.02.2010.

V170. Rehman Arif, M.A., M. Nagel, U. Lohwasser & A. Börner (vorgetragen von Rehman Arif, M. A.): Seed longevity in wheat (*Triticum aestivum* L.): genetics and beyond. – 6th Plant Science Student Conference, IPK, Gatersleben, 15.-18.06.2010.

V171. Rehman Arif, M.A.: Genetics of seed longevity in wheat (*Triticum aestivum* L.). – Oberseminar Pflanzenzüchtung, Martin-Luther-Universität Halle-Wittenberg, Halle/S., 04.11.2010.

V172. Rödder, D., S.S. Jakob, C. Heibl & F. R. Blattner (vorgetragen von Rödder, D.): Linking large-scale analyses of climate niche evolution with population demography. – GfÖ 40th Anniversary Conference, Gießen, 30.08.-03.09.2010

V173. Röder, M.S.: New genes by forward genetics approaches. – Institutstag IPK, Gatersleben, 04.-05.10.2010.

V174. Rutten, T.: Role of transcription factor LEC1 (Leafy Cotyledon 1) in *Arabidopsis* embryogenesis. – Julius Kühn-Institut, Braunschweig, 23.03.2010.

V175. Rutten, T., M. Melzer & D. Daghma (vorgetragen von Rutten, T.): High Pressure Freezing of immature pollen from barley using cyanobacteria as "Filler". – Frühjahrstreffen des Arbeitskreises PANOS der Deutschen Gesellschaft für Elektronenmikroskopie, Martin-Luther-Universität Halle-Wittenberg, Halle/S., 07.05.2010.

V176. Sanei, M., R. Pickering, S. Nasuda & A. Houben (vorgetragen von Sanei, M.): Analysis of uniparental elimination of chromosome in wide crosses. – 6th Plant Science Student Conference, IPK, Gatersleben, 15.-18.06.2010.

V177. Schallau, A., F. Arzenton, A.J. Johnston, U. Hähnel, D. Koszegi, F.R. Blattner, L. Altschmied, G. Haberer, G. Barcaccia & H. Bäumlein (vorgetragen von Bäumlein, H.): Identification and genetic analysis of the APOSPORY locus in *Hypericum perforatum*. – XXI International Congress on Sexual Plant Reproduction, Bristol/UK, 02.-06.08.2010.

V178. Schallau, K.: From subcellular data to kinetic models. – Institut für Theoretische Biologie, Humboldt-Universität zu Berlin, 25.02.2010.

V179. Schallau, K.: Kinetic characteristices of AGPase in barley. – Conference on Regulation of Plant Growth, Potsdam, 12.-14.04.2010.

V180. Schlichting, A.: Evaluierung genetischer Ressourcen der Kartoffel durch innovative Analysen von Inhaltsstoff- und Qualitätsparametern der Knolle. – BLE-Innovationstage, Berlin, 06.-07.10.2010.

V181. Schmid, N., A.R. Meda & N. von Wirén (vorgetragen von Schmid, N.): A role of the SNARE protein VTI11 in intracellular iron efficiency in *Arabidopsis thaliana*. – 6th Plant Science Student Conference, IPK, Gatersleben, 15.-18.06.2010.

V182. Schmidt, B.: The Cucurbitaceae of the German *ex situ* genebank. – ECPGR Cucurbits Working Group, 2nd Meeting, Tiblisi/Georgia, 08.-10.11.2010.

V183. Schmidt, R.: Analysis of seed oil biosynthesis using natural variation in *Arabidopsis thaliana* and *Brassica napus*. – Biowissenschaftliches Netzwerk „Strukturen und Mechanismen der biologischen Informationsverarbeitung", Gesamtarbeitsbesprechung, Martin-Luther-Universität Halle-Wittenberg, Halle/S., 04.-05.03.2010.

V184. Schmidt, R.: Genome plasticity in Brassicaceae. – Institut für Pflanzenbau und Pflanzenzüchtung, Christian-Albrechts-Universität zu Kiel, 04.05.2010.

V185. Schmidt, R.: Analysis of allelic diversity in *Brassica napus*. – Brassica2010, 17th Crucifer Genetics Workshop, Saskatoon/Canada, 05.-09.09.2010.

V186. Schmidt, R.: Transcript level-mediated post-transcriptional gene silencing. – European Networking Summer School (ENSS) Plant Epigenetics 2010, IPK, Gatersleben, 20.-24.09.2010.

V187. Schmidt, R.: Analysis of allelic diversity in *Brassica napus*. – Institutstag IPK, Gatersleben, 04.-05.10.2010.

V188. Schmidt, R.: Analysis of allelic diversity in *Brassica napus*. – 10th Gatersleben Research Conference 2010 (GRCX) "Sequence-informed Crop Research", Quedlinburg (Palais Salfeldt)/Gatersleben (IPK), 22.-24.11.2010.

V189. Schmutzer, T., B. Steuernagel, F. Bull, U. Scholz, A. Houben & N. Stein (vorgetragen von Schmutzer, T.): K-mer analysis to reveal genomic secrets in highly repetitive genomes. – 6th Plant Science Student Conference, IPK, Gatersleben, 15.-18.06.2010.

V190. Schnurbusch, T.: Chasing genes for abiotic stress tolerance in wheat and barley. – Kolloquium in Pflanzenzüchtung, Martin-Luther-Universität Halle-Wittenberg, Halle/S., 22.01.2010.

V191. Schnurbusch, T.: Abiotischer Stress bei Weizen, die australische Sicht. – DLG-/GPZ-/GFP-Symposium: Ertragsbildung bei Weizen, Gustav-Stresemann-Institut, Bonn, 01.-02.03.2010.

V192. Schnurbusch, T.: Chasing genes for boron toxicity tolerance in small grain cereals wheat and barley. – Kolloquium, Technische Universität München-Freising, 24.06.2010.

V193. Schnurbusch, T.: The boron toxicity tolerance locus Bo1 in bread wheat (*Triticum aestivum* L.) encodes a boron efflux-type transporter specific to the genus *Aegilops*. – International Triticeae Mapping Initiative (ITMI) Summer Workshop, Beijing/China, 01.-04.09.2010.

V194. Schnurbusch, T.: Are branched spikes advantageous? – The molecular elucidation of spike branching in wheat and barley. – Institutstag IPK, Gatersleben, 04.-05.10.2010.

V195. Scholz, U.: Assembling the barley genome possibilities, challenges and current status. – Institutstag IPK, Gatersleben, 04.-05.10.2010.

V196. Schreiber, F.: Integrative Bioinformatics – Examples from high-throughput phenotyping and systems biology graphical notation. – ACPFG Adelaide and University of South Australia, Adelaide/Australia, 21.01.2010.

V197. Schreiber, F.: Integrative Bioinformatics. – DSTO, Melbourne/Australia, 28.01.2010.

V198. Schreiber, F.: Integrative Bioinformatics – Examples from modelling plant metabolism and systems biology graphical notation. – Monash University, Melbourne/Australia, 03.02.2010.

V199. Schreiber, F.: Integrative Bioinformatics – network modelling, analysis, and visualisation with examples from crop plant metabolism. – The University of Western Australia, Perth/Australia, 10.02.2010.

V200. Schreiber, F.: Systems Biology Graphical Notation (SBGN) – methods and tools. – 2010 International Summer School on Integrative Biological Pathway Analysis and Simulation, Universität Bielefeld, 21.05.2010.

V201. Schreiber, F.: Biological networks. – Workshop proGD, Konstanz, 21.09.2010.

V202. Schreiber, F.: Modeling, analysis, simulation and visualisation of biological networks. – Maastricht University, Maastricht/The Netherlands, 05.11.2010.

V203. Schreiber, F.: Systems Biology Graphical Notation – eine neue Sprache der Biologen mit Unterstützung aus der Informatik. – Dagstuhl Workshops Wissenschaftsjournalismus „Schreiben und Sprechen über Informatik", Dagstuhl Leibniz-Zentrum für Informatik, 14.-16.06.2010.

V204. Schreiber, F.: Integrative bioinformatics – network modelling, analysis, and visualisation with examples from crop plant metabolism. – CSIRO Canberra/Australia, 26.11.2010.

V205. Schreiber, F.: Systems biology graphical notation. – The University of Western Australia, Perth/Australia, 07.12.2010.

V206. Schreiber, F.: An introduction to flux balance analysis and Vanted/FBASimVis. – The University of Western Australia, Perth/Australia, 08.12.2010.

V207. Schreiber, F.: Analysis and visualisation of biological networks and related information – barley as an example. – Workshop on Analysis and Visualisation of Large and Complex Data Sets, Sydney/Australia, 13.12.2010.

V208. Schubert, I.: Mechanics of chromosome and karyotype evolution – a magnifying lens for palaeogenomics. – Annual Conference of the German Genetics Society (GfG) "Evolution of Primates", Jena, 16.-18.09.2010

V209. Schubert, I.: Modifications of plant interphase chromatin at the microscopic level – an overview. – European Networking Summer School (ENSS) Plant Epigenetics 2010, IPK, Gatersleben, 20.-24.09.2010.

V210. Schubert, I.: Interphase chromosome arrangement is coined by genetic and environmental impacts and determines genome stability. – Institutstag IPK, Gatersleben, 04.-05.10.2010.

V211. Schubert, I.: Mechanics of chromosome evolution and potential pitfalls of genomics. – Mini-Symposium "Plants and the evolution their genomes" on the occasion of the retirement of Prof. Johann Greilhuber, University of Vienna, Vienna/Austria, 05.11.2010.

V212. Schubert, I. & M. Lysak (vorgetragen von Schubert, I.): Mechanics of chromosome evolution – a magnifying lens for paleogenomics. – 10th Gatersleben Research Conference 2010 (GRCX) "Sequence-informed Crop Research", Quedlinburg (Palais Salfeldt)/Gatersleben (IPK), 22.-24.11.2010.

V213. Schulte, D., R. Ariyadasa, N. Poursarebani, R. Zhou, T. Sretenovic-Rajicic, P. Langridge, B.-J. Shi, K. Mayer, T. Close, S. Weise, U. Scholz, A. Graner & N. Stein (vorgetragen von Schulte, D.): Whole genome physical map of barley (*Hordeum vulgare* L.). – Plant and Animal Genome XVIII. Conference, San Diego/USA, 09.-13.01.2010.

V214. Schulte, D., R. Ariyadasa, T. Schmutzer, P. Langridge, B.-J. Shi, A. Graner & N. Stein (vorgetragen von Schulte, D.): Contribution of a random sheared library to whole genome physical mapping in barley (*Hordeum vulgare* cv. Morex). – Plant and Animal Genome XVIII. Conference, San Diego/USA, 09.-13.01.2010.

V215. Schweizer, P.: Multiple WRKY-factor binding sites in the promoters of the GER4 gene cluster of barley cause high transcription upon pathogen attack. – Plant and Animal Genome XVIII. Conference, San Diego/USA, 09.-13.01.2010.

V216. Schweizer, P.: Gene für quantitative Krankheitsresistenz in der Gerste. – GFP – Öffentliche Sitzung der Abteilung Getreide, IPK, Gatersleben, 10.06.2010.

V217. Schweizer, P.: RNA interference as a tool in crop plant genetic analysis. – European Networking Summer School (ENSS) Plant Epigenetics 2010, IPK, Gatersleben, 20.-24.09.2010.

V218. Schweizer, P.: A role of the GER4 gene cluster in quantitative resistance of barley. – Institutstag IPK, Gatersleben, 04.-05.10.2010.

V219. Schweizer, P.: Ein biotechnologischer Ansatz zur Reduktion des Fusariumbefalls in Getreide. – 3. Wiss. Symposium des Verbandes Deutscher Mühlen, Würzburg, 05.11.2010.

V220. Sędzielewska, K., K. Vetter, J. Fuchs, N.M. Nürk, R. Bode, R. Watzke & G. Kunze (vorgetragen von Sędzielewska, K.): Symbiotic glomeromycota *Glomus intraradices* – diagnostic investigation. – 6th Plant Science Student Conference, IPK, Gatersleben, 15.-18.06.2010.

V221. Seifert, M.: Exploiting prior knowlegde and gene distances in the analysis of tumor expression profiles with extended Hidden Markov Models. – Universität Siegen, 19.12.2010.

V222. Seyfarth, M.: Identification and characterization of functional diversity of regulatory proteins controlling plant growth. – Biowissenschaftliches Netzwerk „Strukturen und Mechanismen der biologischen Informationsverarbeitung", Gesamtarbeitsbesprechung, Martin-Luther-Universität Halle-Wittenberg, Halle/S., 04.-05.03.2010.

V223. Sharbel, T.F., M.-L. Voigt, J.M. Corral, G. Galla, J. Kumlehn, C. Klukas, F. Schreiber, H. Vogel & B. Rotter (vorgetragen von Sharbel, T. F.): Apomictic and sexual ovules of *Boechera* display heterochronic global gene expression patterns. – Plant and Animal Genome XVIII. Conference, San Diego/USA, 09.-13.01.2010.

V224. Sharbel, T.F.: Sex and agriculture. – Universität Bayreuth, 28.01.2010.

V225. Sharbel, T.F.: Sex and agriculture. – Systems Biology Workshop, Victoria AgriBiosciences Center, Melbourne/Australia, 17.-28.05.2010.

V226. Sharbel, T.F.: Heterochrony and hybridization: the evolution of apomixis in the genus *Boechera*. – Brassica2010,17th Crucifer Genetics Workshop, Saskatoon/Canada, 05.-09.09.2010.

V227. Sharbel, T.F.: Time travel: a conserved apomixis-specific functional polymorphism has recombined and spread during the post-Pleistocene evolution of apomictic *Boechera*. – Institutstag IPK, Gatersleben, 04.-05.10.2010.

V228. Sharbel, T.F.: Sex and agriculture: evolutionary genomics and next generation sequencing approaches to understanding apomixis. – II Ciclo de seminarios sobre avances en la caracterización genética y molecular de la apomixis en gramíneas forrajeras, Facultad de Ciencias Agrarias, Universidad Nacional de Rosario, Argentina, 23.-24.11.2010.

V229. Sharbel, T.F., M.-L. Voigt, J.M. Corral, J. Kumlehn, C. Klukas, F. Schreiber, H. Vogel & B. Rotter (vorgetragen von Sharbel, T. F.): Heterochrony and hybridization: the evolution of apomixis in the genus *Boechera*. – 10th Gatersleben Research Conference 2010 (GRCX) "Sequence-informed Crop Research", Quedlinburg (Palais Salfeldt)/Gatersleben (IPK), 22.-24.11.2010.

V230. Sharma, R., R.K. Pasam, B. Kilian & A. Graner (vorgetragen von Sharma, R.): Genome-wide association studies for plant architecture traits in barley. – 6th Plant Science Student Conference, IPK, Gatersleben, 15.-18.06.2010.

V231. Sreenivasulu, N.: Molecular basis of terminal drought tolerance. – The University of Western Australia, School of Plant Biology, Perth/Australia, 08.02.2010.

V232. Sreenivasulu, N.: Integrated view of grain development and deciphering the holistic view of reprogrammed seed metabolism under terminal drought. – ARC Excellent Centre of Energy, Perth/Australia, 12.02.2010.

V233. Sreenivasulu, N., C. Seiler, V. Harshavadhan, K. Rajesh, S. Worch, M.S. Röder, H. Rolletschek, J. Kumlehn, N. Staroske, U. Conrad, W. Weschke, A. Börner, M. Strickert, K. Pillen, L. Kuntze, V. Korzun, B. Usadel, R. Sulpice, M. Stitt & U. Wobus (vorgetragen von Sreenivasulu, N.): SEEDs for the FUTURE: developing barley grains with improved yield and grain quality under terminal drought during seed filling. – 10th GABI Status Seminar, Potsdam, 09.-11.03.2010.

V234. Sreenivasulu, N.: SEEDs for the FUTURE: Strategies for improved seed yield and quality under terminal drought in barley. – Martin-Luther-Universität Halle-Wittenberg, Interdisziplinäres Zentrum für Nutzpflanzenforschung, Halle/S., 11.06.2010.

V235. Sreenivasulu, N.: Systems biology of seed metabolism for improving yield stability. – National Institute of Plant Genome Research, New Delhi/India, 10.12.2010.

V236. Stein, N.: Aktueller Stand der Weizengenomsequenzierung und Perspektiven. – DLG-/GPZ-/ GFP-Symposium: Ertragsbildung bei Weizen, Gustav-Stresemann-Institut, Bonn, 01.-02.03.2010.

V237. Stein, N.: How to sequence a 5 Gigabase genome – a case study of barley (*Hordeum vulgare*). – Lunchtime seminar, Justus-Liebig-Universität, Gießen, 05.05.2010.

V238. Stein, N.: Sequencing the 5 Gigabase barley genome - new perspectives for functional genomics in an important cereal model and crop plant. – Seminar, Humboldt-Universität zu Berlin, 11.05.2010.

V239. Stein, N.: New achievements in Crop Genomics – or how to unlock the 5 Gigabase barley genome. – SFB Seminar, Universität Würzburg, 27.05.2010.

V240. Stein, N.: How to sequence a 5 Gigabase genome – a case study of barley (*Hordeum vulgare*). – Seminary at TraitGenetics 10th Anniversary, Gatersleben, 07.-08.06.2010.

V241. Stein, N.: The best-guess barley genome – one step away from barley whole genome sequencing. – Institutstag IPK, Gatersleben, 04.-05.10.2010.

V242. Stein, N.: Barley – get ready for genomics based breeding! – Genomics-based breeding, Justus-Liebig-Universität, Gießen, 26.-28.10.2010.

V243. Stein, N.: How do we access genes in *Triticeae* genetic centromeres? – 10th Gatersleben Research Conference 2010 (GRCX) "Sequence-informed Crop Research", Quedlinburg (Palais Salfeldt)/Gatersleben (IPK), 22.-24.11.2010.

V244. Thiel, T. & T. F. Sharbel (vorgetragen von Thiel, T.): Scrutinizing gene copy number variation (CNV) as a factor for apomixis expression in *Boechera*. – 9th IMPRS Symposium, Dornburg, 15.02.2010.

V245. von Wirén, N.: Ammonium sensing in *Arabidopsis*. – Molekulare Pflanzenphysiologie, Friedrich-Alexander-Universität Erlangen-Nürnberg, 07.01.2010.

V246. von Wirén, N.: Nitrogen sensing and signalling in plants. – Wissenschaftszentrum Weihenstephan für Ernährung, Landnutzung und Umwelt, Technische Universität München, 21.01.2010.

V247. von Wirén, N.: Ansätze aus der Pflanzenernährung zur genetischen Anpassung von Kulturpflanzen an den Klimawandel. – Gesellschaft für Pflanzenzüchtung/ Deutsche Landwirtsch. Gesellschaft, Bonn, 01.03.2010.

V248. von Wirén, N.: Chancen und Risiken der grünen Gentechnik. – Lion's Club, Quedlinburg, 18.03.2010.

V249. von Wirén, N.: Ammonium transport and sensing in plants. – Botanisches Institut und Botanischer Garten, Christian-Albrechts-Universität zu Kiel, 07.06.2010.

V250. Weber, H. & W. Weschke (vorgetragen von Weber, H.): Samenentwicklung in Weizen. – GFP Sommertagung Getreide, IPK, Gatersleben, 09.-10.06.2010.

V251. Weichert, N., A. Hanemann, H. Simkova, J. Dolezel & M. S. Röder (vorgetragen von Röder, M. S.): Exploiting the genomic sequences of rice and *Brachypodium* for delimiting a grain size QTL in wheat. – 10th Gatersleben Research Conference 2010 (GRCX) "Sequence-informed Crop Research", Quedlinburg (Palais Salfeldt)/Gatersleben (IPK), 22.-24.11.2010.

V252. Weier, D., F. Bollenbeck, R. Pielot, U. Seiffert & W. Weschke (vorgetragen von Weier, D.): A 4D atlas of the developing barley grain. – International Conference "Molecular Aspects of Plant Development", Vienna/Austria, 23.-26.02.2010.

V253. Weise, S.: Novel developments of the MetaCrop information system for facilitating systems biological approaches. – 6th International Symposium on Integrative Bioinformatics 2010, Cambridge/UK, 22.-24.03.2010.

V254. Weschke, W.: Molekulare Schalter der Ertragsbildung bei Weizen. – DLG-/GPZ-/GFP-Symposium: Ertragsbildung bei Weizen, Gustav-Stresemann-Institut, Bonn, 01.-02.03.2010.

V255. Weschke, W.: 3-D-Mikrodissektion biologischer Objekte. – BMBF-Projektforum Biotechnica, Hannover, 05.10.2010.

V256. Willner, E.: Forage grasses – *Poa* central crop database development and assigning most original samples towards defining an European Forage Collection (EFC). – Baltic Sea Network for Management and Conservation of Plant Genetic Resources, Tallinn/Estonia, 30.11.2010.

V257. Witzel, K., A. Börner, J. Kumlehn, G. Kunze, M. Melzer, T. Rutten, K.H. Mühling, M. Strickert, A. Weidner & H.-P. Mock (vorgetragen von Witzel, K.): Investigation of salinity stress responses in barley using the genetic variation of mapping populations. – Gordon Res. Conference: Salt & Water Stress in Plants, Les Diablerets/Switzerland, 13.-18.06.2010.

V258. Wobus, A.M.: Embryonale Stammzellen und Analyse der pankreatischen Entwicklung *in vitro*. – 527. Sitzung der Nordrhein-Westfälischen Akademie der Wissenschaften und Künste, Düsseldorf, 03.03.2010.

V259. Wobus, A.M.: Embryonale Stammzellforschung – woher und wohin? – Translationszentrum für Regenerative Medizin (TRM), Universität Leipzig, 11.03.2010.

V260. Wobus, A.M.: Beziehung zwischen Pluripotenz und Tumorigenität. – Novartis Ethical Advisory Board, Novartis International, Basel/Switzerland, 12.11.2010.

V261. Zaynali Nezhad, K., U. Lohwasser, M.S. Röder & A. Börner (vorgetragen von Zaynali Nezhad, K.): Genetic linkage map construction and identification of quantitative trait loci (QTLs) determining post-anthesis drought tolerance and other agronomic traits in bread wheat. – 6th Plant Science Student Conference, IPK, Gatersleben, 15.-18.06.2010.

V262. Zaynali Nezhad, K.: Genetic linkage map construction and identification of QTLs determining post-anthesis drought tolerance and other agronomic traits in bread wheat. – Oberseminar Pflanzenzüchtung, Martin-Luther-Universität Halle-Wittenberg, Halle/S., 08.07.2010.

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V1. Allam, M.: The onset of a study in oilseed rape. – 7th Plant Science Student Conference, IPB, Halle/S., 14.-17.06.2011.

V2. Altmann, T.: Hybridzüchtung: Heterotische Gruppen. – Fachgespräch Weizen-Hybridzüchtung, BMELV, Bonn, 09.02.2011.

V3. Altmann, T.: PLANT-KBBE: CornFed – integration of advanced mapping and phenotyping methods to identify key alleles for building European maize ideotypes. – 11th GABI Status Seminar, Potsdam, 15.-17.03.2011.

V4. Altmann, T.: Phänotypisierung – neue Verfahren für die Erfassung von Pflanzeneigenschaften. – FNR/GFP Strategiedialog II, Pflanzenzüchtung für nachwachsende Rohstoffe, Berlin, 25.03.2011.

V5. Altmann, T.: Analysis of natural variation and heterosis of growth and metabolism in *Arabidopsis* and Maize. – Institutstag IPK, Gatersleben, 04.-06.10.2011.

V6. Altmann, T.: Zugang zu neuen FuE-Konzepten durch innovative Verfahren der Pflanzenphänotypisierung. – 1. Symposium Zierpflanzenzüchtung, Julius Kühn-Institut, Quedlinburg, 15.-16.11.2011.

V7. Amiteye, S., H. Vogel & T. F. Sharbel (vorgetragen von Amiteye, S.): Apomixis and hybridization in the genus *Boechera*: miRNA influences on global gene expression patterns in developing ovules. – Plant and Animal Genome XIX. Conference, San Diego/USA, 15.-19.01.2011.

V8. Amiteye, S., H. Vogel & T. F. Sharbel (vorgetragen von Amiteye, S.): Apomixis and hybridization in the genus *Boechera*: miRNA influences on global gene expression patterns in developing ovules. – EU COST Apomixis Workshop, Valencia/Spain, 04.-05.07.2011.

V9. Banaei Moghaddam, A.M.: Directed nondisjunction of rye B-chromosomes. – Japanese-German JSPS and DFG-funded Workshop "Frontiers of Plant Chromosome Research: Centromeres and Artificial Chromosomes", IPK Gatersleben, 31.10.-03.11.2011.

V10. Bauer, B.: Einfluss der N-Form auf Qualitätsparameter in Winterweizen. – Norddeutsches Marktfruchtforum, Kiel, 23.02.2011.

V11. Bauer, B.: Perspectives of global wheat production. – agri benchmark Cash Crop Conference 2011, Middelfart, Copenhagen/Denmark, 12.-17.06.2011.

V12. Bauer, B.: Unterfußdüngung bei Minimalbodenbearbeitung. Was ist machbar? Was ist erforderlich? – Fachhochschule Südwestfalen, Soest, 17.06.2011.

V13. Bauer, B.: Genotypical differences in the phytohormonal response of wheat to nitrogen fertilisation. – ADAS, Cambridge/UK, 06.09.2011.

V14. Bauer, B.: Influence of nitrogen forms on tillering, cytokinin translocation and yield in cereal plants. – Gemeinsame Tagung der Deutschen Gesellschaft für Pflanzenernährung und der Gesellschaft für Pflanzenbau, Kiel, 27.-29.09.2011.

V15. Bäumlein, H.: Identification and genetic analysis of the apospory locus in *Hypericum perforatum*. – Plant and Animal Genome XIX. Conference, San Diego/USA, 15.-19.01.2011.

V16. Bäumlein, H.: Identification and genetic analysis of the apospory locus in *Hypericum perforatum*. – Institutstag IPK, Gatersleben, 04.-06.10.2011.

V17. Benor, S. & F. R. Blattner (vorgetragen von Benor, S.): Phylogeny and biogeography of the jute genus *Corchorus* (Malvaceae s.l.). – BioSystematics, Berlin, 21.-27.02.2011.

V18. Borisjuk, L.: Unravelling developmental and positional cues for oil storage in rapeseed by 3D-NMR imaging. – Gordon Research Conference on Plant Lipids: Structure, Metabolism & Function, Galverston/USA, 30.01.-04.02.2011.

V19. Borisjuk, L.: Dynamic 13C/1H NMR imaging uncovers sugar allocation in the living seed. – 10th International Conference of the International Society for Seed Science (ISSS), Costa do Sauípe, Bahia/Brazil, 10.-15.04.2011.

V20. Börner, A.: The German *ex situ* genebank in Gatersleben: Conservation and utilisation of plant genetic resources. – Seminar, USDA-ARS, National Center for Genetic Resources Preservation, Fort Collins, Colorado/USA, 13.01.2011.

V21. Börner, A.: Conservation and utilisation of plant genetic resources in the German *ex situ* genebank in Gatersleben. – National Bureau of Plant Genetic Resources, New Delhi/India, 01.03.2011.

V22. Börner, A., M.A. Rehman Arif, K. Neumann, M. Nagel, U. Lohwasser & B. Kobiljski (vorgetragen von Börner, A.): Association genetics – a new strategy to study seed and seedling stress tolerance in crop plants. – 10th International Conference of the International Society for Seed Science (ISSS), Costa do Sauípe, Bahia/Brazil, 10.-15.04.2011.

V23. Börner, A., E.K. Khlestkina, T.A. Pshenichnikova, S. Chebotar, M. Nagel, M.A. Rehman Arif, K. Neumann, B. Kobiljski, U. Lohwasser & M. S. Röder (vorgetragen von Börner, A.): Maintenance and utilisation of wheat genetic resources for future breeding. – International Conference "Wheat Genetic Resources and Genomics", Novosibirsk/Russia, 28.08.-01.09.2011.

V24. Börner, A., E.K. Khlestkina, T.A. Pshenichnikova, K. Neumann, U. Lohwasser, B. Kobiljski, V. Korzun & M. S. Röder (vorgetragen von Börner, A.): Cereal genetic stocks – examples of successful co-operation. – EWAC-EUCARPIA Cereals Section Conference, Novi Sad/Serbia, 07.-11.11.2011.

V25. Brassac, J., S.S. Jakob & F. R. Blattner (vorgetragen von Brassac, J.): Analysis of phylogenetic relationships of *Hordeum* (Poaceae) polyploids. – BioSystematics, Berlin, 21.-27.02.2011.

V26. Budahn, H., T. Bruchmüller, D. Ulrich, H. Krüger, U. Lohwasser & F Marthe (vorgetragen von Budahn, H.): Charakterisierung der intraspezifischen Variabilität bei Petersilie mittels molekularer Marker sowie klassischer und nicht-zielgerichteter Bestimmung flüchtiger Inhaltsstoffe. – 6. Fachtagung Arznei- und Gewürzpflanzen, Berlin, 19.-22.09.2011.

V27. Conrad, U.: Production of very large spider silk proteins by posttranslational fusions *in vivo*. – COST Meeting Cost Action Molecular Farming, Ghent/Belgium, 14.-16.09.2011.

V28. Conrad, U.: Production and characterization of large spider silk protein multimers in transgenic tobacco by posttranslational fusions. – Institutstag IPK, Gatersleben, 04.-06.10.2011.

V29. Conrad, U.: Production of therapeutically and technically important proteins in plants: avian flu antigens and spider silk proteins from tobacco. – Kolloquium, Institut für Biochemie II, Universität Düsseldorf, 19.10.2011.

V30. Conrad, U.: Production and immunological characterization of avian flu hemagglutinin multimers in transgenic plants. – Pharma Planta Open Meeting, Brussels/Belgium, 25.10.2011.

V31. Conrad, U.: Production of spider silk derivatives in transgenic plants: purification and characterization. – Kick-Off Meeting COST-Action Netzwerk "Biological Adhesives: From Biology to Biomimetics", Vienna/Austria, 03.-05.11.2011.

V32. Czauderna, T., M.P. van Iersel & A. C. Villeger (vorgetragen von Czauderna, T.): An introduction to SBGN-ML. – HARMONY 2011: The Hackathon on Resources for Modeling in Biology, New York/USA, 18.-22.04.2011.

V33. Czauderna, T. & F Schreiber (vorgetragen von Schreiber, F.): Using SBGN-ED for the Systems Biology Graphical Notation. – International German/Russian Summer School in "Integrative Biological Pathway Analysis and Simulation", Bielefeld, 04.-07.07.2011.

V34. Czauderna, T. & F Schreiber (vorgetragen von Schreiber, F.): SBGN-ED – working with the Systems Biology Graphical Notation. – COMBINE 2011, Heidelberg, 03.-07.09.2011.

V35. Daghma, D.S.: Structural changes during the initiation of pollen embryogenesis in barley. – International PhD School on Plant Development, Retzbach-Würzburg, 05.-07.10.2011.

V36. Dehmer, K.J.: Diversity analyses in wild potatoes via multiplex fluorescent SSR fingerprints. – 18th Triennial Conference of the European Association for Potato Research (EAPR2011), Oulu/Finland, 24.-29.07.2011.

V37. Demidov, D.: Consequences of spindle checkpoint misfunction in plants by modulation of AtAurora activity. – Japanese-German JSPS and DFG-funded Workshop "Frontiers of Plant Chromosome Research: Centromeres and Artificial Chromosomes", IPK Gatersleben, 31.10.-03.11.2011.

V38. Diekmann, K.: Illustration of the diversity of genebank accessions of cultivated potato using simple sequence repeat markers. – 18th Triennial Conference of the European Association for Potato Research (EAPR2011), Oulu/Finland, 24.-29.07.2011.

V39. Dobrovolskaya, O., J. Salse, P. Martinek, V.S. Arbuzova, O.M. Popova, A. Börner, E.A. Salina & L. I. Laikova (vorgetragen von Dobrovolskaya, O.): Characterization of genes that are involved in control of spike development in wheat and its relatives. – International Conference "Wheat Genetic Resources and Genomics", Novosibirsk/Russia, 28.08.-01.09.2011.

V40. Finke, A., M. Kuhlmann & M. F. Mette (vorgetragen von Finke, A.): Genetic analysis of RNA-directed transcriptional gene silencing in *Arabidopsis*. – 7th Plant Science Student Conference, IPB, Halle/S., 14.-17.06.2011.

V41. Finke, A., M. Kuhlmann & M. F. Mette (vorgetragen von Finke, A.): Genetic analysis of RNA-directed transcriptional gene silencing in *Arabidopsis*. – 2nd European Workshop on Plant Chromatin, Versailles/France, 01.-02.09.2011.

V42. Fleischer, F., C. Volkmar & A. Börner (vorgetragen von Fleischer, F.): Untersuchungen eines Winterweizensortiments 2011 am Standort Gatersleben auf Befall durch Weizengallmücken. – Arbeitskreis „Populationsdynamik und Epidemiologie", Martin-Luther-Universität Halle-Wittenberg, Halle/S., 22.09.2011.

V43. Florschütz, K., A. Schröter, K. Vetter, R. Watzke & G. Kunze (vorgetragen von Florschütz, K.): Nachweis und Quantifizierung von arbuskulären Mykorrhizapilzen. – 15. Jahrestagung der DPG-Projektgruppe Mikrobielle Symbiose des Arbeitskreises Phytomedizin in Gartenbau und Forst und der Vereinigung der Mykorrhizaanwender und -produzenten Deutschlands, Lüneburg, 24.-25.11.2011.

V44. Franke, M., J. Huege, C. Krach, H. Posgar & B. H. Junker (vorgetragen von Franke, M.): Metabolic flux analysis in barley. – 7th Plant Science Student Conference, IPB, Halle/S., 14.-17.06.2011.

V45. Friedel, S.: What can genebank data tell us? – Institutstag IPK, Gatersleben, 04.-06.10.2011.

V46. Fritsch, R.M.: Iran - terra incognita Alliorum? – Institutskolloquium, Conservatoire et Jardin botaniques ville de Genève, Geneva/Switzerland, 20.10.2011.

V47. Giersberg, M.: Nachweis östrogener Aktivitäten mittels A-YES Assay. – Arbeitskreis „Endokrine Wirkungen" – 2. Sitzung, Bundesanstalt für Gewässerkunde, Koblenz, 22.03.2011.

V48. Gils, M.: Hybridzüchtung in Weizen. – Innoplanta Jahrestagung, Gatersleben, 14.03.2011.

V49. Gils, M.: Pollination control systems for hybrid wheat breeding. – German Seed Alliance, Isernhagen, 13.04.2011.

V50. Gils, M.: Pollination control systems for hybrid wheat breeding. – Universität Hohenheim, 21.06.2011.

V51. Gils, M.: Pollination control systems for hybrid wheat breeding. – Visit European Plant Breeding Academy UC Davis, IPK Gatersleben, 23.06.2011.

V52. Gils, M.: Pollination control systems for hybrid wheat breeding. – Institutstag IPK, Gatersleben, 04.-06.10.2011.

V53. Gils, M.: Mit geteilten Genen zum vollen Ertrag – neue Wege in der Weizen-Hybridzucht. – 22. Meeting of Trustees (Stiftungsrat), IPK Gatersleben, 07.10.2011.

V54. Gils, M.: Etablierung eines innovativen Systems zur Herstellung von Hybridweizen. – BMBF-Projektforum, Biotechnica Hannover, 11.10.2011.

V55. Graner, A.: Genomforschung zur Nutzbarmachung pflanzengenetischer Ressourcen. – Institutskolloquium, Christian-Albrechts-Universität, Kiel, 12.01.2011.

V56. Graner, A.: Von der Natur zur Kultur: Nutzpflanzen als Lebensgrundlage des Menschen. – Institutskolloquium, Technische Universität Ilmenau, 26.01.2011.

V57. Graner, A.: Podiumsdiskussion: "Genomics, untapped biodiversity, GMOs and socio-economic concerns". – 15th Annual ADNAT Convention, Intl. Symposium on Genomics and Biodiversity, Hyderabad/India, 23.-25.02.2011.

V58. Graner, A.: Towards a genomics driven valorization of plant genetic resources. – Annual Symposium of the Otto Warburg Centre for Agricultural Biotechnology, Golm, 14.04.2011.

V59. Graner, A.: Grüne Gentechnik – Wahrnehmung und Realität. – Jahrestreffen ehemaliger Absolventen der Ingenieurswissenschaften der Leibniz-Universität Hannover, Quedlinburg, 07.05.2011.

V60. Graner, A.: Genomics informed valorization of plant genetic resources. – Seminarvortrag, National Institute for Plant Genomics Research (NIPGR), New Delhi/India, 18.10.2011.

V61. Graner, A.: Grüne Gentechnik – Rolle der Pflanzenbiotechnologie für die Ernährungssicherung. – Future of Food, Hochschule Anhalt, Bernburg, 26.10.2011.

V62. Hajirezaei, M.R.: Microarray-based identification of genes differentially expressed in stem base of *Petunia hybrida* in different developmental stages of adventitious root formation. – 6th International Symposium on Root Development, Amos/Canada, 07.-11.08.2011.

V63. Hajirezaei, M.R.: Improvement of agronomical important crops by understanding the underlying biological mechanisms. – Symposium on Stress, National Institute of Genetic Engineering and Biotechnology, Tehran/Iran, 14.-16.12.2011.

V64. Harpke, D., H. Kerndorff, T. Rutten & F. R. Blattner (vorgetragen von Harpke, D.): Two times into Asia Minor: phylogeny of *Crocus* (Iridaceae) based on ITS sequences of nuclear rDNA. – BioSystematics, Berlin, 21.-27.02.2011.

V65. Heckmann, S., I. Lermontova, D. Demidov, B. Berckmans, L. de Veylder, H. Bäumlein, I. Schubert & A. Houben (vorgetragen von Heckmann, S.): Transcriptional and posttranslational regulation of the Aurora-substrate CENH3 in *Arabidopsis*. – SFB 648 Meeting, Martin-Luther-Universität Halle-Wittenberg, Halle/S., 04.02.2011.

V66. Heckmann, S., I. Lermontova, D. Demidov, B. Berckmans, L. de Veylder, H. Bäumlein, I. Schubert & A. Houben (vorgetragen von Heckmann, S.): Transcriptional and posttranslational regulation of the Aurora-substrate CENH3 in *Arabidopsis*. – DST-DAAD Project Based Personal Exchange Programme, University of Jammu/India, 16.03.2011.

V67. Heckmann, S.: Holocentric chromosome organization and behaviour during mitosis and meiosis in *Luzula elegans*. – Japanese-German JSPS and DFG-funded Workshop "Frontiers of Plant Chromosome Research: Centromeres and Artificial Chromosomes", IPK Gatersleben, 31.10.-03.11.2011.

V68. Hedtmann, C., A. Matros & H. P. Mock (vorgetragen von Hedtmann, C.): Proteomic approaches to investigate the regulation of stress-inducible proteins from *Arabidopsis* by phosphorylation. – Meeting COST Action FA0603, Dijon/France, 25.-27.05.2011.

V69. Hensel, G., C. Berger, S. Bieri, C. Bollmann, A. Bruchmüller, D. Douchkov, S. Friedel, S. Goedeke, E. Grützemann, M. Gurushidze, A. Himmelbach, S. Lück, C. Marthe, A. Müller, I. Otto, J. Riechen, P. Schweizer & J. Kumlehn (vorgetragen von Hensel, G.): Engineered minichromosomes as vectors in barley. – International Conference "Plant Transformation Technologies II", Vienna/Austria, 19.-22.02.2011.

V70. Hensel, G.: Expression systems for the production of pharmaceutical or technical proteins in barley. – Gentechnik-Workshop der Gesellschaft für Pflanzenbiotechnologie, Quedlinburg und Üplingen, 22.-23.08.2011.

V71. Hensel, G.: Genetic engineering in barley – methods and applications. – Japanese-German JSPS and DFG-funded Workshop "Frontiers of Plant Chromosome Research: Centromeres and Artificial Chromosomes", IPK Gatersleben, 31.10.-03.11.2011.

V72. Hoerandl, E., D. Hojsgaard, T.F. Sharbel, M. Pellino & H. Vogel (vorgetragen von Hoerandl, E.): Effects of hybridization on the expression of apomixis in *Ranunculus auricomus*. – Plant and Animal Genome XIX. Conference, San Diego/USA, 15.-19.01.2011.

V73. Hojsgaard, D., H. Vogel, T.F. Sharbel, M. Pellino & E. Hoerandl (vorgetragen von Hojsgaard, D.): Hybridization delays the sexual development and triggers apomixis in the *Ranunculus auricomus* complex. – EU COST Apomixis Workshop, Valencia/Spain, 04.-05.07.2011.

V74. Houben, A.: Histone phosphorylation – a dynamic affair. – Department of Plant Biochemistry, Polish Academy of Sciences, Warsaw/Poland, 17.05.2011.

V75. Houben, A.: Role of CENH3 in stable and unstable grass hybrids. – Japanese-German JSPS and DFG-funded Workshop "Frontiers of Plant Chromosome Research: Centromeres and Artificial Chromosomes", IPK Gatersleben, 31.10.-03.11.2011.

V76. Junker, B.H.: Integrated analysis and modeling of legume seed metabolism. – FORSYS Young Investigator Seminar, Heidelberg, 14.02.2011.

V77. Junker, B.H.: Analysis and modeling of metabolic fluxes in plants. – Institut für Pharmazie, Martin-Luther-Universität Halle-Wittenberg, Halle/S., 27.04.2011.

V78. Junker, B.H.: Metabolic flux analysis in plant seeds – at the interface between metabolomics and systems biology. – Max-Planck-Institut für Pflanzenzüchtungsforschung, Köln, 06.07.2011.

V79. Junker, B.H.: Towards high-throughput fluxomics in crop seeds. – Institutstag IPK, Gatersleben, 04.-06.10.2011.

V80. Kapusi, E., C.H. Teo, L. Ma, G. Hensel, J. Kumlehn, I. Schubert, M.F. Mette & A. Houben (vorgetragen von Kapusi, E.): Engineered minichromosomes as vectors in barley. – International Conference "Plant Transformation Technologies II", Vienna/Austria, 19.-22.02.2011.

V81. Karimi Ashtiyani, R.: AtHaspin phosphorylates histone H3 at threonine 3 and contributes to embryonic patterning in *Arabidopsis*. – Japanese-German JSPS and DFG-funded Workshop "Frontiers of Plant Chromosome Research: Centromeres and Artificial Chromosomes", IPK Gatersleben, 31.10.-03.11.2011.

V82. Keller, E.R.J., H.M. Schumacher, M. Höfer, A. Meier-Dinkel, K. Zoglauer & I. Pinker (vorgetragen von Keller, E.R.J.): Country Report: Cryopreservation in Germany. – Final Meeting of COST 871 CryoPlanet, Angers/France, 08.-11.02.2011.

V83. Keller, E.R.J., A. Senula, C. Zanke, M. Grübe, A. Kaczmarczyk, A. Nukari, D. Teyssedre, C. Kremer Morales, J. Edesi, M. Pelc & M. Olas-Sochacka (vorgetragen von Keller, E.R.J.): Ways of collaboration – COST short-term scientific missions on three crops and their outcomes – potato, garlic and mint. – Final Meeting of COST 871 CryoPlanet, Angers/France, 08.-11.02.2011.

V84. Keller, E.R.J.: Formalization of vegetatively propagated crop's standards. – 7th Meeting of the ECPGR Allium Working Group, Perea, Thessaloniki/Greece, 06.-08.09.2011.

V85. Keller, E.R.J.: Future development and project ideas for vegetatively propagated alliums. – 7th Meeting of the ECPGR Allium Working Group, Perea, Thessaloniki/Greece, 06.-08.09.2011.

V86. Keller, E.R.J. & C. Zanke (vorgetragen von Keller, E.R.J.): The AEGIS Project "Cryopreservation of young inflorescence bases in bolting garlic for germplasm storage". – 7th Meeting of the ECPGR Allium Working Group, Perea, Thessaloniki/Greece, 06.-08.09.2011.

V87. Keller, E.R.J. & C. Zanke (vorgetragen von Keller, E.R.J.): EURALLIVEG – vegetative *Allium*, Europe's core collection, safe and sound. – 7th Meeting of the ECPGR Allium Working Group, Perea, Thessaloniki/Greece, 06.-08.09.2011.

V88. Keller, E.R.J.: Veranstaltungen und Initiativen zur Kryokonservierung 2010 / 2011: COST 871 – Abschlusstagung in Angers, EU-Projekt-Abschlusstagung in Prag und Erstes Internationales Kryo-Symposium in Yangling, China. – Jahrestagung des Arbeitskreises Deutsche *In-vitro*-Kulturen ADIVK, Bremen, 15.-16.09.2011.

V89. Khlestkina, E.K., O.Y. Tereshchenko, V.S. Arbuzova, A. Börner, L.A. Pershina & E.A. Salina (vorgetragen von Khlestkina, E.K.): A new range of wheat precise genetic stocks application: insights into gene function. – EWAC-EUCARPIA Cereals Section Conference, Novi Sad/Serbia, 07.-11.11.2011.

V90. Kilian, B.: Genetic diversity and domestication of wheat and barley. – Martin-Luther-Universität Halle-Wittenberg, Halle/S., 15.07.2011.

V91. Kittler, J., H. Krüger, W. Schütze, U. Kästner, W. Junghanns, W.D. Blüthner, U. Lohwasser & F Marthe (vorgetragen von Kittler, J.): Charakterisierung unterschiedlicher Genpools der Melisse (*Melissa officinalis*) als Basis für die Entwicklung von züchterisch wertvollem Ausgangsmaterial. – 6. Fachtagung Arznei- und Gewürzpflanzen, Berlin, 19.-22.09.2011.

V92. Klukas, C.: Automated plant phenotyping at the IPK. – College of Life Sciences, Zhejiang University, Hangzhou/China, 26.07.2011.

V93. Klukas, C.: Development of an information system for automated crop plant phenotyping. – Institutstag IPK, Gatersleben, 04.-06.10.2011.

V94. Knüpffer, H.: Chair's report: activities and achievements of the Working Group on Barley since its 6th meeting (Salsomaggiore, Italy, 2000) and the 2nd meeting of the Cereals Network (Foça, Turkey, 2008). – 7th Meeting of the ECPGR Barley Working Group, Nicosia/Cyprus, 10.-12.05.2011.

V95. Knüpffer, H.: *Hordeum* wild species in Europe – crop wild relatives of cultivated barley. – 7th Meeting of the ECPGR Barley Working Group, Nicosia/Cyprus, 10.-12.05.2011.

V96. Knüpffer, H.: European Barley Database and EURISCO, International Barley Core Collection. – 7th Meeting of the ECPGR Barley Working Group, Nicosia/Cyprus, 10.-12.05.2011.

V97. Knüpffer, H.: Rye genetic resources in the world's genebanks. – AEGIS Workshop "Improving the prerequisites for a European rye collection", Radzików/Poland, 13.-14.10.2011.

V98. Kohl, S.: Relationship between senescence-induced N-remobilization and seed filling in barley. – Meeting DFG-Forschergruppe FOR948 „Nitrogen uptake, metabolism and remobilization in leaves during plant senescence", Graz/Austria, 12.-13.05.2011.

V99. Kumlehn, J.: Genetische Transformation bei Getreide. – 2. Quedlinburger Pflanzenzüchtungstage, Quedlinburg, 29.-30.03.2011.

V100. Kumlehn, J.: Genetic engineering and haploid technology in cereals. – University of Cape Town, Cape Town/South Africa, 13.09.2011.

V101. Kumlehn, J.: Investigations on the initiation of pollen embryogenesis. – Institutstag IPK, Gatersleben, 04.-06.10.2011.

V102. Kunze, G.: *Arxula adeninivorans* – a valuable tool for basic research and biotechnological application. – Kolloquium, IPK Gatersleben, 27.04.2011.

V103. Kunze, G.: *Glomus irregulare* AMykor – a molecular approach to characterize and identify the arbuscular mycorrhizal fungus. – Institutstag IPK, Gatersleben, 04.-06.10.2011.

V104. Lange, M.: The LAILAPS information retrieval portal as scalable and integrative database query endpoint. – Workshop "Translational Bioinformatics" of 6th International Symposium on Health Informatics and Bioinformatics (HIBIT2011), Izmir/Turkey, 02.-05.05.2011.

V105. Lermontova, I.: Centromere maintenance via CENH3. – Japanese-German JSPS and DFG-funded Workshop "Frontiers of Plant Chromosome Research: Centromeres and Artificial Chromosomes", IPK Gatersleben, 31.10.-03.11.2011.

V106. Liiving, T. & B. H. Junker (vorgetragen von Liiving, T.): Investigating the starch synthesis pathway for kinetic modeling in pea embryos during seed filling phase. – 7th Plant Science Student Conference, IPB, Halle/S., 14.-17.06.2011.

V107. Lohwasser, U., A. Dittbrenner, F. Marthe & A Börner (vorgetragen von Lohwasser U.): Taxonomy of plant genetic resources – and interaction of morphological, molecular and phytochemical data. – BioSystematics, Berlin, 21.-27.02.2011.

V108. Lohwasser, U., M. Nagel & A Börner (vorgetragen von Lohwasser, U.): Longevity of seeds – intraspecific differences in germplasm collections. – BioSystematics, Berlin, 21.-27.02.2011.

V109. Lohwasser, U.: The umbellifers (Apiaceae) of the German *ex situ* genebank. – ECPGR Umbellifer Working Group Meeting, Quedlinburg, 30.03.-01.04.2011.

V110. Lohwasser, U. & A. Börner (vorgetragen von Lohwasser, U.): Quality standards in genebanks – improvement of sustainability of plant genetic resources. – EUCARPIA Section Genetic Resources, European Plant Genetic Resources Conference 2011, Wageningen/The Netherlands, 05.-07.04.2011.

V111. Lohwasser, U. & A. Börner (vorgetragen von Lohwasser, U.): Genbanken – Ressourcen für künftige Generationen. – Symposium on Biodiversität, Geistiges Eigentum und Innovation, Philipps-Universität Marburg, 20.05.2011.

V112. Lohwasser, U.: Sammlungen alter Kulturpflanzen – Genreservoir für die Zukunft? – Deutsche Biotechnologietage 2011, München, 25.-26.05.2011.

V113. Lohwasser, U., M.A. Rehman Arif, K. Herrmann & A Börner (vorgetragen von Lohwasser, U.): New strategies for discovery loci determining pre-harvest sprouting and dormancy in wheat and barley. – The 12th International Symposium on Pre-Harvest Sprouting in Cereals, Red Deer, Alberta/Canada, 24.-27.07.2011.

V114. Lohwasser, U.: The rye collection of the German genebank. – Workshop "Improving the prerequisites for a European rye collection", Radzików/Poland, 13.-14.10.2011.

V115. Ma, L.: Generation of engineered chromosomes in barley. – Japanese-German JSPS and DFG-funded Workshop "Frontiers of Plant Chromosome Research: Centromeres and Artificial Chromosomes", IPK Gatersleben, 31.10.-03.11.2011.

V116. Marconi, G., G. Galla, M. Conner, L. Ragi, G. Barcaccia, P. Ozias-Akins, T.F. Sharbel, M. Falcinelli & E. Albertini (vorgetragen von Marconi, G.): Cross-species characterization of APOSTART for unveiling its role in apomixis. – EU COST Action Apomixis Workshop, Valencia/Spain, 04.-05.07.2011.

V117. Martín, C., A. Senula, I. González, A. Acosta, M.E. González-Benito & E.R.J. Keller (vorgetragen von Martín, C.): The role of cryopreservation in the long-term conservation of vegetatively propagated plants. – Final Meeting of COST Action 871 CryoPlanet, Angers/France, 08.-11.02.2011.

V118. Mascher, M., U. Scholz & S. Friedel (vorgetragen von Mascher, M.): Chargaff's second parity rule in plant genomes. – JCB Workshop "Nucleotides – Networks – Novelties. Understanding Evolution Beyond Darwin and Haeckel", Jena, 28.-29.03.2011.

V119. Mascher, M.: Chargaff's second parity rule in grass genomes. – 7th Plant Science Student Conference, IPB, Halle/S., 14.-17.06.2011.

V120. Mascher, M.: Chargaff's DNA fragment assembly: an application of graph theory in molecular biology. – Oberseminar Algebra, Fakultät für Mathematik, Otto-von-Guericke-Universität, Magdeburg, 05.07.2011.

V121. Matros, A., M. Peukert, S. Kaspar, W. Weschke & H. P. Mock (vorgetragen von Matros, A.): Spatial protein and metabolite profiling during barley grain development by MALDI-MS imaging and LC-MS approaches. – DGMS-Tagung, Dortmund, 27.02.-02.03.2011.

V122. Matros, A.: Analysis of spatial and temporal changes during barley grain development. – Charles University, Prague/Czech Republic, 18.10.2011.

V123. Mehlhorn, H.: The DBE2 information system. – Workshop "Translational Bioinformatics" of 6th International Symposium on Health Informatics and Bioinformatics (HIBIT2011), Izmir/Turkey, 02.-05.05.2011.

V124. Mehlhorn, H.: Integration of biological networks using VANTED NETS. – 7th Plant Science Student Conference, IPB, Halle/S., 14.-17.06.2011.

V125. Mehlhorn, H.: Integration of biological networks using VANTED NETS. – International German/Russian Summer School in "Integrative Biological Pathway Analysis and Simulation", Bielefeld, 04.-07.07.2011.

V126. Mehlhorn, H.: Analysis of biological networks. – International German/Russian Summer School in "Integrative Biological Pathway Analysis and Simulation", Bielefeld, 04.-07.07.2011.

V127. Mehlhorn, H. & F. Schreiber (vorgetragen von Mehlhorn, H.): Integration and exploration of biological networks. – Workshop „Datenmanagement in den Lebenswissenschaften", Berlin, 06.10.2011.

V128. Melzer, B., T. Guse, C. Kastner, K. Plasun, C. Berger, E. Kapusi, G. Hensel, C. Marthe, P. Hoffmeister & J. Kumlehn (vorgetragen von Melzer, B.): Novel tools for *Brachypodium* research: Genetic transformation using shoot segments and immature pollen-derived generation of instantly homozygous lines. – 1st European *Brachypodium* Workshop, Paris/France, 19.-21.10.2011.

V129. Melzer, M.: The microworld of a plant cell: Microscopy techniques in plant research application. – Faculty of Biology and Environment Protection, University of Silesia, Katowice/Poland, 19.05.2011.

V130. Melzer, M.: Cells in the focus: Microscopy in plant research. – Royal Institute of Technology (KTH), UAlbaNova University Center, Stockholm/Sweden, 22.06.2011.

V131. Melzer, M.: Comparative structural cell biological studies of gametophytic pollen development vs. initiation of pollen embryogenesis in barley. – Institutstag IPK, Gatersleben, 04.-06.10.2011.

V132. Mock, H.-P.: Proteomics to evaluate genetic resources for stress defence responses. – INRA, Clermont-Ferrand/France, 24.05.2011.

V133. Mock, H.-P.: Studying barley seed development by spatially resolved mass spectrometrical analysis. – Danish Technical University, Copenhagen/Denmark, 07.06.2011.

V134. Mock, H.-P.: Analysis of salt stress tolerance mechanisms in barley mapping populations. – Institutstag IPK, Gatersleben, 04.-06.10.2011.

V135. Mock, H.-P.: Phytochemical analysis of anthocyanins. – 1st Annual Meeting Athena, Acireale, Sicily/Italy, 12.-14.10.2011.

V136. Mock, H.-P.: Proteomics to evaluate genetic resources for stress defence responses. – KEW Botanical Gardens/Wakehurst Place, West Sussex/UK, 07.12.2011.

V137. Mostek, A., S. Lüthje, C. Meisrimler, A. Börner & A. Weidner (vorgetragen von Mostek, A.): Proteome differences between salt-sensitive and tolerant barley and alleviating influence of BABA. – Final COST Action Meeting FA0603 'Plant Proteomics in Europe', Dijon/France, 26.05.2011.

V138. Nagel, M. & A. Börner (vorgetragen von Nagel, M.): Impacts of the genetic background on seed deterioration in crops. – 10th International Conference of the International Society for Seed Science (ISSS), Costa do Sauípe, Bahia/Brazil, 10.-15.04.2011.

V139. Nagel, M., I. Kranner & A. Börner (vorgetragen von Nagel, M.): Conservation of germplasm collections – biochemical and genetic impacts on seed ageing in barley. – 10th International Conference of the International Society for Seed Science (ISSS), Costa do Sauípe, Bahia/Brazil, 10.-15.04.2011.

V140. Nagel, M.: Erhaltung von pflanzengenetischen Ressourcen in der Bundeszentralen *ex situ* Genbank Gatersleben. – Interdisziplinäres Wissenschaftlertreffen im Rahmen des Übereinkommens über die Biologische Vielfalt, Naturschutzakademie Vilm, Putbus, 22.-26.08.2011.

V141. Nagel, M., I. Kranner & A. Börner (vorgetragen von Nagel, M.): Biochemical and genetic studies on seed longevity in the German *ex situ* genebank. – Seminar, Wageningen University and Research Centre (WUR), Wageningen/The Netherlands, 17.10.2011.

V142. Neumann, K.: Die Identifizierung von QTLs für die Trockentoleranz in Gerste. – Oberseminar Pflanzenzüchtung, Martin-Luther-Universität Halle-Wittenberg, Halle/S., 10.02.2011.

V143. Neumann, K., A.F. Balint, F. Szira, M. Baum, R.K. Varshney & A. Börner (vorgetragen von Neumann, K.): Genome-wide association mapping for early and late drought tolerance in a diverse barley collection. – Agrisafe Final Conference "Climate change: challenge for training of applied plant scientists", Budapest/Hungary, 21.-23.03.2011.

V144. Neumann, K., B. Kobiljski, S. Denčić, R.K. Varshney & A. Börner (vorgetragen von Neumann, K.): Genome-wide association mapping of agronomic traits in bread wheat. – EWAC-EUCARPIA Cereals Section Conference, Novi Sad/Serbia, 07.-11.11.2011.

V145. Nürk, N.M., S. Uribe-Convers, D. Tank, S. Madriñán, M. Carine, M. Chase & F. R. Blattner (vorgetragen von Nürk, N.M.): Molecular phylogeny and historical biogeography of *Hypericum*. – BioSystematics, Berlin, 21.-27.02.2011.

V146. Nürk, N.M.: Tracing the impact of the Andean uplift – evolutionary history of *Hypericum* in South America. – DFG Nachwuchsakademie "Systematik der Pflanzen und Pilze", Frankfurt am Main, 25.05.2011.

V147. Peruzzi, L., D. Harpke & A. Carta (vorgetragen von Peruzzi, L.): Risultati preliminari sull'evoluzione e filogenesi, nell'ambito della serie *Verni* (*Crocus*, Iridaceae), dei due crochi endemici di Toscana. – Riunione Annuale Gruppo Biosistematica 2011, Castiglioncello (Livorno)/Italy, 11.06.2011.

V148. Peterson, A. & D. Harpke (vorgetragen von Peterson, A.): Molecular insights in the species-rich polyploid Liliaceae genus *Gagea*: impact of molecular data for determination of hybridogenic taxa and species boundaries. – BioSystematics, Berlin, 21.-27.02.2011.

V149. Peukert, M., A. Matros & H. P. Mock (vorgetragen von Peukert, M.): MALDI-imaging for spatial protein and metabolite profiling during barley grain development. – Bruker Anwendertreffen, Kassel, 21.-22.03.2011.

V150. Pistrick, K.: Das wissenschaftliche Werk von Paul Schuster (1876–1965). – Eröffnung einer zusammen mit U. Kison konzipierten und gestalteten Ausstellung „Paul Schuster – Pfarrer und Botaniker in Meisdorf", Patronatskirche Meisdorf, Stadt Falkenstein/Harz, 27.08.2011.

V151. Pshenichnikova, T.A., M.D. Permyakova, S.V. Osipova, A.V. Permyakov, A. Börner, S. Landjeva, T. Karceva, E.K. Khlestkina, A.V. Simonov, E.V. Morozova & L.V. Shchukina (vorgetragen von Pshenichnikova, T.A.): Prospects for the use of cytogenetic collections and their derivative forms in bread wheat for identification and mapping of new genes. – International Conference "Wheat Genetic Resources and Genomics", Novosibirsk/Russia, 28.08.-01.09.2011.

V152. Pshenichnikova, T.A., E. Khlestkina, L.V. Shchukina, A.V. Simonov, A.K. Chistyakova, E.V. Morozova, S. Landjeva, T. Karceva & A. Börner (vorgetragen von Pshenichnikova, T.A.): Exploitation of Saratovskaya 29 / Janetzkis Probat 4D*7A substitution and derivate lines for comprehensive phenotyping and molecular mapping of quantitative traits loci (QTL). – EWAC-EUCARPIA Cereals Section Conference, Novi Sad/Serbia, 07.-11.11.2011.

V153. Rehman Arif, M.A., M. Nagel, U. Lohwasser & A. Börner (vorgetragen von Rehman Arif, M.A.): Long-term seed storability in genebank collections – genetic studies in wheat. – Agrisafe Final Conference "Climate change: challenge for training of applied plant scientists", Budapest/Hungary, 21.-23.03.2011.

V154. Rehman Arif, M.A.: Seed conservation in *ex situ* genebanks – genetic studies on longevity in wheat. – 7th Plant Science Student Conference, IPB, Halle/S., 14.-17.06.2011.

V155. Rohn, H.: Network-based integrative visualization of biological multi-domain data. – International German/Russian Summer School in "Integrative Biological Pathway Analysis and Simulation", Bielefeld, 04.-07.07.2011.

V156. Rolletschek, H.: Combined non-invasive imaging and modelling approaches reveal metabolic compartmentation in the cereal endosperm. – 71st Harden Conference on Metabolic Pathway Analysis, University of Chester, Cheshire, England/UK, 19.-23.09.2011.

V157. Rutten, T.: CENH3 dynamics in the plant cell cycle. – Faculty of Biology and Environment Protection, University of Silesia, Katowice/Poland, 29.11.2011.

V158. Šarhanová, P., R.J. Vašut, K.A. Geetha, T.F. Sharbel, M. Dančák, M. Kitner & B. Trávníček (vorgetragen von Šarhanová, P.): Microevolutionary processes in Central European *Rubus* populations: apomixis versus sexuality – stability versus innovation. – EU COST Action Apomixis Workshop, Valencia/Spain, 04.-05.07.2011.

V159. Schallau, A., F. Arzenton, A.J. Johnston, U. Hähnel, D. Köszegi, F.R. Blattner, L. Altschmied, T.F. Sharbel, G. Haberer, G. Barcaccia & H. Bäumlein (vorgetragen von Schallau, A.): Identification and genetic analysis of the apospory locus in *Hypericum perforatum*. – Plant and Animal Genome XIX. Conference, San Diego/USA, 15.-19.01.2011.

V160. Schallau, A.: The apospory locus of *Hypericum perforatum*. – 4th Annual Hypericum Meeting, Graz/Austria, 23.-24.10.2011.

V161. Schmutzer, T.: RNA-seq in rye (*Secale cereale* L.): Establishment of new resources in Triticeae genomics. – 7th Plant Science Student Conference, IPB, Halle/S., 14.-17.06.2011.

V162. Schmutzer, T.: Tackling repetitiveness in plant genomes: An introduction how to process NGS sequencing data of plants. – International German/Russian Summer School in "Integrative Biological Pathway Analysis and Simulation", Bielefeld, 04.-07.07.2011.

V163. Schnurbusch, T.: Spike branching in wheat and barley. – 11th GABI Status Seminar, Potsdam, 15.-17.03.2011.

V164. Schnurbusch, T.: The rise of developmental mutants in barley and wheat. – Seminar, Carlsberg Research Laboratory, Copenhagen/Denmark, 10.-11.11.2011.

V165. Schreiber, F.: Visualisation of biological data. – Otto-von-Guericke-Universität Magdeburg, 11.02.2011.

V166. Schreiber, F.: Creating views on integrated multi-domain data and representing knowledge in SBGN. – Friedrich-Schiller-Universität, Jena, 16.06.2011.

V167. Schreiber, F.: Von Genen zu Netzen – Bioinformatik in Biologie und Medizin. – Summerbyte, Halle/S., 11.08.2011.

V168. Schreiber, F.: Current developments in pathway-related Bioinformatics. – Novosibirsk State University, Russia, 15.09.2011.

V169. Schreiber, F.: Creating views on integrated multi-domain data. – Institutstag IPK, Gatersleben, 04.-06.10.2011.

V170. Schreiber, F.: Bioinformatics @ IPK Gatersleben. – Institutstag IPK, Gatersleben, 04.-06.10.2011.

V171. Schreiber, F.: The Systems Biology Graphical Notation – methods and tools. – German-Russian Workshop, Biotechnica Hannover, 10.10.2011.

V172. Schreiber, F.: Representing, analysing and visualising plant metabolism. – Rheinische Friedrich-Wilhelms-Universität Bonn, 22.11.2011.

V173. Schubert, I.: Centromere maintenance. – State Key Laboratory of Plant Genomics, Centre for Genome Biology, Institute of Genetics and Developmental Biology, Chinese Academy of Sciences, Beijing/China, 10.05.2011.

V174. Schubert, I.: Mechanics of chromosome and karyotype evolution helps to interprete genomic data correctly. – National Maize Improvement Center, Chinese Agricultural University, Beijing/China, 10.05.2011.

V175. Schubert, I.: Mechanics of chromosome and karyotype evolution helps to interprete genomic data correctly. – Wuhan University, Beijing/China, 13.05.2011.

V176. Schubert, I.: Korrekte Interpretation der Genomevolution erfordert Kenntnis der Chromosomenmutagenese. – Genetik und Epigenetik höherer Pflanzen, Wissenschaftliches Symposium anlässlich des 80. Geburtstages von Professor Rudolf Hagemann, Deutsche Akademie der Naturforscher Leopoldina, Halle/S., 28.10.2011.

V177. Schubert, I.: Plant centromeres. – Japanese-German JSPS and DFG-funded Workshop "Frontiers of Plant Chromosome Research: Centromeres and Artificial Chromosomes", IPK Gatersleben, 31.10.-03.11.2011.

V178. Schubert, V.: Is there CENH3 loading during meiosis in plants? – Japanese-German JSPS and DFG-funded Workshop "Frontiers of Plant Chromosome Research: Centromeres and Artificial Chromosomes", IPK Gatersleben, 31.10.-03.11.2011.

V179. Schweizer, P.: HIGS: Host-induced gene silencing in phytopathogenic fungi. – Plant and Animal Genome XIX. Conference, San Diego/USA, 15.-19.01.2011.

V180. Schweizer, P.: Cell-wall related genes for race-nonspecific resistance of barley to powdery mildew. – University of Adelaide, Adelaide/Australia, 23.09.2011.

V181. Schweizer, P.: Race-nonspecific resistance of barley to powdery mildew: one trait – many genes. – SCIRO Plant Industry, Canberra/Australia, 26.09.2011.

V182. Seifert, M.: Extended Hidden Markov Models for the analysis of MeDIP-chip, tumor expression and Array-

CGH profiles. – Institute of Biology at the Ecole Normale Supérieure, Paris/France, 18.02.2011.

V183. Seifert, M.: Exploiting prior knowledge and gene distances in the analysis of tumor expression profiles with extended Hidden Markov Models. – Jstacs Workshop, Martin-Luther-Universität Halle-Wittenberg, Halle/S., 19.05.2011.

V184. Seifert, M.: Analyzing tumor expression and comparative genomics data with extended Hidden Markov Models. – Interfakultäres Institut für Genetik und Funktionelle Genomforschung, Ernst-Moritz-Arndt-Universität, Greifswald, 04.08.2011.

V185. Sreenivasulu, N.: Strategies for improved seed yield and quality under terminal drought. – University of Agricultural Sciences, Crop Physiology Department, GKVK, Bangalore/India, 11.01.2011.

V186. Sreenivasulu, N.: Reprogramming of seed metabolism under drought. – Kolloquien Pflanzenzüchtung, Martin-Luther-Universität Halle-Wittenberg, Halle/S., 10.06.2011.

V187. Sreenivasulu, N.: Exploring yield enhancement genes influencing grain number and seed growth under drought. – IZN Annual Meeting, Martin-Luther-Universität Halle-Wittenberg, Halle/S., 13.07.2011.

V188. Sreenivasulu, N.: Seed transcriptome reprogramming under terminal drought to harness optimum yield and seed. – PBGB Seminar, International Rice Research Institute, Metro Manila/Philippines, 14.09.2011.

V189. Sreenivasulu, N.: Importance of ABA homeostasis for seed transcriptome reprogramming under terminal drought to harness optimum yield and seed quality. – Institutstag IPK, Gatersleben, 04.-06.10.2011.

V190. Stein, N.: New achievements in crop genomics – or how to unlock the 5 gigabase barley genome. – Seminar, Leibniz-Universität Hannover, 02.02.2011.

V191. Stein, N.: Making the barley genome accessible – progress in physical mapping and sequencing a 5 Gbp genome. – Seminar, University of Bologna/Italy, 23.02.2011.

V192. Stein, N.: Sequencing the 5.1 gigabase genome of barley – new insights into Triticeae genome organization. – Seminar, Carlsberg Research Laboratory, Copenhagen/Denmark, 04.03.2011.

V193. Stein, N.: Beauty and the beast – unlocking the barley genome by chromosomal genomics. – Botanikertagung 2011 "Diversity makes the Difference", Berlin, 18.-23.09.2011.

V194. Steuernagel, B.: Challenges in assembling barley sequences. – 3rd Workshop on TritiGen COST Action FA0604 "Triticeae Genomics for The Advancement of Essential European Crops", Istanbul/Turkey, 03.-04.05.2011.

V195. Teo, C.H.: Induction of telomere-mediated chromosomal truncation and stability of truncated chromosomes in *Arabidopsis thaliana*. – Japanese-German JSPS and DFG-funded Workshop "Frontiers of Plant Chromosome Research: Centromeres and Artificial Chromosomes", IPK Gatersleben, 31.10.-03.11.2011.

V196. Tikhenko, N., A. Börner, N. Tsvetkova, T. Rutten & A. Voylokov (vorgetragen von Tikhenko, N.): Development of a model system to study gene interactions of parental forms in wheat-rye hybrids and primary *Triticale*. – International Conference "Wheat Genetic Resources and Genomics", Novosibirsk/Russia, 28.08.-01.09.2011.

V197. Trautwein, A., D. Jankowska & G. Kunze (vorgetragen von Trautwein A.): Purine degradation pathway in *Arxula adeninivorans* – basis for production of food with low purine content. – Institute of Microbial Technology (IMTECH). Chandigarh/India, 14.02.2011.

V198. van Iersel, M.P. & T. Czauderna (vorgetragen von van Iersel, M.P.): LibSBGN status update. – COMBINE 2011, Heidelberg, 03.-07.09.2011.

V199. von Wirén, N.: Ammonium and iron sensing in *Arabidopsis* plants. – Institut für Pflanzenbiochemie, Halle/S., 11.01.2011.

V200. von Wirén, N.: Ammonium and iron sensing in *Arabidopsis* plants. – Universität Heidelberg, 19.01.2011.

V201. von Wirén, N.: Ammonium and iron sensing in *Arabidopsis* plants. – Freie Universität Berlin, 01.07.2011.

V202. von Wirén, N.: Chancen und Risiken der grünen Gentechnik. – Lion's Club, Wernigerode, 19.07.2011.

V203. von Wirén, N.: Nutrient sensing in *Arabidopsis*. – Institutstag IPK, Gatersleben, 04.-06.10.2011.

V204. Vu, G.T.H. & I Schubert (vorgetragen von Schubert, I. und Vu, G.T.H.): Genome sequencing in carnivorous plants to study genome size and karyotype evolution. – Julius-von-Sachs-Institut für Biowissenschaften, Lehrstuhl Botanik, Molekulare Pflanzenphysiologie und Biophysik, Julius-Maximilians-Universität Würzburg, 21.10.2011.

V205. Weschke, W.: Ertragssteigerungen bei Weizen – der mögliche Beitrag der Grünen Gentechnik. – 25. Getreide-Tagung, Detmold, 17.03.2011.

V206. Weschke, W.: Ertragssteigerungen bei Weizen – der mögliche Beitrag der Grünen Gentechnik. – Sitzung des Ausschusses für Müllerei-Technologie, Würzburg, 22.03.2011.

V207. Weschke, W.: Transgenic solutions to enhance yield structure of high performance lines of wheat. – German-Brazilian Workshop on Transgenic Crops, Hannover, 04.-05.04.2011.

V208. Weschke, W.: Relationship between senescence-induced N-remobilization and seed filling in barley. – Meeting DFG-Forschergruppe FOR948 „Nitrogen uptake, metabolism and remobilization in leaves during plant senescence", Berlin, 23.-24.09.2011.

V209. Weschke, W.: The role of cellular disintegration in crop seed development. – Institutstag IPK, Gatersleben, 04.-06.10.2011.

V210. Witzel, K., A. Matros, A. Møller, C. Finnie, B. Svensson, G. Kunze & H. P. Mock (vorgetragen von Witzel, K.): Label-free quantitative proteomics of the plasma membrane leads to the identification of new candidates for increasing salt tolerance in barley. – Meeting COST Action FA0603, Dijon/France, 25.-27.05.2011.

V211. Zaynali Nezhad, K., W.E. Weber, M.S. Röder, S. Sharma, U. Lohwasser, R.C. Meyer, B. Saal & A Börner (vorgetragen von Zaynali Nezhad, K.): QTL analysis for thousand-grain weight under terminal drought stress in bread wheat (*Triticum aestivum* L.). – International Conference "Wheat Genetic Resources and Genomics", Novosibirsk/Russia, 28.08.-01.09.2011.

Poster/Posters

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P1. Absattarova, A.S., M.S. Röder, S. Kollers, A.I. Morgounov & S. Kenjebaeva: Identification and distribution of the alleles of photoperiod and vernalization responses wheat genes in Kazakhstan. – 8th International Wheat Conference, St. Petersburg/Russia, 01.-04.06.2010.

P2. Agarwal, R., A. Matros, M. Melzer, H.-P. Mock & K. Sainis: Blue native PAGE analysis validates heterogeneity in the thylakoids of Synechocystis 6803. – 15th International Congress of Photosynthesis, Beijing/China, 22.-27.08.2010.

P3. Ahkami, A.H., M. Melzer, B. Hause, P. Franken, U. Drüge & M.R. Hajirezaei: Influence of auxin on primary metabolism at various developmental stages of root formation in *Petunia*. – 20th IPGSA (International Plant Growth Substances Association)-Conference, Tarragona/Spain, 28.06.-02.07.2010.

P4. Alter, P., J.-S. An, B. Steuernagel, T. Schmutzer, U. Scholz, T. Dresselhaus & M. Gahrtz: Maize stem parenchyma – developing tools for the engineering of a potential storage tissue. – Maize Genetics Conference, Riva del Garda/Italy, 18.-21.03.2010.

P5. Altschmied, L.: Promoters of *Arabidopsis thaliana* are characterized by local n-mer frequencies. – Institutstag IPK, Gatersleben, 04.-05.10.2010.

P6. Andeden, E., F. Baloch, B. Kilian, N. Nachit & H. Özkan: Allelic diversity for vernalization and photoperiod genes in bread wheat cultivars and landraces from Turkey. – 8th International Wheat Conference, St. Petersburg/Russia, 01.-04.06.2010.

P7. Angioi, S.A., D. Rau, E. Bellucci, L. Nanni, H. Knüpffer, V. Negri, P.L. Spagnoletti Zeul, R. Papa & G. Attene: European runner bean landraces: genetic diversity and structure assessed by chloroplast microsatellites. – 54th Annual Congress of the Italian Society of Agricultural Genetics (SIGA), Matera/Italy, 27.-30.09.2010.

P8. Appelhagen, I., G. Huep, T. Altmann, B. Weisshaar & M. Sagasser: Weird fingers – functional analysis of WIP domain proteins. – 21st International Conference on *Arabidopsis* Research, Yokohama/Japan, 06.-10.06.2010.

P9. Ariyadasa, R., D. Schulte, N. Poursarebani, R. Zhou, B. Steuernagel, U. Scholz, M. Martis, M. Seidel, H. Gundlach, K. Mayer, S. Taudien, M. Felder, M. Platzer, B. Shi, P. Langridge, T. Close, M. Morgante, P. Hedley, R. Waugh, A. Graner & N. Stein: The physical map of the barley genome. – Institutstag IPK, Gatersleben, 04.-05.10.2010.

P10. Ariyadasa, R., D. Schulte, N. Poursarebani, R. Zhou, B. Steuernagel, U. Scholz, M. Martis, K. Mayer, H. Liu, P. Hedley, R. Waugh, P. Langridge, T. Close, A. Graner & N. Stein: The physical map of barley (*Hordeum vulgare* L.). – 10th Gatersleben Research Conference 2010 (GRCX) "Sequence-informed Crop Research", Quedlinburg (Palais Salfeldt)/Gatersleben (IPK), 22.-24.11.2010.

P11. Bakos, F., C. Kastner, B. Barnabás, E. Kugelmann & J. Kumlehn: Generation of doubled haploid maize plants following inductive treatment of isolated immature pollen. – Conference on Green Plant Breeding Technology, Vienna/Austria, 02.-05.02.2010.

P12. Barunawati, N.: Influence of Nitrogen Fertilizer application on iron retranslocation in wheat plants. – 15th International Symposium on Iron Nutrition and Interactions in Plants, Budapest/Hungary, 26.-30.06.2010.

P13. Berger, C., G. Hensel, M. Gurushidze, D. Douchkov, R. Eichmann, I. Schönborn, L. Loyall, S. Bieri, R. Hückelhoven, P. Schweizer & J. Kumlehn: Generation and molecular analysis of transgenic barley and wheat lines carrying hairpin RNAi constructs directed towards genes involved in plant-pathogen interaction. – 10th GABI Status Seminar, Potsdam, 09.-11.03.2010.

P14. Bohner, A.: Physiological functions of the urea transporter AtDUR3 in *Arabidopsis thaliana*. – 6th Plant Science Student Conference, IPK, Gatersleben, 15.-18.06.2010.

P15. Bohner, A.: Physiological functions of the urea transporter AtDUR3 during senescence in *Arabidopsis thaliana*. – 5th European Plant Senescence Network Meeting (SENnet 2010), Wokefield Park, Reading/UK, 31.08.-03.09.2010.

P16. Bohner, A.: Physiological function of the urea transporter AtDUR3 during senescence in *Arabidopsis thaliana*. – Deutsche Gesellschaft für Pflanzenernährung (DGP) Symposium, Hannover, 30.09.-02.10.2010.

P17. Borisova, B., G. Jovtchev, I. Schubert & M.F. Mette: Genetic analysis of tandem repeat mediated control of nuclear architecture in *A. thaliana*. – Biowissenschaftliches Netzwerk „Strukturen und Mechanismen der biologischen Informationsverarbeitung", Gesamtarbeitsbesprechung, Martin-Luther-Universität Halle-Wittenberg, Halle/S., 04.-05.03.2010.

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P20. Boudichevskaia, A., J. Koppolu & R. Schmidt: Analysis of regulators of seed oil biosynthesis. – 6th Plant Science Student Conference, IPK, Gatersleben, 15.-18.06.2010.

P21. Boudichevskaia, A., J. Koppolu & R. Schmidt: Genetic analysis of seed traits in *Arabidopsis thaliana*. – Institutstag IPK, Gatersleben, 04.-05.10.2010.

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P23. Bruchmüller, A., M. Kuhlmann, J. Kumlehn, R. Schmidt & M.F. Mette: RNA-directed RNA polymerase RDR5 is essential for transcript level-mediated post-transcriptional gene silencing. – 21st International Conference on *Arabidopsis* Research, Yokohama/Japan, 06.-10.06.2010.

P24. Cao, H.X., A. Boudichevskaia & R. Schmidt: Exploiting BAC libraries for the study of the *Brassica napus* genome. – Institutstag IPK, Gatersleben, 04.-05.10.2010.

P25. Chesnokov, Y.V., N.V. Pochepnya, L. Kozlenko, O.P. Mitrofanova, U. Lohwasser & A. Börner: Localization of QTLs for agronomic important characters in spring wheat (*Triticum aestivum* L.) grown in different ecological places in Russia and Germany. – 8th International Wheat Conference, St. Petersburg/Russia, 01.-04.06.2010.

P26. Colmsee, C., S. Sonnewald, U. Schlüter, A. Bräutigam, N. Zellerhoff, A. Weber, M. Bucher, U. Sonnewald & U. Scholz: OPTIMAS-OC: Development of an oligo chip to explore the maize transcriptome. – 10th GABI Status Seminar, Potsdam, 09.-11.03.2010.

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P30. Czauderna, T., C. Klukas, A. Junker & F. Schreiber: Editing, validating, and translating of SBGN maps with SBGN-ED. – 11th International Conference on Systems Biology (ICSB 2010), Edinburgh, Scotland/UK, 10.-15.10.2010.

P31. Czernicka, M., E. Böer, B. Steuernagel, S. Flemming, N. Stein, U. Scholz & G. Kunze: The *Arxula adeninivorans* genome: Sequencing, assembly and annotation. – Institutstag IPK, Gatersleben, 04.-05.10.2010.

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P37. Dehmer, K.J. & L. Krawetzke: An SSR-based assessment of diversity in wild species of potato. – 2nd International Symposium on Genomics of Plant Genetic Resources, Bologna/Italy, 24.-27.04.2010.

P38. Dehmer, K.J.: Assessing genetic diversity in potato wild species via SSR markers. – EAPR – EUCARPIA Congress on Potato Breeding after Completion of the DNA Sequence of the Potato Genome, Wageningen/The Netherlands, 27.-30.06.2010.

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P43. Douchkov, D., S. Lück & P. Schweizer: A high-throughput RNAi screen for defense- or susceptibility-related genes in barley (GABI-Phenome). – 10th GABI Status Seminar, Potsdam, 09.-11.03.2010.

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P60. Fuchs, J., B. Borisova, G. Jovtchev & I. Schubert: Epigenetic modifications of sex chromatin in dioecious plants. – Institutstag IPK, Gatersleben, 04.-05.10.2010.

P61. Galla, G., T.F. Sharbel & G. Barcaccia: Apospory in *Hypericum perforatum* L.: from cytohistological investigations of sporogenesis and gametogenesis to transcriptome analysis. – 14th International Biotechnology Symposium and Exhibition, Rimini/Italy, 14.-18.09.2010.

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P171. Pistrick, K., M. Akhalkatsi & J. Ekhvaia: Plant genetic resources of higher altitudes in southeastern Georgia (Samcche-Džavacheti and Atčara). – Institutstag IPK, Gatersleben, 04.-06.10.2011.

P172. Poskar, C.H., C. Krach, M. Franke, N. Schäfer, L. Fichtmüller, F. Kellner, J. Hüge & B.H. Junker: A pipeline for the derivation of intracellular metabolic fluxes in developing legume seeds. – Society for Experimental Biology Annual Main Meeting, Glasgow/UK, 01.-04.07.2011.

P173. Poursarebani, N., R. Ariyadasa, D. Schulte, R. Zhou, B. Steuernagel, M. Martis, K.F.X. Mayer, U. Scholz, A. Graner & N. Stein: Potential of grass genome synteny for genetic anchoring of the physical map of barley (*Hordeum vulgare* L.) – A case study on chromosome 2H. – Plant and Animal Genome XIX. Conference, San Diego/USA, 15.-19.01.2011.

P174. Radchuk, V., D. Weier, R. Radchuk, H. Weber & W. Weschke: Expression of distinct VPE genes coincides with the disintegration processes in developing barley grains. – 1st Plant Protease Conference, Hemavan/Sweden, 11.-14.04.2011.

P175. Rajesh, K., V. Harshavadhan, H. Rolletschek, K.-P. Götz, C. Seiler, M. Strickert, V. Korzun, B. Usadel, R. Sulpice, M. Stitt, U. Wobus & N. Sreenivasulu: Importance of senescence induced remobilization in determining the crop yield in elite lines of barley under terminal drought. – 11th GABI Status Seminar, Potsdam, 15.-17.03.2011.

P176. Rehman Arif, M.A., M. Nagel, K. Neumann, U. Lohwasser, B. Kobiljski & A. Börner: Genome-wide association mapping of longevity, dormancy and pre-harvest sprouting in bread wheat (*Triticum aestivum* L.). – EWAC-EUCARPIA Cereals Section Conference, Novi Sad/Serbia, 07.-11.11.2011.

P177. Rohn, H., C. Klukas & F. Schreiber: Visual analytics of multimodal biological data. – International Conference on Information Visualization Theory and Applications (IVAPP2011), Vitamoura/Portugal, 05.-07.03.2011.

P178. Rohn, H. & F. Schreiber: Combining different types of biological data. – International Symposium on Integrative Bioinformatics 2011 (IB2011), Wageningen/The Netherlands, 21.-23.03.2011.

P179. Róis, A.S., D. Espírito-Santo, T.F. Sharbel & A.D. Caperta: Cytogenetic diversity and ploidy variation in diploid and polyploid *Limonium* species. – 13th Congress of the European Society for Evolutionary Biology (ESEB2011), Tübingen, 20.-25.08.2011.

P180. Rolletschek, H., G. Melkus, E. Grafahrend-Belau, J. Fuchs, N. Heinzel & L. Borisjuk: Combined non-invasive imaging and modeling approaches reveal metabolic compartmentation in the barley endosperm. – 12th International Conference on Systems Biology (ICSB2011), Heidelberg/Mannheim, 28.08.-01.09.2011.

P181. Rolletschek, H., G. Melkus, E. Grafahrend-Belau, J. Fuchs, N. Heinzel, F. Schreiber, P.M. Jakob & L. Borisjuk: Combined non-invasive imaging and modelling approaches reveal metabolic compartmentation in the cereal endosperm. – 71st Harden Conference on Metabolic Pathway Analysis, University of Chester, Cheshire, England/UK, 19.-23.09.2011.

P182. Rolletschek, H., N. Heinzel, H. Tschiersch, J. Fuchs, T. Altmann & L. Borisjuk: Modelling of growth and storage metabolism in crop seeds. – Institutstag IPK, Gatersleben, 04.-06.10.2011.

P183. Rubtsova, M., K. Kempe & M. Gils: A split gene approach for hybrid wheat production. – Institutstag IPK, Gatersleben, 04.-06.10.2011.

P184. Rutten, T., D. Köszegi, A.J. Johnston, A. Czihal, J. Kumlehn, S. Wuest, O. Kirioukhova, J. Gheyselinck, L. Altschmied, G. Mönke, M. Melzer & H. Bäumlein: Studies on the egg-cell specific transcription factors RKD1 & RKD2. – 9th International Botanical Microscopy Meeting, Wageningen/The Netherlands, 16.-21.04.2011.

P185. Sainis, J.K., R. Agarwal, K.H. Süss & M. Melzer: Immune electron microscopy suggests that soluble enzymes form a thin layer on the surface of thylakoid membranes. – Gordon Research Conference on Photosynthesis, Davidson/USA, 12.-17.06.2011.

P186. Salem, K.F.M., M.S. Röder & A. Börner: Evaluation of genetic diversity among Egyptian bread wheat (*Triticum aestivum* L.) varieties during the period 1947-2004 using microsatellites. – EWAC-EUCARPIA Cereals Section Conference, Novi Sad/Serbia, 07.-11.11.2011.

P187. Sanei, M., R. Pickering, K. Kumke, S. Nasuda & A. Houben: Loss of CENH3 from centromeres precedes uniparental chromosome elimination in interspecific barley hybrids. – 18th International Chromosome Conference, University Place, Manchester/UK, 29.08.-02.09.2011.

P188. Sanei, M., R. Pickering, K. Kumke, S. Nasuda & A. Houben: Loss of CENH3 from centromeres precedes uniparental chromosome elimination in interspecific barley hybrids. – Institutstag IPK, Gatersleben, 04.-06.10.2011.

P189. Saur, A., I.P. Pathuri, G. Hensel, D. Zajic, R. Pröls, R. Hückelhoven, J. Kumlehn & L.M. Voll: Suppression of starch biosynthesis compromises non-host resistance in barley. – SFB 648 International Meeting "Communication in Plants and their Responses to the Environment", Halle/S., 19.-21.05.2011.

P190. Schallau, K., S. Bundtzen, T. Liiving, S. Weber, S.M. Baker, V. Peter & B.H. Junker: Metabolic engineering based on predictions from computational models of starch synthesis in plant seeds. – Institutstag IPK, Gatersleben, 04.-06.10.2011.

P191. Schlereth, A., H. Tschoep, W.R. Scheible, R.C. Meyer, M. Müller, H. Schön, T. Altmann & M. Stitt: GABI-ENERGY: Biomass production in maize – genomics guided breeding of energy maize and a systems-oriented analysis; genotyping of inbred line panel and phenotyping of inbreds and test crosses under glass house conditions. – 11th GABI Status Seminar, Potsdam, 15.-17.03.2011.

P192. Schreiber, F. & T. Czauderna: SBGN-ED – working with the Systems Biology Graphical Notation. – 12th International Conference on Systems Biology (ICSB2011), Heidelberg/Mannheim, 28.08.-01.09.2011.

P193. Schubert, I., V. Schubert & J. Fuchs: DNA double-strand break recombination repair in plants – is 'Break-Induced Replication' a real phenomenon? – Institutstag IPK, Gatersleben, 04.-06.10.2011.

P194. Sedzielewska, K.A., D. Klemann, J. Fuchs, N.M. Nürk, K. Vetter, R. Watzke & G. Kunze: A molecular approach to characterize *Glomus* AMykor isolate. – 26th Fungal Genetic Conference, Boston/USA, 15.-20.03.2011.

P195. Seeber, E., G. Winterfeld, T.F. Sharbel, W. Durka, I. Hensen, J. Liu, H. Miehe & K. Wesche: A study on generative reproduction, clonal growth and polyploidy. – 7th Sino-German Workshop on Tibetan Plateau Research, Hamburg, 03.-05.03.2011.

P196. Seidensticker, T., A. Börner & T. Schnurbusch: Towards genetic elucidation of gene(s) regulating inflorescence branching in wheat and barley. – 11th GABI Status Seminar, Potsdam, 15.-17.03.2011.

P197. Seidensticker, T., A. Börner & T. Schnurbusch: Towards the molecular elucidation of 'Miracle Wheat' - wheats with branched inflorescences. – 21st Workshop of the International Triticeae Mapping Initiative (ITMI), Mexico City/Mexico, 05.-09.09.2011.

P198. Seidensticker, T., L. Rossini, U. Lundqvist & T. Schnurbusch: Compositum barley – towards genetic elucidation of gene(s) regulating inflorescence branching. – 21st Workshop of the International Triticeae Mapping Initiative (ITMI), Mexico City/Mexico, 05.-09.09.2011.

P199. Seidensticker, T., A. Börner & T. Schnurbusch: Towards the molecular elucidation of 'Miracle Wheat' – wheats with branched inflorescences. – Annual Conference of the German Genetics Society (GfG), Würzburg, 14.-16.09.2011.

P200. Seidensticker, T., L. Rossini, A. Börner, U. Lundqvist & T. Schnurbusch: Towards genetic elucidation of gene(s) regulating inflorescence branching in wheat and barley. – Institutstag IPK, Gatersleben, 04.-06.10.2011.

P201. Seifert, M., A.M. Banaei Moghaddam, A. Gohr, M. Strickert & I. Grosse: Parsimonious higher-order Hidden Markov Models for enhanced comparative genomics. – Institutstag IPK, Gatersleben, 04.-06.10.2011.

P202. Seiler, C., V. Harshavadhan, R. Kalladan, G. Henzel, J. Kumlehn & N. Sreenivasulu: Fine tuned modulation of receptor kinase RPK1 in source and sink tissues lead to altered ABA homeostasis and improved drought tolerance in barley. – Institutstag IPK, Gatersleben, 04.-06.10.2011.

P203. Seyfarth, M., K. Weigelt, D. Riewe, R.C. Meyer & T. Altmann: Identification and characterization of functional diversity of regulatory proteins controlling plant growth. – 7th Plant Science Student Conference, IPB, Halle/S., 14.-17.06.2011.

P204. Seyfarth, M., K. Weigelt, R.C. Meyer & T. Altmann: Identification and characterization of functional diversity of regulatory proteins controlling plant growth. – Botanikertagung 2011 "Diversity makes the Difference", Berlin, 18.-23.09.2011.

P205. Shi, R.: Senescence-induced iron remobilization in source leaves as a prerequisite for iron retranslocation in barley plants. – Botanikertagung 2011 "Diversity makes the Difference", Berlin, 18.-23.09.2011.

P206. Springmann, C., S. Hörding, T. Mechanik, F. Bakos & J. Kumlehn: Development of commercially applicable methods to generate doubled haploid lines in cereals. – 11th GABI Status Seminar, Potsdam, 15.-17.03.2011.

P207. Steuernagel, B., T. Wicker, H. Gundlach, K.F.X. Mayer, N. Stein & U. Scholz: Assembly validation and scaffolding using transposable element information. – Plant and Animal Genome XIX. Conference, San Diego/USA, 15.-19.01.2011.

P208. Steuernagel, B., S. Taudien, H. Gundlach, M. Groth, M. Felder, T. Nussbaumer, M. Platzer, K.F.X. Mayer, U. Scholz & N. Stein:

WGS sequencing of barley: A current status. – 11th GABI Status Seminar, Potsdam, 15.-17.03.2011.

P209. Szira, F., A. Börner, K. Neumann, K. Zaynali Nezhad, G. Galiba & A.F. Balint: EST-based markers associated with QTLs for drought tolerance in barley (*Hordeum vulgare*) could be used for marker-assisted selection. – Agrisafe Final Conference "Climate change: challenge for training of applied plant scientists", Budapest/Hungary, 21.-23.03.2011.

P210. Tavakol, E., G. Verderio, T. Fusca, S. Ciannamea, T.J. Close, A. Druka, R. Waugh, K.F.X. Mayer, M. Martis, R. Ariyadasa, D. Schulte, R. Zhou, N. Stein, G. Muehlbauer & L. Rossini: Fine mapping and steps towards map-based cloning of Cul4, a Mendelian locus required for tillering in barley. – Plant and Animal Genome XIX. Conference, San Diego/USA, 15.-19.01.2011.

P211. Teo, C.H., L. Ma, E. Kapusi, G. Hensel, J. Kumlehn, I. Schubert, A. Houben & M.F. Mette: Construction of engineered minichromosomes in *Hordeum vulgare* and *Arabidopsis thaliana*. – 18th International Chromosome Conference, University Place, Manchester/UK, 29.08.-02.09.2011.

P212. Teo, C.H., L. Ma, E. Kapusi, G. Hensel, J. Kumlehn, I. Schubert, A. Houben & M.F. Mette: Towards construction of engineered plant minichromosomes. – Institutstag IPK, Gatersleben, 04.-06.10.2011.

P213. Thiel, T. & T.F. Sharbel: Scrutinizing gene copy number variation (CNV) as a factor for apomixis expression in *Boechera*. – 9th IMPRS Symposium, Dornburg, 15.02.2011.

P214. Tison, J.M., A. Peterson, D. Harpke & L. Peruzzi: Phylogenetic analysis shed new light into taxonomy and reticulate evolution of the critical Mediterranean *Gagea* sect. *Didymobulbos* (Liliaceae). – BioSystematics, Berlin, 21.-27.02.2011.

P215. Tschiersch, H., L. Borisjuk & H. Rolletschek: Modelling seed photosynthesis by IMAGING-PAM reveals gradient distribution and adjustments to low light supply. – International Conference on Tetrapyrole Photoreceptors of Photosynthetics Organisms (ICTPPO), Berlin, 24.-28.07.2011.

P216. van Iersel, M.P., S.E. Boyd, F. Bergmann, S. Moodie, F. Schreiber, T. Czauderna, E. Demir, N. Le Novère, A. Sorokin, H. Mi, A. Luna, U. Dogrusoz, Y. Matsuoka, A. Funahashi, H. Kitano, M.I. Aladjem, M.L. Blinov & A.C. Villéger: LibSBGN: electronic exchange of SBGN maps. – HARMONY 2011: The Hackathon on Resources for Modeling in Biology, New York/USA, 18.-22.04.2011.

P217. van Iersel, M.P., S.E. Boyd, F. Bergmann, S. Moodie, F. Schreiber, T. Czauderna, E. Demir, N. Le Novère, A. Sorokin, H. Mi, A. Luna, U. Dogrusoz, Y. Matsuoka, A. Funahashi, H. Kitano, M.I. Aladjem, M.L. Blinov & A.C. Villéger: LibSBGN: electronic processing of SBGN maps. – COMBINE 2011, Heidelberg, 03.-07.09.2011.

P218. Vu, G.T.H., H.X. Cao, F. Bull, J. Fuchs, T. Schmutzer, G. Jovtchev, A. Pecinka, P. Dear, U. Scholz & I. Schubert: Genome size evolution in the genus *Genlisea* from half of the *A. thaliana* genome to the twenty-fold. – "Plant Genome Evolution" (A Current Opinion Conference), Amsterdam/The Netherlands, 04.-06.09.2011.

P219. Weigelt, K., R.C. Meyer, D. Riewe, B. Ebert, J. Lisec, R. Schmidt, L. Willmitzer & T. Altmann: GABI-GNADE: Genome-wide natural diversity exploitation in the *Arabidopsis* population; Identification and characterization of genes controlling vegetative biomass accumulation in *Arabidopsis thaliana*. – 11th GABI Status Seminar, Potsdam, 15.-17.03.2011.

P220. Weigelt, K., R.C. Meyer, D. Riewe, I. Mücke & T. Altmann: Use of high-throughput phenotyping platforms to identify and characterize genes controlling vegetative biomass accumulation in *Arabidopsis thaliana*. – 2nd International Plant Phenotyping Symposium, Forschungszentrum Jülich, 05.-07.09.2011.

P221. Wicker, T., K.F.X. Mayer, H. Gundlach, B. Steuernagel, U. Scholz, A. Graner, J. Dolezel, H. Simkova, F. Choulet, C. Feuillet, T. Fahima, H. Budak, B. Keller & N. Stein: Report on low-pass sequencing of flow-sorted wheat group 1 chromosome arms. – Plant and Animal Genome XIX. Conference, San Diego/USA, 15.-19.01.2011.

P222. Wicker, T., K.F.X. Mayer, H. Gundlach, B. Steuernagel, U. Scholz, A. Graner, J. Dolezel, H. Simkova, F. Choulet, C. Feuillet, T. Fahima, H. Budak, B. Keller & N. Stein: Too many genes and pseudogenes – runaway amplification of genic sequences in barley and wheat? – Plant and Animal Genome XIX. Conference, San Diego/USA, 15.-19.01.2011.

P223. Willner, E., S. Nehrlich & K.J. Dehmer: A European Forage Collection (EFC) as basis for AEGIS and the planned Euro Genebank – Which final requirements are needed? – EUCARPIA Section Genetic Resources, European Plant Genetic Resources Conference 2011, Wageningen/The Netherlands, 05.-07.04.2011.

P224. Witter, S. & K.J. Dehmer: Establishment of heterotic pools in *Lolium perenne* L. as basis for biomass hybrid breeding. – 7th Plant Science Student Conference, IPB, Halle/S., 14.-17.06.2011.

P225. Witter, S., S. Weise, J. Förster & K.J. Dehmer: Heterotic pools in perennial ryegrass as basis for biomass hybrid breeding. – Botanikertagung 2011 "Diversity makes the Difference", Berlin, 18.-23.09.2011.

P226. Worch, S., N. Sreenivasulu, K. Rajesh, L. Kunze & M.S. Röder: Candidate genes for grain yield and quality under terminal drought stress in barley. – 11th GABI Status Seminar, Potsdam, 15.-17.03.2011.

P227. Ye, F. & N. von Wirén: Iron as a determinant of virulence and resistance in the *Colletotrichum graminicola* – maize interaction. – Botanikertagung 2011 "Diversity makes the Difference", Berlin, 18.-23.09.2011.

P228. Zhou, R., G. Haseneyer, T. Schmutzer, M. Seidel, C.C. Schön, E. Bauer, U. Scholz, K.F.X. Mayer & N. Stein: A high density transcript map of rye (*Secale cereale* L.) comprising 3,000 EST-SNPs loci. – Plant and Animal Genome XIX. Conference, San Diego/USA, 15.-19.01.2011.

Vom Institut organisierte Tagungen und Veranstaltungen/ Conferences and Meetings Organised by IPK

2010

Veranstaltung zur Verabschiedung des Administrativen Leiters, Herrn Bernd Eise und zur Einführung seiner Nachfolgerin, Frau Sybille-Andrea Lorenz
21. Januar 2010, Gatersleben
188 Teilnehmer

Arbeitstagung der Arbeitsgemeinschaft Saatgut- und Sortenwesen der Gesellschaft für Pflanzenbauwissenschaften (GPW) und der Gesellschaft für Pflanzenzüchtung (GPZ) „Saatgut als Kulturerbe – Produktion, Nutzung und Erhaltung“
24. - 25. Februar 2010, Gatersleben
ca. 100 Teilnehmer

10. Sitzung der ECPGR-Arbeitsgruppe Forages
28. - 29. April 2010, Malchow/Poel
33 Teilnehmer

InWent – Weiterbildung und Entwicklung gGmbH „The Role of Plant Genetic Resources in Climate Change Adaptation“
17. - 22. Mai 2010, Gatersleben und Berlin
16 Teilnehmer

Mini-Symposium Association Studies Task Force (ASTF)
27. Mai 2010, Gatersleben

Tag der offenen Tür in der Genbank Teilsammlungen Nord zum Motto „2010 – Jahr der Biologischen Vielfalt“
5. Juni 2010, Malchow/Poel
ca. 200 Teilnehmer

GFP-Sommertagung
Öffentliche Sitzung der Abteilung Getreide
9. - 10. Juni 2010, Gatersleben
70 Teilnehmer

Tag der offenen Tür „Biodiversität als Herausforderung und Chance“ und 5. Fest der Begegnung
12. Juni 2010, Gatersleben
ca. 500 Teilnehmer

6th Plant Science Student Conference (PSSC)
15. - 18. Juni 2010, Gatersleben
70 Teilnehmer

Workshop „Bestimmung von Schlafmohn und anderen Mohnarten“ für Kriminalämter der BRD
1. - 2. Juli 2010, Gatersleben
10 Teilnehmer

3. Gaterslebener Gespräch „Globale Aspekte der Grünen Gentechnik“
16. - 17. September 2010, Gatersleben
80 Teilnehmer

Abb. 53
Wie hier am Stand der chinesischen Mitarbeiter/-innen konnten sich die Besucher über das Leben und die Bräuche in den Heimatländern unserer ausländischen Wissenschaftler/-innen informieren bzw. auf kulinarische Entdeckungsreise gehen. (Foto: B. Schäfer/IPK Gatersleben)
Fig. 53
Visitors to the Muliti-cultural Event showed great interest in the life, habits and customs in the home countries of our foreign scientists - exemplary the Chinese community. Especially tempting seemed the specialties from the different countries. (Photo: B. Schäfer/ IPK Gatersleben)

European Networking Summer School (ENSS) Plant Epigenetics 2010 „Epigenetische Genregulation in Pflanzen“
20. - 24. September 2010, Gatersleben
43 Teilnehmer

Institutstag 2010
Vortragsveranstaltung, Posterpräsentation aller wissenschaftlichen Arbeitsgruppen
4. - 5. Oktober 2010, Gatersleben
ca. 200 Teilnehmer

Gaterslebener Forum zum Wissenschaftsmanagement und Technologietransfer
15. Oktober 2010, Gatersleben
22 Teilnehmer

Mini-Symposium „Stem Cell Research and Applications“ anlässlich der Verabschiedung von Frau Prof. Dr. Anna M. Wobus
17. November 2010, Gatersleben
60 Teilnehmer

10th Gatersleben Research Conference (GRC X) “Sequence-informed Crop Research”
22. - 24. November 2010, Gatersleben und Quedlinburg
160 Teilnehmer

Jahresversammlung BarleyGenomeNet
26. November 2010, Gatersleben
15 Teilnehmer

2011

Gaterslebener Begegnung XII „Wachstum und Reifung in Natur und Gesellschaft“
12. - 14. Mai 2011, Gatersleben
110 Teilnehmer

Tag der offenen Tür „Der Wissenschaftsstandort Malchow stellt sich vor“
21. Mai 2011, Arbeitsgruppe Teilsammlungen Nord der IPK-Genbank, Malchow/Peol
ca. 300 Teilnehmer

Tag der offenen Tür am Biotechnologie-Campus Gatersleben
28. Mai 2011, Gatersleben
ca. 300 Teilnehmer

Institutstag 2011
Vortragsveranstaltung, Posterpräsentation aller wissenschaftlichen Arbeitsgruppen
4. - 5. Oktober 2011, Gatersleben
ca. 200 Teilnehmer

JSPS-DFG Workshop „Frontiers of Plant Chromosome Research: Centromeres and Artificial Chromosomes“
31. Oktober - 3. November 2011, Gatersleben
30 Teilnehmer

Festveranstaltung anlässlich der Verleihung der Forschungspreise für Grundlagenforschung und angewandte Forschung des Landes Sachsen-Anhalt
5. Dezember 2011, Gatersleben
ca. 100 Teilnehmer

Abb. 54
Die Teilnehmer genießen die herbstliche Atmosphäre am IPK während des gemeinsamen JSPS-DFG-finanzierten Workshops "Frontiers of Plant Chromosome Research: Centromeres and Artificial Chromosomes" vor dem Hörsaal. (Foto: H. Ernst/IPK Gatersleben)
Fig. 54
Indian Summer in Gatersleben: Participants of the joint JSPS-DFG-financed Workshop "Frontiers of Plant Chromosome Research: Centromeres and Artificial Chromosomes" in front of IPK's lecture hall. (Photo: H. Ernst/IPK Gatersleben)

Beteiligung an der Organisation externer Veranstaltungen/ Participation in Organising External Meetings

Thema	Zeitpunkt der Veranstaltung Ort/Land	Veranstalter/Mitorganisatoren (beteiligte Einrichtungen)	Art der Veranstaltung (national/ internat.)	Anzahl Teilnehmer
2010				
6th International Symposium on Integrative Bioinformatics	20.-22.03.2010 Cambridge UK	University of Cambridge and Rothamsted Research Prof. F. Schreiber Dr. U. Scholz	international	120
Systems Biology Graphical Notation Workshop (SBGN 5.5)	21.-23.04.2010 Wittenberg	IPK und Martin-Luther-Universität Halle-Wittenberg Prof. F. Schreiber T. Czauderna	international	40
2nd International Symposium on Genomics of Plant Genetics Resources	24.-27.04.2010 Bologna Italy	Alma Mater Studiorum Università di Bologna Prof. A. Graner PD Dr. A. Börner	international	400
8th International Wheat Conference	01.-04.06.2010 St. Petersburg Russia	N.I. Vavilov Research Institute of Plant Industry (VIR) International Maize and Wheat Improvement Center (CIMMYT) PD Dr. A. Börner	international	650
16th International Conference for Renewable Resources and Plant Biotechnology NAROSSA 2010	07.-08.06.2010 Magdeburg	PPM Pilot Pflanzenöltechnologie Magdeburg e.V. Prof. G. Kunze	international	ca. 100
European Conference on Machine Learning and Principles and Practice of Knowledge Discovery in Databases (ECML PKDD)	20.-24.09.2010 Barcelona Spain	Universitat Politècnica de Catalunga BarcelonaTech (UPC) Centre National de la Recherche Scientifique (CnrS) Dr. J. Keilwagen	international	460
Frontier in Agriculture Proteome Research	18.11.2010 Tsukuba Japan	National Institute of Crop Science PD Dr. H.-P. Mock	international	ca. 220

Thema	Zeitpunkt der Veranstaltung Ort/Land	Veranstalter/Mitorganisatoren (beteiligte Einrichtungen)	Art der Veranstaltung (national/ internat.)	Anzahl Teilnehmer
2011				
COST Action 871, CryoPlaNet Final meeting	08.-11.02.2011 Angers France	Agrocampus Quest of INHP Dr. J. Keller	international	68
7th International Symposium on Integrative Bioinformatics	21.-23.03.2011 Wageningen The Netherlands	University of Wageningen Dr. M. Lange, Dr. U. Scholz, Prof. F. Schreiber	international	ca. 120
Joint AGRISAFE-EUCARPIA Cereals Section Workshop for Young Cereal Scientists "Climate Change and Plant Breeding Answers"	21.-23.03.2011 Budapest Hungary	Agricultural Research Institute of the Hungarian Academy of Sciences, Martonvásár PD Dr. A. Börner	international	160
Seventh meeting of the ECPGR Barley Working Group	10.-12.05.2011 Nicosia Cyprus	ECPGR Secretariat Dr. H. Knüpffer	international	28
Workshop Java framework for statistical analysis and classification of biological sequences (Jstacs)	19.05.2011 Halle/S.	Martin-Luther-Universität Halle-Wittenberg Dr. S. Friedel	national	20
First International Symposium on Cryopreservation of Horticultural Crops in China	28.-30.06.2011 Shaanxi China	Northwest A & F University, Yangling Dr. J. Keller	international	70
21st International Triticeae Mapping Initiative Workshop	05.-09.09.2011 Mexico City Mexico	Internationale Triticeae Mapping Initiative Dr. N. Stein	international	ca. 300
Seventh meeting of the ECPGR Allium Working Group	06.-08.09.2011 Perea, Thessaloniki Greece	European Cooperative Programme for Plant Genetic Resources (ECPGR) Dr. J. Keller	international	22
Non-conventional Yeast in the Postgenomic Era (NCY)	11.-14.09.2011 Lviv Ukraine	Institute of Cell Biology, NAS of Ukraine, Ukrainian Society of Cell Biology Prof. G. Kunze	international	ca. 200
7th International Symposium on *In vitro* Culture and Horticultural Breeding „Biotechnological Advances in *In vitro* Horticultural Breeding"	18.-22.09.2011 Ghent Belgium	International Society for Horticultural Science, University Ghent, Belgium Dr. J. Keller	international	260
6. Fachtagung Arznei- und Gewürzpflanzen	19.-22.09.2011 Berlin	Deutscher Fachausschuss für Arznei-, Gewürz- und Aromapflanzen (DFA) und Landwirtschaftlich-Gärtnerische Fakultät der Humboldt-Universität zu Berlin Dr. U. Lohwasser	international	ca. 150
Joint EWAC-EUCARPIA Cereals Section Conference „Development and Utilisation of Cereal Stocks for Gene Identification and Molecular Mapping"	07.-11.11.2011 Novi Sad Serbia	Institute of Field and Vegetable Crops, Novi Sad PD Dr. A. Börner	international	60
Parlamentarischer Abend „Pflanzen-basierte Bioökonomie: Wertstoffproduktion und Ernährungssicherung"	12.12.2011 Berlin	Ministerium für Wissenschaft und Wirtschaft Sachsen-Anhalt, IPB Halle/S., IPK Gatersleben	national	70

Ehrungen, Preise/Honours, Awards

2010

Der Biologe **Dr. Nils Stein** hat am 15. März 2010 den erstmals verliehenen Günter und Anna Wricke-Forschungspreis erhalten. Damit wurden seine Arbeiten zur Genforschung an Getreide durch die gleichnamige Stiftung gewürdigt (http://www.wricke-stiftung.de).

Auf der 45. Vortragstagung der Deutschen Gesellschaft für Qualitätsforschung präsentierte sich **Manuela Nagel** mit einem Poster, das am 23. März 2010 als „Hervorragender wissenschaftlicher Posterbeitrag" ausgezeichnet wurde. Die Veranstaltung fand in Berlin-Dahlem statt.

Am 25. März 2010 erhielt **Jemanesh Kifatew Haile** den „Jeanie Borlaug Laube Women in Triticum Award 2010". Die äthiopische Wissenschaftlerin arbeitet in der Arbeitsgruppe Gen- und Genomkartierung bei Dr. M. Röder.

Bei der 6th Plant Science Student Conference (PSSC), die vom 15. bis 18. Juni 2010 im IPK stattfand, wurden folgende Preise vergeben:

Jury Award - Best Talks

1. Platz: **Rico Lippmann**, IPK, Abt. Physiologie und Zellbiologie, Arbeitsgruppe Angewandte Biochemie;

2. Platz: **Naser Poursarebani,** IPK, Abt. Genbank, Arbeitsgruppe Genomdiversität;

3. Platz: **Katarzyna Plasun**, IPK, Abt. Physiologie und Zellbiologie, Arbeitsgruppe Pflanzliche Reproduktionsbiologie.

Jury Award - Best Poster

2. Platz: **Tina Seidensticker**, IPK, Abt. Genbank, Arbeitsgruppe Pflanzliche Baupläne;

3. Platz: **Anne Bohner**, IPK, Abt. Physiologie und Zellbiologie, Arbeitsgruppe Molekulare Pflanzenernährung.

Audience Award – Best Talk

Katarzyna Plasun, IPK, Abt. Physiologie und Zellbiologie, Arbeitsgruppe Pflanzliche Reproduktionsbiologie.

Audience Award – Best Poster

Young-Min Kim, IPK, Abt. Physiologie und Zellbiologie, Arbeitsgruppe Molekulare Pflanzenernährung.

M.Sc. Manuela Nagel erhielt auf dem 29th International Seed Testing Association (ISTA) Congress, der vom 15. bis 18. Juni 2010 in Köln stattfand, den „Seed Symposium Award 2010" für hervorragende Leistungen ihrer Darstellung.

Honorable mention of BEST Performer (2nd place) in the DREAM5 international initiative of Columbia University and IBM, challenge: „Transcription-Factor/DNA-Motif Recognition" for **Jens Keilwagen**, Jan Grau, Ivo Grosse, Stefan Posch, November 2010.

2011

Die Nationale Akademie der Wissenschaften LEOPOLDINA ehrte ihre Mitglieder Frau **Prof. Dr. Anna M. Wobus** und Herrn **Prof. Dr. Ulrich Wobus** mit der Cothenius-Medaille in Gold. Sie erhielten diese Ehrung für ihr wissenschaftliches Lebenswerk. Die Medaillen wurden im Rahmen der feierlichen Eröffnung der Leopoldina-Jahresversammlung am 23. September 2011 in Halle/S. überreicht.

Dr. Manuela Nagel, Dr. Astrid Junker und **Nicolai Nürk** wurden am 5. Oktober 2011 mit dem „Beagle Award" ausgezeichnet. Sie erhielten diesen Preis, der an Nachwuchswissenschaftler des IPK vergeben wird, für ihre wissenschaftliche Arbeit und ihr soziales Engagement. Die Preisverleihung erfolgte im Anschluss an den Institutstag durch den Geschäftsführenden Direktor und das Student Board.

Am 5. Dezember 2011 wurde der Forschungspreis für angewandte Forschung des Landes Sachsen-Anhalt an den langjährigen Mitarbeiter des IPK und Leiter der Arbeitsgruppe Hefegenetik, Herrn **Prof. Dr. Gotthard Kunze**, verliehen und im Rahmen einer Festveranstaltung durch Herrn Staatssekretär Marco Tullner, Ministerium für Wissenschaft und Wirtschaft des Landes Sachsen-Anhalt, überreicht.

Von der Ag Dateninspektion nahmen Dr. Jens Keilwagen und Dr. Michael Seifert erfolgreich am 6. „Bioinformatics DREAM 2011" Wettbewerb teil. Gemeinsam mit sechs anderen Teams errangen beide unabhängig voneinander den 1. Platz.

Arbeitsaufenthalte von Gästen im IPK/
Guest Researchers at the IPK

(ab einer Woche, ohne Schüler, Praktikanten, Studenten)

Abteilung Genbank

Dr. Sven Gottwald, Justus-Liebig-Universität, Gießen, 01.01.2010 bis 28.02.2011, Eigenfinanzierung (Prof. Dr. A. Graner, Dr. N. Stein/Arbeitsgruppe Genomdiversität).

Dr. Dragan Perovic, Julius Kühn-Institut Quedlinburg, Quedlinburg, 01.01.2010 bis 30.04.2010, Finanzierung durch JKI Quedlinburg; 01.06.2010 bis 31.12.2010, Eigenfinanzierung (Dr. N. Stein/Arbeitsgruppe Genomdiversität).

Salar Shaaf, Department of Agronomy and Plant, University of Teheran, Teheran, Iran, 11.02.2010 bis 25.09.2010, Finanzierung durch iranische Regierung (Dr. B. Kilian/Arbeitsgruppe Genomdiversität).

Agostino Fricano, Università degli Studi di Milano, Lodi, Italien, 22.03.2010 bis 26.03.2010, Finanzierung durch BMBF (Dr. N. Stein/Arbeitsgruppe Genomdiversität).

Benedikt Athmer, 01.04.2010 bis 31.12.2011, Eigenfinanzierung (Dr. N. Stein/Arbeitsgruppe Genomdiversität).

Dr. Jan Bartos, Laboratory of Molecular Cytogenetics and Cytometry, Institute of Experimental Botany, Olomouc, Tschechische Republik, 22.03.2010 bis 26.03.2010, Eigenfinanzierung (Dr. N. Stein/Arbeitsgruppe Genomdiversität).

Ping Yang, 24.08.2010 bis 31.08.2010, Eigenfinanzierung (Dr. N. Stein/Arbeitsgruppe Genomdiversität).

Dr. Daniela Schulte, 01.02.2010 bis 31.12.2010, Eigenfinanzierung (Dr. N. Stein/Arbeitsgruppe Genomdiversität).

Therese Gradin, School of Life Sciences, Södertörn University, Södertörn, Schweden, 01.02.2010 bis 28.02.2010, Finanzierung durch Södertörn University (Dr. N. Stein/Arbeitsgruppe Genomdiversität).

Dr. Fedor A. Konovalov, N. I. Vavilov Institute of General Genetics, Moskau, Russland, 01.03.2010 bis 31.05.2010, Finanzierung durch DFG; 18.11.2010 bis 18.12.2010, Eigenfinanzierung; 04.06.2011 bis 19.06.2011, IPK (Dr. B. Kilian/Arbeitsgruppe Genomdiversität).

Dr. Marianna Paquariello, University of Modena, Modena, Italien, 15.03.2010 bis 30.05.2010; 28.08.2011 bis 27.09.2011, Eigenfinanzierung (Dr. N. Stein, Dr. A. Himmelbach/Arbeitsgruppe Genomdiversität).

Dr. Minne Turktas, Szbzrci University of Istanbul, Istanbul, Türkei, 22.03.2010 bis 26.03.2010, Eigenfinanzierung (Dr. N. Stein/Arbeitsgruppe Genomdiversität).

Dr. Cedric Moisy, MTT/BI Plant Genomics Laboratory, Helsinki, Finnland, 22.03.2010 bis 26.03.2010, Eigenfinanzierung (Dr. N. Stein/Arbeitsgruppe Genomdiversität).

Dr. Outi Manninen, MTT/Agrifood Research, Helsinki, Finnland, 22.03.2010 bis 26.03.2010, Eigenfinanzeirung (Dr. N. Stein/Arbeitsgruppe Genomdiversität).

Dr. Marco Maccaferri, Department of Agro-Environmental Science and Technology, University of Bologna, Bologna, Italien, 22.03.2010 bis 26.03.2010, Finanzierung durch University of Bologna (Dr. N. Stein/Arbeitsgruppe Genomdiversität).

Dr. Bu-Jun Shi, Australian Center for Plant Functional Genomics (ACPFG), Adelaide, Australien, 27.02.2011 bis 02.03.2011, Finanzierung durch University of Adelaide (Dr. N. Stein/Arbeitsgruppe Genomdiversität).

Oskar Obidiegwu, University Hohenheim, Institute of Plant Breeding, Seed Science and Population Genetics, Stuttgart-Hohenheim, 28.08.2011 bis 02.09.2011, Finanzierung durch IPK und University of Hohenheim (Dr. B. Kilian/Arbeitsgruppe Genomdiversität).

Ben-Israel Imri, Hebrew University, Faculty of Agricultural Science, Jerusalem, Israel, 19.06.2011 bis 26.06.2011, Finanzierung durch IPK und Eigenfinanzierung (Dr. B. Kilian/Arbeitsgruppe Genomdiversität).

Dr. Anna Filatenko, Vavilov Institute (VIR), St. Petersburg, Russland, 22.05.2011 bis 31.10.2011, Finanzierung durch DFG (Dr. B. Kilian/Arbeitsgruppe Genomdiversität).

Dr. Maria Munoz Amatriain, University of Minnesota, Department of Agronomy and Plant Genetics, Minnesota, USA, 06.06.2011 bis 17.07.2011, Finanzierung durch University of Minnesota (Dr. N. Stein/Arbeitsgruppe Genomdiversität und Dr. U. Scholz/Arbeitsgruppe Bioinformatik und Informationstechnologie).

Dr. Marzena Kurowska, University of Silesia, Faculty of Biology and Environmental Protection, Department of Genetics, Katowice, Polen, 29.10.2011 bis 31.01.2012, Finanzierung durch IAEA-Stipendium (Dr. N. Stein/Arbeitsgruppe Genomdiversität).

Dr. Helmy Mohamed Youssef, Plant Physiology & Biotech Department, Faculty of Agriculture, Kairo, Ägypten, 09.05.2010 bis 09.07.2010, Finanzierung durch DAAD-Stipendium (Dr. T. Schnurbusch/Arbeitsgruppe Pflanzliche Baupläne).

Arash Fazeli, University of Sari, Sari, Iran, 13.04.2011 bis 12.10.2011, Finanzierung durch Ministry of Science, Research & Technology, Iran; 13.10.2011 bis 31.12.2011, Eigenfinanzierung; 01.01.2012 bis 29.02.2012, Finanzierung durch IPK (Dr. T. Schnurbusch/Arbeitsgruppe Pflanzliche Baupläne).

Dr. Yuri Shavrukov, Australian Centre for Plant Functional Genomics, Glen Osmond, Australien, 19.05.2010 bis 21.05.2010, Eigenfinanzierung (Dr. T. Schnurbusch/Arbeitsgruppe Pflanzliche Baupläne).

Lucia Stimolo, Institute of Plant Genetics, Genebank Bari, Bari, Italien, 23.08.2010 bis 27.08.2010, Eigenfinanzierung (Dr. U. Lohwasser/Arbeitsgruppe Ressourcengenetik und Reproduktion).

Mian Abdur Rehman Arif, University of Arid Agriculture, Rawalpindi, Pakistan, 01.01.2010 bis 31.03.2012, Finanzierung durch DAAD (Dr. A. Börner/Arbeitsgruppe Ressourcengenetik und Reproduktion).

Khalil Zaynali Nezhad, Department of Agronomy and Plant Breeding, College of Agriculture, Isfahan Institute of Technology, Isfahan, Iran, 01.01.2010 bis 30.09.2010, Finanzierung durch iranische Regierung (Dr. A. Börner/Arbeitsgruppe Ressourcengenetik und Reproduktion).

Kerstin Neumann, 01.01.2010 bis 31.08.2010, Eigenfinanzierung (Dr. A. Börner/Arbeitsgruppe Ressourcengenetik und Reproduktion).

Dr. Oxana Dobrovolskaya, Institute of Cytology and Genetics, Nowosibirsk, Russland, 02.03.2010 bis 03.04.2010 und 31.10.2010 bis 23.12.2010, Finanzierung durch DFG (Dr. A. Börner/Arbeitsgruppe Ressourcengenetik und Reproduktion).

Dr. Annette Weidner, 01.01.2010 bis 30.06.2010, Eigenfinanzierung (Dr. A. Börner/Arbeitsgruppe Ressourcengenetik und Reproduktion).

Dr. Abdolrazagh Danesh-Shahraki, University of Shahrekord, Department of Agronomy and Plant Breeding, Faculty of Agriculture, Shahrekord, Iran, 13.07.2010 bis 29.07.2010, Finanzierung durch Shahrekord University (Dr. A. Börner/Arbeitsgruppe Ressourcengenetik und Reproduktion).

Dr. Natalia Tikhenko, St. Petersburg State University, Biological Research Institute, St. Petersburg, Russland, 04.04.2010 bis 14.04.2010, Eigenfinanzierung (Dr. A. Börner/Arbeitsgruppe Ressourcengenetik und Reproduktion).

Klaudia Kruppa, Martonvásár, Agricultural Research Institute, Martonvásár, Ungarn, 10.01.2011 bis 09.04.2011, Finanzierung durch Agricultural Research Institute Martonvásár (Dr. A. Börner/Arbeitsgruppe Ressourcengenetik und Reproduktion).

Mai Allam, National Research Center (NRC), Plant Biotechnology Department, Kairo, Ägypten, 04.04.2011 bis 03.04.2014, Finanzierung durch DAAD (Dr. A. Börner/Arbeitsgruppe Ressourcengenetik und Reproduktion).

Dr. Isaac Daniel, University of Agriculture, Department of Plant Breeding & Seed Technology, Abeokuta, Nigeria, 01.07.2011 bis 26.09.2011, Finanzierung durch ein Stipendium der Humboldt-Stiftung (Dr. A. Börner/Arbeitsgruppe Ressourcengenetik und Reproduktion).

Serik Jantassov, Kasakh Research Institute of Potato and Vegetables Production, Almaty Oblast, Karasay Rayon, Kasachstan, 11.09.2011 bis 17.09.2011, Finanzierung durch GIZ Bonn/Eschborn (Dr. U. Lohwasser/Arbeitsgruppe Ressourcengenetik und Reproduktion).

Dr. Malgorzata Pelc, Warsaw University of Life Science, Department of Vegetable and Medicinal Plants, Warschau, Polen, 07.04.2010 bis 28.05.2010, Finanzierung durch COST Action 871 (Dr. J. Keller/Arbeitsgruppe *In vitro*-Erhaltung und Cryo-Lagerung).

Marta Olas-Sochacka, Research Institute of Vegetable Crops (RIVC), Warschau, Polen, 19.10.2010 bis 18.11.2010, Finanzierung durch COST Action 871 (Dr. J. Keller/Arbeitsgruppe *In vitro*-Erhaltung und Cryo-Lagerung).

Dr. Magfrat Muminova, Academy of Science, Institute of Genetics and Plant Experimental Biology, Tashkent, Usbekistan, 12.09.2011 bis 11.12.2011, Finanzierung durch DAAD (Dr. J. Keller/Arbeitsgruppe *In vitro*-Erhaltung und Cryo-Lagerung).

Andreas Stephanik, 01.02.2010 bis 31.12.2010, Eigenfinanzierung (Dr. H. Knüpffer/Arbeitsgruppe Genbankdokumentation).

Tamar Jinjikhadze, Ilia State University Tbilisi, Botanical Garden and Institute of Botany, Cultural Flora Department, Tbilisi, Georgien, 19.03.2011 bis 29.03.2011, Finanzierung durch Tbilisi Botanical Garden (Dr. H. Knüpffer/Arbeitsgruppe Genbankdokumentation).

Solomon Benor, Debub University, Department of Plant Sciences, Awassa, Äthiopien, 01.01.2010 bis 30.09.2011, Finanzierung durch DAAD (Dr. F. Blattner/Arbeitsgruppe Experimentelle Taxonomie).

Christina Baier, 01.09.2010 bis 31.03.2011 und 01.07.2011 bis 31.12.2011, Eigenfinanzierung (Dr. F. Blattner/Arbeitsgruppe Experimentelle Taxonomie).

Dr. Anna A. Filatenko, N. I. Vavilov-Institute (VIR), St. Petersburg, Russland, 15.02.2010 bis 10.03.2010, Eigenfinanzierung (Dr. F. Blattner/Arbeitsgruppe Experimentelle Taxonomie).

Prof. Dr. Konrad Bachmann, 01.01.2010 bis 31.05.2011, Eigenfinanzierung (Dr. F. Blattner/Arbeitsgruppe Experimentelle Taxonomie).

Dr. Reinhard Fritsch, 01.01.2010 bis 30.04.2012, Finanzierung durch DFG (Dr. F. Blattner/Arbeitsgruppe Taxonomie pflanzengenetischer Ressourcen).

Abteilung Cytogenetik und Genomanalyse

Emilia Cincu, Humboldt-Universität zu Berlin, Berlin, 31.05.2010 bis 04.06.2010, Eigenfinanzierung (Dr. J. Fuchs/Arbeitsgruppe Karyotypevolution).

Aslihan Temel, Universität Istanbul, Türkei, 04.01.2010 bis 30.09.2010, Finanzierung durch Stipendium der Universität Istanbul (Prof. Dr. I. Schubert/Arbeitsgruppe Karyotypevolution).

Katharina Seeliger, KIT Campus Süd, Institut für Botanik II, Karlsruhe, 11.04.2010 bis 17.04.2010, Eigenfinanzierung (Prof. Dr. I. Schubert/Arbeitsgruppe Karyotypevolution).

Prof. Takashi R. Endo, Universität Kyoto, Japan, 20.11.2010 bis 25.11.2010, Finanzierung durch IPK (Prof. Dr. I. Schubert/ Arbeitsgruppe Karyotypevolution).

Dr. Insa Schröder, Martin-Luther-Universität Halle-Wittenberg, Halle/S., 01.01.2011 bis 30.06.2011, Finanzierung durch Kooperationsvertrag mit der MLU Halle/S. (Prof. Dr. I. Schubert/Arbeitsgruppe Karyotypevolution).

Prof. Dr. Anna Magdalene Wobus, 01.01.2011 bis 31.03.2012, Eigenfinanzierung (Prof. Dr. I. Schubert/Arbeitsgruppe Karyotypevolution).

Tran Duc Trung, Plant Resource Center (PRC), Division of Agricultural Biodiversity, Vietnam Academy of Agricultural Science, Hanoi, Vietnam, 17.09.2011 bis 30.09.2014, Finanzierung durch MOET-Stipendium Vietnam (Prof. Dr. I. Schubert/Arbeitsgruppe Karyotypevolution).

Dr. Thi Ha Giang Vu, Max-Planck-Institut für Pflanzenzüchtungsforschung, Köln, 25.05.2011 bis 03.06.2011 und 30.09.2011 bis 10.10.2012, Eigenfinanzierung (Prof. Dr. I. Schubert/Arbeitsgruppe Karyotypevolution).

Miriam Gonzalez Garcia, Universität Madrid, Spanien, 02.05.2010 bis 02.08.2010, Finanzierung durch Universität Madrid, Ministerio de Educacion, Spanien (Dr. A. Houben/Arbeitsgruppe Chromosomenstruktur und -funktion).

Francesco Agueci, 01.01.2010 bis 30.06.2010, Eigenfinanzierung (Dr. A. Houben/Arbeitsgruppe Chromosomenstruktur und -funktion).

Dr. Elena Evtushenko, Institute of Chemical Biology and Fundamental Medicine, Laboratory of Molecular Genetics, Nowosibirsk, Russland, 01.09.2010 bis 29.11.2010, Finanzierung durch DFG (Dr. A. Houben/Arbeitsgruppe Chromosomenstruktur und -funktion).

Gurmeet Kaur, Jammu Universität, Indien, 17.10.2010 bis 01.12.2010, Finanzierung durch DAAD (Dr. A. Houben/Arbeitsgruppe Chromosomenstruktur und -funktion).

Maria Cuacos, University Madrid, Madrid, Spanien, 01.06.2011 bis 31.08.2011, Finanzierung durch University Madrid, Ministerio de Educacion (Dr. A. Houben/Arbeitsgruppe Chromosomenstruktur und -funktion).

Aretuza Sousa, Ludwig-Maximilians-Universität, München, 28.02.2011 bis 11.03.2011, Finanzierung durch Ludwig-Maximilians-Universität München (Dr. A. Houben/Arbeitsgruppe Chromosomenstruktur und -funktion).

Maryam Sanei, 01.07.2011 bis 01.10.2011, Eigenfinanzierung (Dr. A. Houben/Arbeitsgruppe Chromosomenstruktur und -funktion).

Erwann Caillieux, Institut de Biologie de l' école normale supérieure (IBENS), Paris, Frankreich, 10.10.2011 bis 28.10.2011, Finanzierung durch DAAD (Dr. A. Houben/Arbeitsgruppe Chromosomenstruktur und -funktion).

Takayoshi Ishii, Tottori University, Laboraty of Molecular Breeding Arid Lund Research Center, Tottori, Japan, 17.10.2011 bis 30.10.2011, Eigenfinanzierung (Dr. A. Houben/Arbeitsgruppe Chromosomenstruktur und -funktion).

Johanna Acevedo-Garcia, Max-Planck-Institut für Pflanzenzüchtungsforschung Köln, Department of Plant Microbe Interactions, Köln, 31.07.2011 bis 13.08.2011, Eigenfinanzierung (Dr. A. Houben/Arbeitsgruppe Chromosomenstruktur und -funktion).

Samuel Amiteye, International Max Planck Research School, Asutsuare, Ghana, 01.01.2010 bis 22.02.2012, Finanzierung durch International Max Planck Research School (Dr. T. Sharbel/ Arbeitsgruppe Apomixis).

Thomas Thiel, International Max Planck Research School, Jena, 01.01.2010 bis 31.12.2011, Finanzierung durch International Max Planck Research School/Max-Planck-Institut für Chemische Ökologie, Jena (Dr. T. Sharbel/Arbeitsgruppe Apomixis).

Susanne Scheffknecht, Universität Wien, Abteilung Pharmakognosie, Wien, Österreich, 01.08.2010 bis 14.08.2010, Finanzierung durch FWF (Dr. T. Sharbel/Arbeitsgruppe Apomixis).

Charlotte Scheriau, Heidelberg Institute for Plant Science, Biodiversity and Plant Systematics, Universität Heidelberg, Heidelberg, 28.02.2010 bis 06.03.2010, Finanzierung durch DFG (Dr. T. Sharbel/Arbeitsgruppe Apomixis).

Marcin Piwczynski, Max-Planck-Institut für Chemische Ökologie Jena, Jena, 30.8.2010 bis 27.09.2010, Finanzierung durch Nicolaus Copernicus University, Poland (Dr. T. Sharbel/Arbeitsgruppe Apomixis).

Dr. Diego Hojsgaard, Universität Wien, Department of Systematic and Evolutionary Botany, Wien, Österreich, 17.10.2010 bis 23.10.2010 und 23.03.2011 bis 31.05.2011, Finanzierung durch FWF (Dr. T. Sharbel/Arbeitsgruppe Apomixis).

Dr. Christoph Dobes, Universität Wien, Abteilung Pharmakognosie, Wien, Österreich, 01.08.2010 bis 08.08.2010, Finanzierung durch FWF (Dr. T. Sharbel/Arbeitsgruppe Apomixis).

Ingrid Jordon-Thadeus, Heidelberg Institute for Plant Science, Biodiversity and Plant Systematics, Universität Heidelberg, Heidelberg, 28.02.2010 bis 06.03.2010, Finanzierung durch DFG (Dr. T. Sharbel/Arbeitsgruppe Apomixis).

Dr. Lars-Gernot Otto, 01.01.2010 bis 31.07.2010, 11.08.2010 bis 14.02.2011 und 15.08.2011 bis 31.12.2011, Eigenfinanzierung (Dr. T. Sharbel/Arbeitsgruppe Apomixis).

Giulio Galla, University of Padova, Department of Enviromental Agronomy & Crop Science, Padua, Italien, 08.03.2010 bis 12.04.2010 und 05.08.2011 bis 26.08.2011, Eigenfinanzierung (Dr. T. Sharbel/Arbeitsgruppe Apomixis).

Francisco Valverde, University of Granada, Granada, Spanien, 21.02.2011 bis 18.04.2011, Finanzierung durch University of Granada (Dr. T. Sharbel/Arbeitsgruppe Apomixis).

Javier Morillas, University of Granada, Granada, Spanien, 21.02.2011 bis 18.04.2011, Finanzierung durch University of Granada (Dr. T. Sharbel/Arbeitsgruppe Apomixis).

Ana Sofia Rois, Instituto Superior de Agronomia (ISA), Lissabon, Portugal, 24.01.2011 bis 04.02.2011, Finanzierung durch Instituto Superior de Agronomia (Dr. T. Sharbel/Arbeitsgruppe Apomixis).

Anna Weber, Poznań University of Life Sciences, Poznań, Polen, 14.08.2011 bis 10.09.2011, Finanzierung durch EU COST Action (Dr. T. Sharbel/Arbeitsgruppe Apomixis).

Lúbos Majeský, University of Olomouc, Olomouc, Tschechische Republik, 12.09.2011 bis 12.12.2011, Finanzierung durch University of Olomouc (Dr. T. Sharbel/Arbeitsgruppe Apomixis).

John Thomsen Lovell, Colorado State University, Fort Collins, USA, 25.09.2011 bis 05.12.2011, Finanzierung durch DFG-Stipendium (Dr. T. Sharbel/Arbeitsgruppe Apomixis).

Jana Koperdakova, Pavol Jozef Šafárik University, Institute of Biology and Ecology, Košice, Slovakische Republik, 01.09.2011 bis 19.09.2011, Finanzierung durch EU COST Action (Dr. T. Sharbel/Arbeitsgruppe Apomixis).

E. Eradasappa, Central Potato Research Station, Sahaynagar, Indien, 14.10.2011 bis 11.01.2012, Finanzierung durch ein Stipendium der World Bank (Dr. T. Sharbel/Arbeitsgruppe Apomixis).

K. A. Geetha, Directorate of Medicinal and Aromatic Plants Research, Boriavi, Indien, 02.05.2011 bis 31.07.2011, Finanzierung durch Stipendium der World Bank (Dr. T. Sharbel/Arbeitsgruppe Apomixis).

Dr. Marta Puente Molins, 15.06.2011 bis 15.03.2012, Eigenfinanzierung (Dr. T. Sharbel/Arbeitsgruppe Apomixis).

Dr. Insa Schröder, Martin-Luther-Universität Halle-Wittenberg, Halle/S., 01.01.2010 bis 31.12.2010, Finanzierung durch Kooperationsvertrag mit der MLU Halle (Prof. Dr. A.M. Wobus/Arbeitsgruppe *In vitro*-Differenzierung).

Anna Daniel-Wojcik, 01.03.2010 bis 31.08.2010, Eigenfinanzierung (Prof. Dr. A.M. Wobus/Arbeitsgruppe *In vitro*-Differenzierung).

Dung Phuong Le, Martin-Luther-Universität Halle-Wittenberg, Halle/S., 24.09.2011 bis 30.09.2015, Finanzierung durch MOET/DAAD-Stipendium (Dr. R. Schmidt/Arbeitsgruppe Genomplastizität).

Astrid Bruchmüller, 01.04.2010 bis 30.09.2010, Eigenfinanzierung (Dr. M. Mette/Arbeitsgruppe Epigenetik).

Alexandra Plochotnikova, University of Vilnius, Institute of Biotechnology, Vilnius, Litauen, 06.06.2011 bis 18.06.2011, Eigenfinanzierung und Finanzierung durch IPK (Dr. M. Mette/Arbeitsgruppe Epigenetik).

Simona Jachimoviciute, University of Vilnius, Institute of Biotechnology, Vilnius, Litauen, 06.06.2011 bis 18.06.2011, Eigenfinanzierung und Finanzierung durch IPK (Dr. M. Mette/Arbeitsgruppe Epigenetik).

Dr.-Ing. Alexander Ihlow, Technische Hochschule Ilmenau, Ilmenau, 01.01.2010 bis 30.11.2011, Finanzierung durch TH Ilmenau (Dr. P. Schweizer/Arbeitsgruppe Transkriptomanalyse).

Stephan Marzin, 01.01.2010 bis 31.01.2010, Eigenfinanzierung (Dr. P. Schweizer/Arbeitsgruppe Transkriptomanalyse).

Luo Liu, 01.01.2010 bis 30.06.2010, Eigenfinanzierung (Dr. P. Schweizer/Arbeitsgruppe Transkriptomanalyse).

Ernst Metzner, Martin-Luther-Universität Halle-Wittenberg, Halle/S., 01.01.2010 bis 31.07.2010, Eigenfinanzierung (Dr. P. Schweizer/Arbeitsgruppe Transkriptomanalyse).

Dr. Clara Pliego Prieto, Imperial College London, Großbritannien, 20.09.2010 bis 20.10.2010, Eigenfinanzierung (Dr. P. Schweizer/Arbeitsgruppe Transkriptomanalyse).

Gerald Siegwart, Universität für Bodenkultur, Wien, Österreich, 20.09.2010 bis 16.10.2010, Eigenfinanzierung (Dr. P. Schweizer/Arbeitsgruppe Transkriptomanalyse).

Tobias Baum, Fraunhofer-Institut für Fabrikbetrieb und -automatisierung, Magdeburg, 09.03.2011 bis 30.06.2011, Finanzierung durch BMBF (Dr. P. Schweizer/Arbeitsgruppe Transkriptomanalyse).

Jemanesh Kifetew Haile, Ethiopian Institute of Agricultural Research, Addis Abeba, Äthiopien, 01.01.2010 bis 30.04.2012, Finanzierung durch DAAD-Stipendium (Dr. M. Röder/Arbeitsgruppe Gen- und Genomkartierung).

Rajneesh Paliwal, Banaras Hindu University, Varanasi, Indien, 01.01.2010 bis 30.06.2010, Finanzierung durch DAAD-Stipendium (Dr. M. Röder/Arbeitsgruppe Gen- und Genomkartierung).

Dr. Jose Luis Diaz De Léon, Universidad de Baja California, La Paz, Mexiko, 28.07.2010 bis 29.09.2010, Finanzierung durch CONACYT-BMBF; 04.09.2011 bis 04.10.2011, Finanzierung durch BMBF; 05.10.2011 bis 13.10.2011, Eigenfinanzierung (Dr. M. Röder/Arbeitsgruppe Gen- und Genomkartierung).

Aiman Absattarova, Kazakh Scientific Production Center of Farming and Plant Growth, Almalybak, Kasachstan, 11.01.2010 bis 19.03.2010, Finanzierung durch IAOE-Stipendium (Dr. M. Röder/Arbeitsgruppe Gen- und Genomkartierung).

Dr. Elena Salina, Institute of Cytology and Genetics, Nowosibirsk, Russland, 04.10.2010 bis 23.10.2010, Finanzierung durch BLE-Projekt (Dr. M. Röder/Arbeitsgruppe Gen- und Genomkartierung).

Dr. Thelma Castellanos, Universidad de Baja California, La Paz, Mexiko, 28.07.2010 bis 29.09.2010, Finanzierung durch CONACYT-BMBF (Dr. M. Röder/Arbeitsgruppe Gen- und Genomkartierung).

Dr. Irina Leonova, Institute of Cytology and Genetics, Nowosibirsk, Russland, 10.10.2010 bis 09.12.2010, Finanzierung durch DFG (Dr. M. Röder/Arbeitsgruppe Gen- und Genomkartierung).

Merit Mora, Universidad de Baja California, La Paz, Mexiko, 03.08.2010 bis 29.09.2010, Finanzierung durch CONACYT-BMBF (Dr. M. Röder/Arbeitsgruppe Gen- und Genomkartierung).

Mehmoona Ilyas, University of Arid Agriculture, Shamsabad, Pakistan, 18.08.2011 bis 17.02.2012, Finanzierung durch Research Fellowship of Higher Education Commission (Dr. M. Röder/Arbeitsgruppe Gen- und Genomkartierung).

Dr. Uttam Kumar, Plant Tissue Culture & Molecular Biology (TERI), New Delhi, Indien, 01.06.2011 bis 22.08.2012, Finanzierung durch BMBF (Dr. M. Röder/Arbeitsgruppe Gen- und Genomkartierung).

Dr. Malgorzata Czernicka, University of Agriculture Krakow, Department of Genetics, Plant Breeding and Seed Science, Krakow, Polen, 28.02.2010 bis 31.12.2011, Finanzierung durch DAAD-Stipendium (Dr. U. Scholz, M. Lange/Arbeitsgruppe Bioinformatik und Informationstechnologie).

Dr. Urte Schlüter, Friedrich-Alexander-Universität Erlangen-Nürnberg, Erlangen, 06.06.2011 bis 10.06.2011, Eigenfinanzierung (Dr. U. Scholz/Arbeitsgruppe Bioinformatik und Informationstechnologie).

Maria Munoz Amatriain, University of Minnesota, Department of Agronomy and Plant Genetics, Minnesota, USA, 06.06.2011 bis 17.07.2011, Finanzierung durch University of Minnesota (Dr. U. Scholz/Arbeitsgruppe Bioinformatik und Dr. N. Stein/ Arbeitsgruppe Genomdiversität).

Abteilung Molekulare Genetik

Mehrana Koohi, Shahrekord University, Department of Plant Breeding, College of Agriculture, Shahrekord, Iran, 10.01.2010 bis 31.08.2010 und 01.12.2010 bis 30.09.2011, Finanzierung durch Iranian Ministry of Science, Research and Technology (Prof. Dr. T. Altmann, Dr. R. Meyer/Arbeitsgruppe Heterosis).

Hea-Jung Jeon, Kyung Hee University, Department of Horticultural Biotechnology, College of Life Science, Youngin-si, Republik Korea, 27.09.2010 bis 26.09.2013, Finanzierung durch Stipendium der koreanischen Regierung (Prof. Dr. T. Altmann/ Arbeitsgruppe Heterosis).

Dr. Michaela Ernst, Forschungszentrum Jülich, 01.09.2010 bis 31.03.2011 und 25.11.2011 bis 31.05.2012, Eigenfinanzierung (Prof. Dr. T. Altmann/Arbeitsgruppe Heterosis).

Dr. Marc Strickert, Universität Siegen, Fakultät Medieninformatik, 01.02.2010 bis 31.10.2010, Eigenfinanzierung (Dr. W. Weschke/Arbeitsgruppe Samenentwicklung).

Dr. Christiane Seiler, 01.07.2010 bis 31.10.2010, Eigenfinanzierung (Dr. W. Weschke, Dr. N. Sreenivasulu/Arbeitsgruppe Samenentwicklung).

Dr. Manoj Prasad, National Institute of Plant Genome Research, Aruna Asaf Ali Marg, New Delhi, Indien, 12.02.2010 bis 28.02.2010 und 18.11.2010 bis 27.11.2010, Finanzierung durch DLR (Dr. N. Sreenivasulu/Arbeitsgruppe Samenentwicklung).

Nicole Staroske, 01.04.2011 bis 30.04.2011 und 01.08.2011 bis 31.12.2011, Eigenfinanzierung (Dr. W. Weschke/Arbeitsgruppe Samenentwicklung).

Van Tran Thi Thuy, Agricultural Science Institute of Northern Central Vietnam, Vinh City, Vietnam, 21.08.2011 bis 31.08.2014, Finanzierung durch Ministry of Education and Training (Dr. W. Weschke/Arbeitsgruppe Samenentwicklung).

Maria Isabel Mora Ramirez, Universidad de Costa Rica, San José, Costa Rica, 01.10.2011 bis 30.09.2015, Finanzierung durch DAAD-Stipendium (Dr. W. Weschke/Arbeitsgruppe Samenentwicklung).

Dr. Yaroslav Pirko, National Academy of Science, Institute of Food Biotechnology and Genomics, Department of Genomics and Molecular Biotechnology, Kiew, Ukraine, 03.07.2011 bis 30.09.2012, Finanzierung durch DFG (Dr. W. Weschke/Arbeitsgruppe Samenentwicklung).

Maria Mildner, 01.10.2010 bis 31.10.2010, Eigenfinanzierung (Dr. H. Bäumlein/Arbeitsgruppe Genregulation).

Dr. Amal Joseph Johnston, Eidgenössische Technische Hochschule Zürich, Abteilung Biologie, Zürich, Schweiz, 01.09.2010 bis 31.08.2012, Finanzierung durch Stipendium der A. von Humboldt-Stiftung (Dr. H. Bäumlein/Arbeitsgruppe Genregulation).

Diep Le Hong, Vietnamese Academy of Science and Technology, Institute of Biotechnology, Hanoi, Vietnam, 01.01.2010 bis 31.03.2010 und 01.10.2010 bis 14.03.2011, Finanzierung durch Ministry of Education & Training/Vietnam (Dr. H. Bäumlein/Arbeitsgruppe Genregulation).

Anna Schallau, 11.08.2010 bis 28.02.2011, Eigenfinanzierung und Finanzierung durch IPK (Dr. H. Bäumlein/Arbeitsgruppe Genregulation).

Petra Sarahnova, Palacky University, Department of Botany, Tschechische Republik, 28.10.2010 bis 07.02.2011 und 04.10.2011 bis 31.03.2012, Finanzierung durch DAAD-Stipendium (Dr. H. Bäumlein/Arbeitsgruppe Genregulation).

Isabella Herrmann, Martin-Luther-Universität Halle-Wittenberg, Halle/S., 01.01.2010 bis 30.06.2010, Eigenfinanzierung (Dr. U. Conrad/Arbeitsgruppe Phytoantikörper).

Phan Trong Hoang, University of Science, Institute of Biotechnology, Hanoi, Vietnam, 01.01.2010 bis 29.02.2012, Finanzierung durch Stipendium vom Ministry of Education and Training, Vietnam (Dr. U. Conrad/Arbeitsgruppe Phytoantikörper).

Dr. Nguyen Huu Cuong, Institute of Biotechnology, Hanoi, Vietnam, 08.08.2010 bis 04.10.2010, Finanzierung durch DAAD (Dr. U. Conrad/Arbeitsgruppe Phytoantikörper).

Alejandro Sarriòn Perdigones, Instituto des Biologia Molecular y Celular de Plantas, Valencia, Spanien, 17.09.2011 bis 19.11.2011, Finanzierung durch Ministerium für Wissenschaft und Innovation, Spanien (Dr. U. Conrad/Arbeitsgruppe Phytoantikörper).

Dr. Urs Hähnel, Julius Kühn-Institut, Quedlinburg, 01.01.2010 bis 16.05.2010, Finanzierung durch Julius Kühn-Institut (Dr. L. Altschmied/Arbeitsgruppe Expressionskartierung).

Prof. Ali Masoudi-Nejad, Universität Teheran, Teheran, Iran, 01.08.2010 bis 10.09.2010, Finanzierung durch DAAD-Stipendium (Prof. Dr. F. Schreiber/Arbeitsgruppe Pflanzenbioinformatik).

Dr. Michael Wybrow, Monash University, Melbourne, Australien, 19.08.2010 bis 27.08.2010, Finanzierung durch Monash Universitiy (Prof. Dr. F. Schreiber/Arbeitsgruppe Pflanzenbioinformatik).

Yasdan Asgari, University of Tehran, Institute of Biochemistry and Biophysics, Tehran, Iran, 22.06.2011 bis 21.08.2011, Finanzierung durch University of Tehran (Prof. Dr. F. Schreiber/Arbeitsgruppe Pflanzenbioinformatik).

Dr. Kambiz Baghalian, University of Agriculture Tokyo, Tokyo, Japan, 03.04.2011 bis 30.11.2011, Eigenfinanzierung (Prof. Dr. F. Schreiber/Arbeitsgruppe Pflanzenbioinformatik).

Dr. Christiane Seiler, 01.11.2010 bis 30.04.2011, Eigenfinanzierung (Dr. N. Sreenivasulu/Arbeitsgruppe Stress-Genomik).

Dr. Marc Strickert, Universität Siegen, Fakultät Medieninformatik, 01.11.2010 bis 30.09.2012, Eigenfinanzierung (Dr. N. Sreenivasulu/Arbeitsgruppe Stress-Genomik).

Dr. Sudhakar Reddy Palakolanu, 06.11.2011 bis 05.11.2012, Finanzierung durch Leibniz-DAAD-Stipendium (Dr. N. Sreenivasulu/Arbeitsgruppe Stress-Genomik).

Abteilung Physiologie und Zellbiologie

Nunun Barunawati, Brawijaya University, Malang, Indonesien, 01.01.2010 bis 30.06.2012, Finanzierung durch indonesische Regierung (Prof. Dr. N. von Wirén/Arbeitsgruppe Molekulare Pflanzenernährung).

Dmitriy Fedoseyenko, Universität Hohenheim, Stuttgart-Hohenheim, 01.01.2010 bis 31.12.2010 und 01.07.2011 bis 31.07.2011, Eigenfinanzierung (Prof. Dr. N. von Wirén/Arbeitsgruppe Molekulare Pflanzenernährung).

Mariela Monteoliva, University of Córdoba, Department of Biological Chemistry, Córdoba, Argentinien, 14.11.2010 bis 20.12.2010, Finanzierung durch BMBF (Prof. Dr. N. von Wirén/Arbeitsgruppe Molekulare Pflanzenernährung).

Amirhossein Ahkami, Universität Hohenheim, Stuttgart-Hohenheim, 01.04.2010 bis 30.09.2010, Finanzierung über Universität Hohenheim (Prof. Dr. N. von Wirén/Arbeitsgruppe Molekulare Pflanzenernährung).

Ricardo Fabiano Hettwer Giehl, Universität Hohenheim, Stuttgart-Hohenheim, 03.05.2010 bis 31.03.2011, Finanzierung durch Brasilianisches Bildungsministerium - CAPES (Prof. Dr. N. von Wirén/Arbeitsgruppe Molekulare Pflanzenernährung).

Zeynep Isik, Universität Hohenheim, Stuttgart-Hohenheim, 18.03.2010 bis 26.03.2010, Finanzierung durch Stipendium der Universität Hohenheim (Prof. Dr. N. von Wirén/Arbeitsgruppe Molekulare Pflanzenernährung).

Fengying Duan, China Agricultural University, Beijing, China, 01.11.2010 bis 31.10.2012, Finanzierung durch chinesische Regierung (Prof. Dr. N. von Wirén/Arbeitsgruppe Molekulare Pflanzenernährung).

Baris Boylu, Middle East Technical University, Ankara, Türkei, 26.08.2011 bis 31.08.2011, Eigenfinanzierung (Prof. Dr. N. von Wirén/Arbeitsgruppe Molekulare Pflanzenernährung).

Michiko Takahashi, Utsunomiya University, Utsunomiya, Japan, 22.04.2011 bis 21.09.2011, Eigenfinanzierung (Prof. Dr. N. von Wirén/Arbeitsgruppe Molekulare Pflanzenernährung).

Prof. Lixing Yuan, Chinese Agricultural University, Beijing, China, 12.08.2011 bis 02.09.2011, Finanzierung durch Robert-Bosch-Foundation (Prof. Dr. N. von Wirén/Arbeitsgruppe Molekulare Pflanzenernährung).

Susanne Schmidt, University of Queensland, School of Agriculture & Food Science, Queensland, Australien, 14.05.2011 bis 30.06.2011, Finanzierung durch Humboldt-Stipendium (Prof. Dr. N. von Wirén/Arbeitsgruppe Molekulare Pflanzenernährung).

Majid Ghorbani Javid, Tarbiar Modares University, Department of Agronomy, Agriculture Faculty, Teheran, Iran, 11.03.2010 bis 10.09.2010, Finanzierung durch Ministry of Science, Research and Technology in Teheran (Dr. M. Hajirezaei/Arbeitsgruppe Molekulare Pflanzenernährung).

Dr. Mathias Zurbriggen, Universidad de Rosario, Rosario, Argentinien, 21.06.2010 bis 30.06.2010 und 29.08.2010 bis 23.09.2010, Finanzierung durch DFG (Dr. M. Hajirezaei/Arbeitsgruppe Molekulare Pflanzenernährung).

Dr. Nestor Carillo, Universidad de Rosario, Rosario, Argentinien, 09.09.2010 bis 23.09.2010, Finanzierung durch DFG; 12.05.2011 bis 17.05.2011, Finanzierung durch IPK (Dr. M. Hajirezaei/Arbeitsgruppe Molekulare Pflanzenernährung).

Maria Alvarez, Universidad Nacional de Córdoba, Córdoba, Argentinien, 11.09.2010 bis 21.09.2010, Finanzierung durch MINCYT - BMBF (Dr. M. Hajirezaei/Arbeitsgruppe Molekulare Pflanzenernährung).

Young-Min Kim, 01.02.2011 bis 31.01.2012, Eigenfinanzierung (Dr. M. Hajirezaei/Arbeitsgruppe Molekulare Pflanzenernährung).

Medhi Ghaboli, Agricultural Biotechnology Research Institute of Iran (ABRII), Karaj, Iran, 05.08.2011 bis 04.04.2012, Finanzierung durch Ministry of Science and Technology of Iran (Dr. M. Hajirezaei/Arbeitsgruppe Molekulare Pflanzenernährung).

Dr. Vanesa Tognetti, Ghent University, VIB Department of Plant Systems Biology, Gent, Belgien, 12.05.2011 bis 17.05.2011, Finanzierung durch IPK (Dr. M. Hajirezaei/Arbeitsgruppe Molekulare Pflanzenernährung).

Yanelis Karina Capdesuner Ruiz, Institute Centro de Bioplantas, Ciego de Avila, Cuba, 01.01.2010 bis 29.08.2010 und 16.06.2011 bis 10.12.2011, Finanzierung durch DAAD-Stipendium (Dr. H.-P. Mock/Arbeitsgruppe Angewandte Biochemie).

Jan Fila, Institute of Experimental Botany, Prag, Tschechische Republik, 02.03.2010 bis 28.03.2010, Finanzierung durch EU-COST; 14.11.2010 bis 27.11.2010, Eigenfinanzierung; 31.07.2011 bis 18.09.2011, Finanzierung durch DAAD (Dr. H.-P. Mock/Arbeitsgruppe Angewandte Biochemie).

Mohsen Janmohammadi, University of Tehran, Department of Agronomy and Plant Breeding, Teheran, Iran, 01.01.2010 bis 22.04.2010, Finanzierung durch Forschungsstipendium der Republik Iran (Dr. H.-P. Mock/Arbeitsgruppe Angewandte Biochemie).

Manuela Eick, Institut für Botanik und Landschaftsökologie EMAU, Greifswald, 18.07.2010 bis 30.07.2010, Eigenfinanzierung (Dr. A. Matros/Arbeitsgruppe Angewandte Biochemie).

Giuseppe Lattanzio, Estación Experimental de Aula Dei, Dpto. Nutrición Vegetal, Italien, 01.08.2010 bis 22.11.2010, Eigenfinanzierung (Dr. H.-P. Mock/Arbeitsgruppe Angewandte Biochemie).

Dr. Katja Witzel, Universität Kiel, Fakultät für Agrar- und Ernährungswissenschaften, 08.11.2010 bis 26.11.2010; 16.05.2011 bis 20.05.2011 und 01.11.2011 bis 08.11.2011, Eigenfinanzierung (Dr. H.-P. Mock/Arbeitsgruppe Angewandte Biochemie).

Dr. Elisabetta Mazzucotelli, Genomic Research Centre, Fiorenzuola d´Arda, Italien, 18.04.2010 bis 28.05.2010, Finanzierung durch EU COST Action (Dr. H.-P. Mock/Arbeitsgruppe Angewandte Biochemie).

José Àngel Huerta Ocampo, Potosi Institute of Scientific Research and Technology, San Luis Potosi, Mexico, 04.04.2011 bis 30.11.2011, Eigenfinanzierung (Dr. H.-P. Mock/Arbeitsgruppe Angewandte Biochemie).

Amenehsadat Hashemi, Agricultural Biotechnology Research Institute of Iran (ABRII), Department of Physiology and Proteomics, Karaj, Iran, 19.06.2011 bis 18.12.2011, Finanzierung durch Ministry of Science, Research and Technology in Teheran (Dr. H.-P. Mock/Arbeitsgruppe Angewandte Biochemie).

Sunita Yadav, University of Delhi, Department of Botany, New Delhi, Indien, 01.09.2011 bis 30.11.2011, Finanzierung durch DAAD-Fellowship (Dr. H.-P. Mock/Arbeitsgruppe Angewandte Biochemie).

Marek Marzec, University of Silesia, Katowice, Polen, 01.01.2010 bis 29.03.2010, Finanzierung durch UPGOW-Europäische Union; 01.04.2011 bis 21.04.2011, 02.06.2011 bis 28.06.2011 und 29.09.2011 bis 20.10.2011, Finanzierung durch DAAD (Dr. M. Melzer/Arbeitsgruppe Strukturelle Zellbiologie).

Dr. Ahmed Eisa Mahmoud Ghoniem, University of Cairo, Botany Department, Agriculture Faculty, Kairo, Ägypten, 10.10.2010 bis 09.11.2010, Finanzierung durch Universität Kairo (Dr. M. Melzer/Arbeitsgruppe Strukturelle Zellbiologie).

Pooja Pandey, Integral University of Lucknow, Indien, 24.09.2011 bis 30.09.2011, Finanzierung durch DAAD-Siemens-Stipendium (Dr. M. Melzer/Arbeitsgruppe Strukturelle Zellbiologie).

Prof. Louise Andersen, University of Illinois, Department of Biological Sciences, Chicago, USA, 28.04.2011 bis 17.05.2011, Eigenfinanzierung (Dr. M. Melzer/Arbeitsgruppe Strukturelle Zellbiologie).

Stefanie Goedeke 01.04.2010 bis 31.12.2010, Eigenfinanzierung (Dr. J. Kumlehn/Arbeitsgruppe Pflanzliche Reproduktionsbiologie).

Malik Zahid Abbas, Wheat Biotechnology Laboratory, Plant Transformation Group Agricultural Biotechnology Division, NIBGE, Faisalabad, Pakistan, 17.06.2010 bis 16.12.2010, Finanzierung über Stipendium der Higher Education Commision (Dr. J. Kumlehn/Arbeitsgruppe Pflanzliche Reproduktionsbiologie).

Katarzyna Plasun, 01.01.2011 bis 31.03.2012, Eigenfinanzierung (Dr. J. Kumlehn/Arbeitsgruppe Pflanzliche Reproduktionsbiologie).

Inés Cambra, University of Madrid, Madrid, Spanien, 11.04.2011 bis 14.07.2011, Finanzierung durch University of Madrid; 15.08.2011 bis 14.09.2011, Finanzierung durch IPK (Dr. J. Kumlehn/Arbeitsgruppe Pflanzliche Reproduktionsbiologie).

Katarzyna Szyrajew, University of Silesia, Katowice, Polen, 19.09.2011 bis 18.12.2011, Finanzierung durch ERASMUS-Stipendium (Dr. J. Kumlehn/Arbeitsgruppe Pflanzliche Reproduktionsbiologie).

Monika Gajecka, University of Silesia, Department of Genetics, Katowice, Polen, 06.06.2011 bis 05.09.2011, Finanzierung durch ERASMUS-Stipendium (Dr. J. Kumlehn/Arbeitsgruppe Pflanzliche Reproduktionsbiologie).

Stefan Hiekel, Friedrich-Schiller-Universität, Jena, 10.10.2011 bis 30.11.2011, Finanzierung durch IPK (Dr. J. Kumlehn/Arbeitsgruppe Pflanzliche Reproduktionsbiologie).

Dr. Federica Bini, 01.09.2011 bis 28.02.2012, Eigenfinanzierung (Dr. J. Kumlehn/Arbeitsgruppe Pflanzliche Reproduktionsbiologie).

Dr. Francesca Tedeschi, University of Tuscia, Viterbo, Italien, 01.10.2010 bis 30.09.2011, Finanzierung durch University of Tuscia (Dr. J. Kumlehn/Arbeitsgruppe Pflanzliche Reproduktionsbiologie).

Dr. Mohammad Pourkheirandish, National Institute of Agrobiological Sciences (NIAS), Tsukuba, Japan, 03.01.2011 bis 08.01.2011, Finanzierung durch NIAS (Dr. J. Kumlehn/Arbeitsgruppe Pflanzliche Reproduktionsbiologie).

Dr. Prasanthi Perera, International Center for Tropical Agriculture (CIAT), Cali, Colombia, 23.09.2011 bis 23.10.2011, Finanzierung durch CIAT (Dr. J. Kumlehn/Arbeitsgruppe Pflanzliche Reproduktionsbiologie).

Miguel Alvaro Benito, Universidad Autonoma de Madrid, Centro de Biología Molecular „Severo Ochoa", Madrid, Spanien, 23.08.2010 bis 26.11.2010, Finanzierung durch CBMSO/Universidad Autonoma de Madrid (Prof. Dr. G. Kunze/Arbeitsgruppe Hefegenetik).

Thi Minh Ha Pham, Institute of Biotechnology, Vietnam Academy of Science and Technology, Hanoi, Vietnam, 01.01.2010 bis 31.07.2011, Finanzierung durch MOET-Stipendium Vietnam (Prof. Dr. G. Kunze/Arbeitsgruppe Hefegenetik).

Kinga Sedzielewska, AMykor GmbH, 01.01.2010 bis 14.09.2010, Finanzierung durch Kooperationsvertrag mit AMykor GmbH (Prof. Dr. G. Kunze/Arbeitsgruppe Hefegenetik).

Tabias Samuel Lemanski, Wrocław University of Technology, Wrocław, Polen, 08.02.2010 bis 07.05.2010, Finanzierung durch ComEAST (Prof. Dr. G. Kunze/Arbeitsgruppe Hefegenetik).

Mauricio Toro Nahuelpan, University of La Serena, La Serena, Chile, 19.08.2010 bis 03.03.2011, Finanzierung durch Stipendium der Bayer-Stiftung (Prof. Dr. G. Kunze/Arbeitsgruppe Hefegenetik).

Ravi Kumar Yelchuri, Institute of Microbial Technology, Council of Scientific and Industrial Research Sector, Indien, 16.11.2010 bis 10.12.2010, Finanzierung durch BMBF (Prof. Dr. G. Kunze/Arbeitsgruppe Hefegenetik).

Dr. Burla Sashidar, The Energy and Resources Institute (TERI), New Delhi, Indien, 08.04.2010 bis 28.06.2010, Finanzierung durch DLR (Prof. Dr. G. Kunze/Arbeitsgruppe Hefegenetik).

Prof. Keith Baronian, University of Canterbury, School of Biological Sciences, Christchurch, Neuseeland, 17.06.2010 bis 28.06.2010, Eigenfinanzierung (Prof. Dr. G. Kunze/Arbeitsgruppe Hefegenetik).

Dr. Viviana Ordenes, CEAZA Campus Andreas Bello, Chile, 11.10.2010 bis 25.10.2010, Eigenfinanzierung (Prof. Dr. G. Kunze/Arbeitsgruppe Hefegenetik).

Sabine Nutz, Julius Kühn-Institut, Quedlinburg, 01.02.2011 bis 04.03.2011, Finanzierung durch IPK (Prof. Dr. G. Kunze/Arbeitsgruppe Hefegenetik).

Arbeitsaufenthalte von IPK-Wissenschaftlern in anderen Einrichtungen/ Stays of IPK Researchers at Other Institutions

Abteilung Genbank

Tina Seidensticker/Arbeitsgruppe Pflanzliche Baupläne, Università degli Studi di Milano, Lodi, Italien, 21.06.2010 bis 10.07.2010, Finanzierung durch BMBF.

Piotr Gawroński/Arbeitsgruppe Pflanzliche Baupläne, University of Liverpool, Liverpool, UK, 31.03.2011 bis 16.04.2011, Finanzierung durch IPK.

Manuela Nagel/Arbeitsgruppe Ressourcengenetik und Reproduktion, Seed Conservation Department, Millennium Seed Bank, Kew Gardens, Großbritannien, 13.03.2010 bis 08.05.2010 und 08.11.2010 bis 24.11.2010, Finanzierung durch IPK und Millennium Seed Bank.

Dr. Frank Blattner/Arbeitsgruppe Experimentelle Taxonomie, Department of Botany, Mongolian National University, Ulaan Baator, Mongolei, 03.08.2010 bis 01.09.2010, Finanzierung durch DFG.

Dr. Frank Blattner und **Dr. Sabine Jakob**/Arbeitsgruppe Experimentelle Taxonomie, Feldarbeit, Südost-Argentinien, 15.01.2011 bis 17.02.2011, Finanzierung durch DFG.

Dr. Frank Blattner/Arbeitsgruppe Experimentelle Taxonomie, Feldarbeit, Kalifornien, USA, 01.06.2011 bis 16.06.2011, Finanzierung durch DFG.

Dr. Reinhard Fritsch/Arbeitsgruppe Taxonomie pflanzengenetischer Ressourcen, Iranian Research Institute of Plant Protection, Teheran, Iran, 24.04.2010 bis 15.05.2010, Finanzierung durch DFG.

Dr. Klaus Pistrick/Arbeitsgruppe Taxonomie pflanzengenetischer Ressourcen, Institut für Botanik und Botanischer Garten, Tbilisi, Georgien, 20.07.2010 bis 04.08.2010, Finanzierung durch IPK.

Nikolai Matthias Nürk/Arbeitsgruppe Experimentelle Taxonomie, University Idaho, Stillinger Herbarium, Idaho, USA, 05.11.2010 bis 28.11.2010, Finanzierung durch DFG.

Dr. Sabine Jakob/Arbeitsgruppe Experimentelle Taxonomie, Dushanbe, Tadschikistan, 18.06.2010 bis 10.07.2010, Finanzierung durch DFG.

Abteilung Cytogenetik und Genomanalyse

Dr. Gabriele Jovtchev/Arbeitsgruppe Karyotypevolution, Institute of Biophysics, Department of Plant Developmental Genetics, Brno, Tschechische Republik, 26.07.2010 bis 30.07.2010, Finanzierung durch Projekt des Landes Sachsen-Anhalt.

Dr. Andreas Houben/Arbeitsgruppe Chromosomenstruktur und -funktion, Chinese Academy of Sciences, Institute of Genetics, Peking, China, 06.11.2011 bis 20.11.2011, Finanzierung durch Chinese Academy of Sciences.

Stefan Heckmann/Arbeitsgruppe Chromosomenstruktur und -funktion, Jammu University, Jammu, Indien, 12.03.2011 bis 24.03.2011, Finanzierung durch DAAD.

Jeyaraman Rajaraman/Arbeitsgruppe Transkriptomanalyse, Technische Universität München, München, 25.04.2010 bis 08.05.2010, Finanzierung durch IPK.

Jemanesh Kifetew Haile/Arbeitsgruppe Gen- und Genomkartierung, Institute for Maize and Wheat Improvement Centre, CIMMYT, Mexiko, 05.03.2011 bis 29.03.2011, Finanzierung durch „Jeanie Borlaug Women in Triticum Award 2010".

Abteilung Molekulare Genetik

Gerd Melkus/Arbeitsgruppe Heterosis, University Park, Park, USA, 12.04.2010 bis 01.05.2010, Finanzierung durch BMBF (GABI-SysSEED).

Dr. Ljoudmilla Borisjuk/Arbeitsgruppe Heterosis, Penn State University, Pennsylvania, USA, 20.12.2010 bis 09.01.2011 und 31.05.2011 bis 20.06.2011, Finanzierung durch Industrieprojekt.

Olga Kirioukhova/Arbeitsgruppe Genregulation, National Institute for Basic Biology, Obazaki, Japan, 19.11.2010 bis 01.01.2011, Finanzierung durch Humboldt-Stipendium.

Valeska Hauptmann/Arbeitsgruppe Phytoantikörper, INRA, Nantes, Frankreich, 15.03.2010 bis 30.04.2010, Finanzierung durch COST Action der Europäischen Union.

Prof. Dr. Falk Schreiber/Arbeitsgruppe Pflanzenbioinformatik, University of Sydney; ACPFG Adelaide und University of South Australia; University of Newcastle; Monash University Melbourne und DSTO Melbourne; NICTA Sydney; University Western Australia Perth; CSIRO Canberra, Australien, 11.01.2010 bis 15.02.2010, teilweise Finanzierung durch University of South Australia und University Western Australia Perth.

Prof. Dr. Falk Schreiber/Arbeitsgruppe Pflanzenbioinformatik, University of Newcastle; CSIRO Canberra; University of Sydney und NICTA Sydney; Monash University Melbourne; University Western Australia Perth, Australien, 21.11.2010 bis 13.12.2010, teilweise Finanzierung durch CSIRO Canberra und University Western Australia Perth.

Dr. Christian Klukas/Arbeitsgruppe Bildanalyse, Zhejiang University, Department of Bioinformatics, College of Life Sciences, Hangzhou, China, 22.07.2010 bis 04.08.2010 und 17.07.2011 bis 29.07.2011, Finanzierung durch Research Fund for International Young Scientists, NSFC of China.

Dr. Nese Sreenivasulu/Arbeitsgruppe Stress-Genomik, National Institute of Plant Genome Research, New Delhi; University of Agricultural Sciences, Department of Crop Physiology, Bangalore, Indien, 30.11.2010 bis 31.01.2011, Finanzierung durch BMBF.

Abteilung Physiologie und Zellbiologie

Dr. Mohammad-Reza Hajirezaei/Arbeitsgruppe Molekulare Pflanzenernährung, Institute of Molecular and Cell Biology, Department of Physiology and Cell Biology, Rosario, Argentinien, 21.02.2010 bis 25.02.2010, Finanzierung durch DLR und MINCYT/BMBF.

Dr. Michael Melzer/Arbeitsgruppe Strukturelle Zellbiologie, Molecular Biology and Agriculture Division, Bhaba Atomic Research Center, Mumbai, Indien, 04.03.2010 bis 11.04.2010, Finanzierung durch DLR/BMBF.

Dr. Michael Melzer/Arbeitsgruppe Strukturelle Zellbiologie, Department of Genetics, Faculty of Biology and Environment Protection, University of Silesia, Katowice, Polen, 17.05.2011 bis 22.05.2011, Finanzierung durch DAAD.

Dr. Twan Rutten/Arbeitsgruppe Strukturelle Zellbiologie, Department of Genetics, Faculty of Biology and Environment Protection, University of Silesia, Katowice, Polen, 28.11.2011 bis 02.12.2011, Finanzierung durch DAAD.

Prof. Dr. Gotthard Kunze/Arbeitsgruppe Hefegenetik, University of Canterbury, School of Biological Sciences, Canterbury, Neuseeland, 18.11.2010 bis 25.11.2010, Finanzierung durch Industrieprojekt mit Neuseeland.

Dagmara Jankowska/Arbeitsgruppe Hefegenetik, Institute of Microbial Technology, Chandigarh, Indien, 13.12.2010 bis 17.12.2010, Finanzierung durch DAAD.

Anke Trautwein/Arbeitsgruppe Hefegenetik, Institute of Microbial Technology, Chandigarh, Indien, 13.12.2010 bis 17.12.2010, Finanzierung durch DAAD.

Lehrtätigkeit/Teaching

2010

Name der/des Lehrenden	Thema	Universität/ Hochschule	Fakultät/ Fachbereich (FB)	SWS*
Prof. Dr. A. Graner (GB) Priv.-Doz. Dr. A. Börner (GB) Dr. N. Stein (GB) Dr. B. Kilian (GB)	Masterstudiengang Nutzpflanzenwissenschaften, Mastermodul: Pflanzengenetische Ressourcen und Genomforschung (Vorlesung und Praktikum)	Martin-Luther-Universität Halle-Wittenberg	Naturwissenschaftliche Fakultät III Institut für Agrar- und Ernährungswissenschaften	4
Priv.-Doz. Dr. A. Börner (GB) Dr. J. Keller (GB) Dr. U. Lohwasser (GB) Dr. A. Senula (GB)	Erhaltungsstrategien und Management pflanzengenetischer Ressourcen (Vorlesung und Praktikum)	Martin-Luther-Universität Halle-Wittenberg	Naturwissenschaftliche Fakultät III Institut für Agrar- und Ernährungswissenschaften	1
Dr. A. Senula (GB)	Kryokonservierung von Minze-Akzessionen (*Mentha*) (Praktikum)	Martin-Luther-Universität Halle-Wittenberg	Naturwissenschaftliche Fakultät I Institut für Pharmazie	10
Dr. T. Schnurbusch (GB)	Quantitative Genetik und Populationsgenetik in der Pflanzenzüchtung (Vorlesung)	Martin-Luther-Universität Halle-Wittenberg	Naturwissenschaftliche Fakultät III Institut für Agrar- und Ernährungswissenschaften	2
Prof. Dr. I. Schubert (CYG) Dr. J. Fuchs (CYG)	Klassische und molekulare Cytogenetik (Komplexpraktikum)	Universität Kassel	Fachbereich Genetik	7
Priv.-Doz. Dr. V. Schubert (CYG) Dr. J. Fuchs (CYG) Dr. M. Melzer (PZB)	Moderne Techniken der Mikroskopie und Cytogenetik (Bachelor-Studentenpraktikum)	Martin-Luther-Universität Halle-Wittenberg	Naturwissenschaftliche Fakultät III Institut für Agrar- und Ernährungswissenschaften	1
Dr. A. Houben (CYG) Dr. H. Bäumlein (MOG)	Biotechnologie in der Pflanzenproduktion (Vorlesung und Praktikum)	Hochschule Anhalt Bernburg	FB Landwirtschaft	7
Dr. A. Houben (CYG) Priv.-Doz. Dr. V. Schubert (CYG) Dr. J. Kumlehn (PZB)	Zytogenetik und Gentechnologie der Nutzpflanzen (Praktikum)	Martin-Luther-Universität Halle-Wittenberg	Naturwissenschaftliche Fakultät III Institut für Agrar- und Ernährungswissenschaften	1
Priv.-Doz. Dr. R. Schmidt (CYG)	Einblicke durch Genomprojekte: Was machen Pflanzen anders? (Seminar)	Universität Potsdam	Mathematisch-Naturwissenschaftliche Fakultät	2
Priv.-Doz. Dr. R. Schmidt (CYG)	Struktur-/Funktionsbeziehungen in Eukaryontengenomen (Seminar)	Universität Potsdam	Mathematisch-Naturwissenschaftliche Fakultät	2
Prof. Dr. A.M. Wobus (CYG)	Grundlagen der Zell- und Gewebekultur und aktuelle Aspekte der Stammzellforschung (Vorlesung)	Martin-Luther-Universität Halle-Wittenberg	Medizinische Fakultät	1
Dr. U. Scholz (CYG) Dr. M. Lange (CYG) Dr. S. Weise (CYG)	Einführung in die Bioinformatik (Vorlesung und Übung)	Hochschule Anhalt Köthen	FB Biotechnologie, Lebensmitteltechnologie, Verfahrens- und Umwelttechnik	4
Dr. M. Lange (CYG) Dr. S. Weise (CYG)	Datenbankmanagementsysteme Medieninformatik Bachelor-Studiengang (Vorlesung und Übung)	Hochschule Harz Wernigerode	FB Automatisierung und Informatik	6

* SWS = Semesterwochenstunden

Name der/des Lehrenden	Thema	Universität/ Hochschule	Fakultät/ Fachbereich (FB)	SWS*
Prof. Dr. T. Altmann (MOG) Dr. R.C. Meyer (MOG) Dr. W. Weschke (MOG) Dr. H. Weber (MOG) Dr. U. Conrad (MOG) Dr. habil. L. Altschmied (MOG) Dr. S. Friedel (MOG)	Projektmodul Molekulare Genetik (Vorlesung)	Martin-Luther-Universität Halle-Wittenberg	Naturwissenschaftliche Fakultät I Institut für Biologie	15
Prof. Dr. T. Altmann (MOG) Dr. H. Rolletschek (MOG)	Biologie der Samenentwicklung (Praktikum)	Universität Hannover	FB Pflanzenproteomik Institut für Pflanzengenetik	6
Dr. U. Conrad (MOG)	Grundlagen der Genetik (Vorlesung)	Martin-Luther-Universität Halle-Wittenberg	Naturwissenschaftliche Fakultät I FB Pharmazie	1
Dr. U. Conrad (MOG)	Molecular Pharming im Masterkurs Pharmazeutische Biotechnologie (Vorlesung)	Martin-Luther-Universität Halle-Wittenberg	Naturwissenschaftliche Fakultät I FB Pharmazie	1
Dr. habil. L. Altschmied (MOG)	Pflanzenphysiologisches Praktikum	Friedrich-Schiller-Universität Jena	Institut für Pflanzen-physiologie	4
Prof. Dr. F. Schreiber (MOG) H. Mehlhorn (MOG)	Analyse biologischer Netzwerke (Vorlesung und Übung)	Martin-Luther-Universität Halle-Wittenberg	Naturwissenschaftliche Fakultät III Institut für Informatik	4
Prof. Dr. F. Schreiber (MOG) Dr. U. Scholz (CYG) Dr. S. Friedel (MOG) Dr. C. Klukas (MOG) Dr. B. Junker (PZB) Dr. H. Knüpffer (GB)	Bioinformatik-Intensivkurs Master-Studiengang Agrarwissenschaften (Vorlesung und Übung)	Christian-Albrechts-Universität zu Kiel	Agrar- und Ernährungs-wissenschaftliche Fakultät	4
Dr. N. Sreenivasulu (MOG) Senior Lecturer	Molecular basis of terminal drought tolerance (Vorlesung)	University of Western Australia, Perth	Summer school of plant biology	1
Prof. Dr. N. von Wirén (PZB)	Pflanzenphysiologie: Transportprozesse über pflanzliche Membranen; Molekularer Mineralstoffwechsel	Martin-Luther-Universität Halle-Wittenberg	Naturwissenschaftliche Fakultät I Institut für Biologie	2
Priv.-Doz. Dr. H.-P. Mock (PZB)	Pflanzenphysiologie (Grundpraktikum)	Martin-Luther-Universität Halle-Wittenberg	Naturwissenschaftliche Fakultät I Institut für Biologie	4
Prof. Dr. G. Kunze (PZB)	Molekulargenetik Teil I (Vorlesung)	Hochschule Anhalt Köthen	FB Biotechnologie, Lebensmitteltechnologie, Verfahrens- und Umwelttechnik	3
Prof. Dr. G. Kunze (PZB)	Molekulargenetik Teil II (Vorlesung)	Hochschule Anhalt Köthen	FB Biotechnologie, Lebensmitteltechnologie, Verfahrens- und Umwelttechnik	3
Prof. Dr. G. Kunze (PZB)	Biosensoren für die Umweltkontrolle (Vorlesung)	Hochschule Anhalt Köthen	FB Biotechnologie, Lebensmitteltechnologie, Verfahrens- und Umwelttechnik	2
Prof. Dr. G. Kunze (PZB)	Hefegenetik (Praktikum)	Ernst-Moritz-Arndt-Universität Greifswald	Mathematisch-Natur-wissenschaftliche Fakultät, FB Biologie Institut für Genetik und Biochemie	4
Semesterwochenstunden (SWS) insgesamt:				102

* SWS = Semesterwochenstunden

2011

Name der/des Lehrenden	Thema	Universität/ Hochschule	Fakultät/ Fachbereich (FB)	SWS*
Prof. Dr. A. Graner (GB) Priv.-Doz. Dr. A. Börner (GB) Dr. N. Stein (GB) Dr. B. Kilian (GB)	Masterstudiengang Nutzpflanzenwissenschaften Mastermodul: Pflanzengenetische Ressourcen und Genomforschung (Vorlesung und Praktikum)	Martin-Luther-Universität Halle-Wittenberg	Naturwissenschaftliche Fakultät III Institut für Agrar- und Ernährungswissenschaften	4
Priv.-Doz. Dr. A. Börner (GB) Dr. J. Keller (GB) Dr. U. Lohwasser (GB) Dr. A. Senula (GB)	Erhaltungsstrategien und Management pflanzengenetischer Ressourcen (Vorlesung und Praktikum)	Martin-Luther-Universität Halle-Wittenberg	Naturwissenschaftliche Fakultät III Institut für Agrar- und Ernährungswissenschaften	1
Dr. T. Schnurbusch (GB)	Quantitative Genetik und Populationsgenetik in der Pflanzenzüchtung (Vorlesung)	Martin-Luther-Universität Halle-Wittenberg	Naturwissenschaftliche Fakultät III Institut für Agrar- und Ernährungswissenschaften	2
Dr. J. Keller (GB)	Cryopreservation and *in vitro* storage for plant germplasm conservation (Vorlesung)	Martin-Luther-Universität Halle-Wittenberg	Biozentrum der Universität Halle	1,5
Prof. Dr. I. Schubert (CYG) Dr. J. Fuchs (CYG)	Klassische und molekulare Cytogenetik (Komplexpraktikum)	Universität Kassel	Fachbereich Genetik	7
Priv.-Doz. Dr. V. Schubert (CYG) Dr. J. Fuchs (CYG) Dr. M. Melzer (PZB)	Moderne Techniken der Mikroskopie und Cytogenetik (Bachelor-Studentenpraktikum)	Martin-Luther-Universität Halle-Wittenberg	Naturwissenschaftliche Fakultät III Institut für Agrar- und Ernährungswissenschaften	0,5
Priv.-Doz. Dr. V. Schubert (CYG)	Grundlagen und moderne Techniken der Mikroskopie im Masterstudiengang „Nutzpflanzenwissenschaften“ (Vorlesung und Praktikum)	Martin-Luther-Universität Halle-Wittenberg	Naturwissenschaftliche Fakultät III Institut für Agrar- und Ernährungswissenschaften	1,5
Dr. A. Houben (CYG) Dr. H. Bäumlein (MOG)	Biotechnologie in der Pflanzen- und Tierproduktion (Vorlesung und Praktikum)	Hochschule Anhalt Bernburg	FB Landwirtschaft	7
Priv.-Doz. Dr. R. Schmidt (CYG)	Einblicke durch Genomprojekte: Was machen Pflanzen anders? (Seminar)	Universität Potsdam	Mathematisch-Naturwissenschaftliche Fakultät	2
Priv.-Doz. Dr. R. Schmidt (CYG)	Struktur-/Funktionsbeziehungen in Eukaryontengenomen (Seminar)	Universität Potsdam	Mathematisch-Naturwissenschaftliche Fakultät	2
Prof. Dr. A.M. Wobus (CYG)	Grundlagen der Zell- und Gewebekultur und aktuelle Aspekte der Stammzellforschung (Vorlesung)	Martin-Luther-Universität Halle-Wittenberg	Medizinische Fakultät	1
Dr. U. Scholz (CYG) B. Steuernagel (CYG) Prof. Dr. A. Graner (GB) Dr. N. Stein (GB) Dr. B. Kilian (GB) K. Wolf (GB) M. Ziems (GB) A. Kusserow (GB) J. Perovic (GB) R.K. Pasam (GB) R. Sharma (GB)	Genomkartierung/Molekulare Diversität	Martin-Luther-Universität Halle-Wittenberg	Naturwissenschaftliche Fakultät III Institut für Agrar- und Ernährungswissenschaften	2
Dr. U. Scholz (CYG)	Einführung in die Bioinformatik Bachelor-Studiengang Biotechnologie (Vorlesung und Übung)	Hochschule Anhalt Köthen	Fachbereich 7 – Angewandte Biowissenschaften und Prozesstechnik	8

* SWS = Semesterwochenstunden

Name der/des Lehrenden	Thema	Universität/ Hochschule	Fakultät/ Fachbereich (FB)	SWS*
Dr. M. Lange (CYG) Dr. S. Weise (CYG)	Datenbankmanagementsysteme Bachelor-Studiengang Medieninformatik (Vorlesung und Übung)	Hochschule Harz, Wernigerode	Fachbereich Automatisierung und Informatik	4
Prof. Dr. T. Altmann (MOG) Dr. W. Weschke (MOG) Dr. H. Weber (MOG) Dr. U. Conrad (MOG) Dr. habil. L. Altschmied (MOG) Dr. S. Friedel (MOG)	Projektmodul Molekulare Genetik Bachelor-Studiengang Biologie (Vorlesung)	Martin-Luther-Universität Halle-Wittenberg	Naturwissenschaftliche Fakultät I Institut für Biologie	15
Dr. habil. L. Altschmied (MOG)	Praktikum für Pflanzenphysiologie (Lehramts- und Diplomstudenten)	Friedrich-Schiller-Universität Jena	Institut für Pflanzenphysiologie	4
Prof. Dr. F. Schreiber (MOG)	Analyse biologischer Netzwerke (Vorlesung und Übung)	Martin-Luther-Universität Halle-Wittenberg	Naturwissenschaftliche Fakultät III Institut für Informatik	4
Prof. Dr. F. Schreiber (MOG) Dr. U. Scholz (CYG) Dr. B. Junker (PZB) Dr. H. Knüpffer (GB) M. Oppermann (GB) Dr. C. Klukas (MOG) Dr. S. Friedel (MOG)	Bioinformatik (Vorlesung und Übung)	Christian-Albrechts-Universität zu Kiel	Agrar- und Ernährungswissenschaftliche Fakultät	4
Prof. Dr. N. von Wirén (PZB)	Transportprozesse über pflanzliche Membranen (Vorlesung und Praktikum)	Martin-Luther-Universität Halle-Wittenberg	Naturwissenschaftliche Fakultät I Fach Pflanzenphysiologie	1
Prof. Dr. N. von Wirén (PZB)	Molekularer Mineralstoffwechsel (Vorlesung)	Martin-Luther-Universität Halle-Wittenberg	Naturwissenschaftliche Fakultät I Fach Pflanzenphysiologie	1
Priv.-Doz. Dr. H.-P. Mock (PZB)	Pflanzenphysiologie (Grundpraktikum)	Martin-Luther-Universität Halle-Wittenberg	Naturwissenschaftliche Fakultät I Institut für Biologie	4
Dr. J. Kumlehn (PZB)	Cytogenetik und Gentechnik (Master-Studiengang)	Martin-Luther-Universität Halle-Wittenberg	Naturwissenschaftliche Fakultät III, Agrarwissenschaften, Geowissenschaften und Informatik	1,3
Prof. Dr. G. Kunze (PZB)	Molekulargenetik Teil I (Vorlesung)	Hochschule Anhalt Köthen	FB Biotechnologie, Lebensmitteltechnologie, Verfahrens- und Umwelttechnik	3
Prof. Dr. G. Kunze (PZB)	Molekulargenetik Teil II (Vorlesung)	Hochschule Anhalt Köthen	FB Biotechnologie, Lebensmitteltechnologie, Verfahrens- und Umwelttechnik	3
Prof. Dr. G. Kunze (PZB)	Biosensoren für die Umweltkontrolle (Vorlesung)	Hochschule Anhalt Köthen	FB Biotechnologie, Lebensmitteltechnologie, Verfahrens- und Umwelttechnik	2
Prof. Dr. G. Kunze (PZB)	Hefegenetik (Praktikum)	Ernst-Moritz-Arndt-Universität Greifswald	Mathematisch-Naturwissenschaftliche Fakultät, FB Biologie	4
Dr. B. Junker (PZB)	Mikrobiologie (Vorlesung)	Martin-Luther-Universität Halle-Wittenberg	Pharmazie	2
Dr. B. Junker (PZB)	Biogene Arzneimittel (Seminar)	Martin-Luther-Universität Halle-Wittenberg	Pharmazie	1
Semesterwochenstunden (SWS) insgesamt:				**92,8**

* SWS = Semesterwochenstunden

Mitarbeit an wissenschaftlichen Zeitschriften/ Editing Scientific Journals

Mitarbeiter des Leibniz-Instituts für Pflanzengenetik und Kulturpflanzenforschung sind Herausgeber bzw. Mitherausgeber folgender Zeitschriften:

Agriculture, Piestany, Slovak Republic (A. Börner, Editorial Board).

BBA Gene Regulatory Mechanisms, Elsevier, Maryland Heights, USA (A. Houben, Board Member).

Biotechnology in Forestry and Agriculture, Springer, Berlin-Heidelberg (J. Kumlehn, Editor).

Biotechnology Research International, Hindawi, Publishing Corporation, New York, USA (U. Conrad, Subject Editor).

BMC Biotechnology, BioMed Central Ltd, London, UK (U. Conrad, Associate Editor).

BMC Plant Biology, BioMed Central Ltd, London, UK (N. Stein and N. Sreenivasulu, Associate Editor).

BMC Research Notes, BioMed Central, London, UK (B. Junker, Associate Editor).

BMC Systems Biology, BioMed Central, London, UK (F. Schreiber, Associate Editor).

Botanical Journal of Iran, Rostaniha, Tehran, Iran (R. Fritsch, Editorial Board).

Cell Biology and Toxicology, Springer, Dordrecht, The Netherlands (Anna M. Wobus, Consulting Editor).

Cells Tissues Organs, Karger AG, Basel, Switzerland (Anna M. Wobus, Associate Editor).

Cereal Research Communications, Akadémiai Kiadó, Budapest, Hungary (A. Börner, Editorial Board).

Chromosoma, Springer, New York, USA (I. Schubert, Associate Editor).

Chromosome Research, Springer, Dordrecht, The Netherlands (A. Houben, Editorial Advisory Board).

Comparative and Functional Genomics (T. Altmann, Supporting Editorial Board Member).

Current Trends in Biotechnology and Pharmacy, USA (N. Sreenivasulu, Editorial Board Member).

Cytogenetics & Genome Research (CGR), Karger AG, Basel, Switzerland (I. Schubert, Editorial Board).

Electronic Wheat Information Service, Shizuoka, Japan (A. Houben, Editorial Advisory Board).

Field and Vegetable Crops Research, Novi Sad, Serbia (A. Börner, Editorial Board).

Frontiers in Crop Science and Horticulture, Lausanne, Switzerland (A. Börner, Editorial Board).

Frontiers in Plant Genetics and Genomics, Frontiers Lausanne, Switzerland (I. Schubert, Associate Editor; A. Houben, Editorial Advisory Board).

Frontiers in Plant Nutrition, Frontiers Media, Genève, Switzerland (N. von Wirén, Editor-in-Chief).

Functional & Integrative Genomics, Springer, Berlin-Heidelberg (N. Stein, Associate Editor).

Genetic Resources and Crop Evolution (GRACE), Springer, Dordrecht, The Netherlands (K. Pistrick, Managing Editor; F. R. Blattner, Editorial Board).

Genetics, Journal of the Genetics Society of America (A. Houben, Editorial Board).

Genetics and Breeding, Bulgarian Academy of Sciences for the Bulgarian Genetical Society, Sofia, Bulgaria (I. Schubert, Editorial Board).

GM Crops, Landes Bioscience, Austin, USA (J. Kumlehn, Editorial Board).

International Scholarly Research Network (ISRN) Agronomy, New York, USA (N. Sreenivasulu, Editorial Board).

Japanese Journal of Breeding Science, The Japanese Society of Breeding, Tsukuba, Japan (N. Stein, Associate Editor).

Journal of Integrative Bioinformatics (JIB), IMBio, Bielefeld (F. Schreiber, Associate Editor; M. Lange and U. Scholz, Editorial Board; C. Klukas, M. Lange and S. Weise, Editorial Management).

Journal of Plant Physiology, Elsevier, Amsterdam, The Netherlands (J. Kumlehn, Editorial Board).

Journal of Stem Cells, Nova Science Publishers, Inc., New York, USA (Anna M. Wobus, Editorial Advisory Board Member).

Journal of Tissue Engineering and Regenerative Medicine, John Wiley & Sons, Ltd., UK (Anna M. Wobus, Editorial Board Member).

Medizinische Informatik, Biometrie und Epidemiologie, Köln (F. Schreiber, Advisory Board).

Molecular Breeding, Springer, Dordrecht, The Netherlands (A. Graner and J. Kumlehn, Editorial Board).

Molecular Plant-Microbe Interactions, APS Press, St. Paul, USA (P. Schweizer, Associate Editor).

New Phytologist, Lancaster, UK (N. von Wirén, Scientific Advisor).

Plant Biotechnology Journal, Blackwell Publishing, Bristol, UK (R. Schmidt, Advisory Board).

Plant Cell Reports, Springer, Berlin-Heidelberg (R. Schmidt, Editorial Board).

Plant Molecular Biology Reporter, Springer, Berlin-Heidelberg (R. Schmidt und A. Houben, Editorial Board).

Plant Systematics and Evolution, Springer, Berlin-Heidelberg (F.R. Blattner, Editorial Board).

Proteomics, Wiley-VCH, Weinheim (H.-P. Mock, Editorial Board).

Stem Cells, AlphaMed Press, Durham, USA (Anna M. Wobus, Editorial Board Member).

The International Journal of Developmental Biology, The University of the Basque Country Press, Bilbao, Spain (Anna M. Wobus, Editorial Advisory Board Member).

The Nucleus, MD Publications Pvt Ltd., New Delhi, India (I. Schubert, Advisory Board).

The Open Mycology Journal, Bentham Science Publishers Ltd., USA (G. Kunze, Editorial Advisory Board).

The Plant Journal, Blackwell Publishing, Oxford, UK (T. Altmann, Editor).

Theoretical and Applied Genetics, Springer, Berlin-Heidelberg (A. Graner, Editorial Board).

Vegetable Crops Research Bulletin, RIVC, Skierniewice, Poland (J. Keller, Editorial Advisory Board).

Tätigkeit in Gremien/Activities in Boards

Geschäftsführender Direktor

Prof. Dr. A. Graner
- Mitglied der Deutschen Akademie der Naturforscher LEOPOLDINA – Nationale Akademie der Wissenschaften Halle/S.;
- Mitglied des Vorstandsrates der Gesellschaft für Pflanzenzüchtung e.V. (GPZ) und Leiter der Ag Genomanalyse;
- Mitglied des Beirates für nachwachsende Rohstoffe, Ministerium für Landwirtschaft und Umwelt des Landes Sachsen-Anhalt;
- Vorsitzender des Scientific Advisory Boards des Max-Planck-Instituts für Pflanzenzüchtungsforschung, Köln;
- Mitglied im Wissenschaftlichen Beirat des Julius Kühn-Instituts (JKI), Quedlinburg;
- Mitglied des Beratungs- und Koordinierungsausschusses (BEKO) des Nationalen Fachprogramms zur Erhaltung und nachhaltigen Nutzung pflanzengenetischer Ressourcen landwirtschaftlicher und gartenbaulicher Kulturpflanzen, BMELV, Bonn;
- Mitglied des Wissenschaftlichen Beirates Otto Warburg Center for Agricultural Biotechnology, Hebrew University, Jerusalem, Israel;
- Honorary Fellow des James Hutton Institute, Dundee, UK;
- Steering Committee, International Barley Sequencing Consortium (IBSC);
- Stellvertretender Vorsitzender der Gemeinschaft zur Förderung der Kulturpflanzenforschung Gatersleben e.V.;
- Review Panel Research Program: Integrated Biological Systems, Australian Government Department of Innovation, Industry, Science and Research (DIISR) (2010);
- Mitglied Executive Board, Generation Challenge Program, Consultative Group of International Agricultural Research (CGIAR);
- Mitglied des Direktoriums, Interdisziplinäres Zentrum für Nutzpflanzenforschung (IZN), Martin-Luther-Universität Halle/S;
- acatech, Arbeitsgruppe Anpassungsstrategien in der Klimapolitik;
- Mitglied des Kuratoriums der Sparkassenstiftung Aschersleben-Staßfurt;
- Vorsitzender des Fördervereins des Schülerlabors „Grünes Labor Gatersleben".

Abteilung Genbank

Dr. N. Stein
- Chair of International Barley Genome Sequencing Consortium (IBSC, http://barleygenome.org);
- European Triticeae Genomics Initiative (ETGI, http://www.etgi.org) (Koordinator);
- Management Committee and National Representative of COST-Action Tritigen FA0604;
- Chair of the Scientific Coordinating Committee (SCC) of the German Plant Biotechnology Program.

Dr. H. Knüpffer
- Koordinator des Cereals Network sowie Chairman der Barley Working Group des European Cooperative Programme for Plant Genetic Resources (ECPGR);
- Mitglied der Network Coordinating Group des Documentation and Information Network des ECPGR;
- Mitglied der Arbeitsgruppe zum Europäischen Kooperationsprogramm pflanzengenetischer Ressourcen (ECPGR) des Beratungs- und Koordinierungsausschusses für pflanzengenetische Ressourcen (BeKo) von Bund und Ländern (unter Leitung des BMELV);
- Mitglied des International Barley Core Collection Committee (Bioversity International);
- Mitglied der Arbeitsgruppe Biodiversity Information Standards (TDWG – ehem. Taxonomic Databases Working Group).

Priv.-Doz. Dr. A. Börner
- Koordinator der European Cereals Genetics Co-operative (EWAC);
- Vorsitzender der Cereals Section of the European Association for Research on Plant Breeding (EUCARPIA);
- Mitglied des Seed Storage Committee of the International Seed Testing Association (ISTA);
- German Representative of Working Group Wheat of the European Cooperative Programme for Plant Genetic Resources (ECPGR);
- Vorsitzender der Arbeitsgemeinschaft Saatgut und Sortenwesen der Gesellschaft für Pflanzenbauwissenschaften (GPW) und der Gesellschaft für Pflanzenzüchtung (GPZ);
- Mitglied der Beratungsgruppe Entwicklungsorientierte Agrarforschung (BEAF) der Deutschen Gesellschaft für Technische Zusammenarbeit (GTZ).

Dr. U. Lohwasser
- Mitglied des Expertengremiums zur Entwicklung von Genbankstandards bei Bioversity;
- Core Advisory Group bzw. Reviewer bei Bioversity;
- Vorstandsmitglied in der Gemeinschaft zur Förderung der Kulturpflanzenforschung;
- Mitglied des beratenden Gremiums zum Aufbau der Genbanken WEL und Zierpflanzen in Deutschland;
- Deutscher Vertreter of Working Group Solanaceae of the European Cooperative Programme for Plant Genetic Resources (ECPGR).

Dr. J. Keller
- Mitglied der Koordinierungsgruppe des ECPGR Vegetables Network und Vice Chairman der *Allium*-Arbeitsgruppe;
- Chairman der *Allium* Working Group im European Cooperative Programme for Plant Genetic Resources (ECPGR);
- Mitglied im Lenkungsausschuss der europäischen COST-Initiative 871 „Kryokonservierung in Europa".

Dr. K.J. Dehmer
- Mitglied in der ECPGR Working Group on Potato;
- Councellor der European Association for Potato Research (EAPR).

E. Willner
- Stellvertretende Vorsitzende der ECPGR Working Group on Forages.

Dr. K. Pistrick
- Mitglied im Nomenclature Committee of the International Seed Testing Association (ISTA).

Abteilung Cytogenetik und Genomanalyse

Priv.-Doz. Dr. R. Schmidt
- Gewähltes Mitglied des DFG-Fachkollegiums „Pflanzenwissenschaften".

Prof. Dr. Anna M. Wobus
- Mitglied der Deutschen Akademie der Naturforscher LEOPOLDINA – Nationale Akademie der Wissenschaften, Halle/S.;
- Ordentliches Mitglied der Berlin-Brandenburgischen Akademie der Wissenschaften (BBAW);
- Mitglied der Zentralen Ethik-Kommission für Stammzellenforschung (ZES) am Robert-Koch-Institut, Berlin (stellvertretende Vorsitzende);
- Mitglied des Novartis Ethics Advisory Board (NEAB) von NOVARTIS Pharma International, Basel, Schweiz;
- Mitglied des Programmbeirats des Wissenschaftszentrums Sachsen-Anhalt (WZW).

Dr. habil. P. Schweizer
- Mitglied der Zentralen Kommission für Biologische Sicherheit (ZKBS), Bereich Pflanzenzucht.

Abteilung Molekulare Genetik

Prof. Dr. T. Altmann
- Mitglied des Multinational Arabidopsis Steering Committee;
- Mitglied des Scientific Co-Ordination Committee (SCC) of the BMBF-funded German Plant Biotechnology Program;
- Mitglied des Scientific Advisory Board of the French plant genome program Génoplante;
- Mitglied des Scientific Advisory Board of the Nottingham Arabidopsis Stock Centre (NACS);
- Program Board Member of the DFG-funded Program „Heterosis bei Pflanzen".
- Mitglied im Wissenschaftlichen Beirat der Gemeinschaft zur Förderung der privaten deutschen Pflanzenzüchtung e.V. (GFP).

Prof. Dr. F. Schreiber
- Mitglied des Lenkungsgremiums der Gesellschaft für Informatik (GI) und der Gesellschaft für Medizinische Informatik, Biometrie und Epidemiologie (GMDS) des Fachbereichs „Informatik in den Lebenswissenschaften";
- Mitglied im German/Russian Virtual Network on Bioinformatics;
- Mitglied im Sino/German Network of Computational & Integrative Biology;
- Sprecher der Fachgruppe Informationsmanagement in der Biotechnologie der Gesellschaft für Informatik (GI).

Abteilung Physiologie und Zellbiologie

Prof. Dr. N. von Wirén
- Mitglied des „IPNC-Steering Committees" (International Plant Nutrition);
- Vizepräsident der Deutschen Gesellschaft für Pflanzenernährung;
- Fachgutachter der Deutschen Forschungsgemeinschaft im Fachkollegium 207 „Agrar-, Forstwissenschaften, Gartenbau und Tiermedizin";
- Mitglied des Scientific Advisory Boards des „Department of Agriculture & Ecology of the University of Copenhagen";
- Mitglied des Wissenschaftlichen Beirats des Leibniz-Instituts für Pflanzenbiochemie, Halle/S.;
- Mitglied des Direktoriums des Leibniz-Wissenschaftscampus „Pflanzenbasierte Bioökonomie" mit der Martin-Luther-Universität Halle-Wittenberg, Halle/S.

Prof. Dr. G. Kunze
- Mitglied im wissenschaftlichen Beirat der Fa. ARTES Biotechnology GmbH.

Dr. B.H. Junker
- Mitglied im Zukunftsforum Biotechnologie der DECHEMA e.V., Arbeitskreis Systembiologie und Synthetische Biologie;
- Mitglied der Fachgruppe Systembiologie und Synthetische Biologie der DECHEMA e.V.

Öffentlichkeitsarbeit/Public Relations

Informationsveranstaltungen und Führungen/Informative Events and Guided Tours

2010

8. Januar 2010
Besuch von Studenten des 1. Semesters Landwirtschaft (Bachelorstudiengang) der Hochschule Anhalt, Köthen, 30 Personen, Vorstellung des Instituts, Besuch der Abteilungen Molekulare Genetik und Cytogenetik und Genomanalyse, Besichtigung der Genbank, des Samenkühllagers und der *In vitro*-Erhaltung und Kryolagerung (R. Schnee, Dr. habil. H. Bäumlein, Dr. A. Houben, Dr. U. Lohwasser, Dr. J. Keller).

13. Januar 2010
Besuch von Studenten der Agrarwirtschaft an der Fachhochschule Soest, 11 Personen, Vorstellung des Instituts und der Aufgaben der Genbank, Führung durch die Genbank, Elektronenmikroskopie in der Pflanzenforschung und Besichtigung der Gewächshäuser (R. Schnee, Dr. U. Lohwasser, Dr. M. Melzer, E. Geyer).

22. Januar 2010
Besuch von Studenten des 1. Semesters Landwirtschaft (Bachelorstudiengang) der Hochschule Anhalt, Köthen, 30 Personen, Vorstellung des Instituts, Besuch der Abteilungen Molekulare Genetik und Cytogenetik und Genomanalyse, Besichtigung der Genbank mit Samenkühllager, Labor und *In vitro*-Erhaltung und Kryo-Lagerung (R. Schnee, Dr. habil. H. Bäumlein, Dr. A. Houben, Dr. U. Lohwasser, Dr. J. Keller).

27. Januar 2010
Besuch von Herrn Detlef Gürth, MdL Sachsen-Anhalt, wirtschaftspolitischer Sprecher der CDU-Fraktion, Besuch der Genbank und Rundgang durch das IPK und *SunGene*, Vorstellung der Forschungsschwerpunkte Grüne Gentechnik und Diskussion über den Standort (Prof. Dr. A. Graner, Prof. Dr. Th. Altmann, Prof. Dr. I. Schubert, Prof. Dr. N. von Wirén, S.-A. Lorenz, R. Schnee).

27. Januar 2010
Genbankführung für Dr. Likyelesh Gugsa aus Äthiopien (Dr. U. Lohwasser, Dr. J. Keller).

18. Februar 2010
Besuch von Mitarbeitern der Psychiatrischen Tagesklinik, Aschersleben, 20 Personen, Vorstellung des Instituts sowie der Aufgaben der Genbank und anschließende Besichtigung, Erläuterung der *In vitro*-Erhaltung und Kryo-Konservierung, Gewächshausführung und Besichtigung des Phytokammerhauses (Priv.-Doz. Dr. A. Börner, Dr. J. Keller, P. Schreiber, E. Geyer).

31. März 2010
Führung durch die Malchower Öl- und Futterpflanzen-Sortimente der IPK-Genbank für Futterpflanzenzüchter der NPZ und der Universität Kiel, 5 Personen, Sammelreisestrategie für alte Grünlandstandorte (E. Willner).

7. April 2010
Besuch von Lehrern der Sächsischen Bildungsagentur (SBA) Chemnitz, 20 Personen, Überblick zur Geschichte der Biotechnologie und zur Genregulation bei Pflanzen, Produktion von Vakzinen und Antikörpern in Pflanzen, Anwendung von Hefen in der Pflanzenforschung und zur Entwicklung von Hormon-Sensoren, Führung durch die Labore der Arbeitsgruppe Hefegenetik, Neue Verfahren und Methoden in der Chromosomenbiologie, Systembiologie – an der Schnittstelle zwischen Dry und Wetlab, Erzeugung von transgenen Pflanzen, Besichtigung der Gewächshäuser und Gewebekulturen, Rundgang im Grünen Labor (Dr. habil. H. Bäumlein, Priv.-Doz. Dr. U. Conrad, Prof. Dr. G. Kunze, Dr. A. Houben, Dr. B. Junker, Dr. J. Kumlehn).

12. April 2010
Besucher vom Umwelt-, Planungs-, Verkehrs- und Wirtschaftsausschuss im Biotech-Gründerzentrum Gatersleben, 13 Personen, Erläuterung der Aufgaben in der Genbank mit anschließender Führung (Priv.-Doz. Dr. A. Börner).

28. April 2010
Führung durch die Malchower Öl- und Futterpflanzen-Sortimente der IPK-Genbank im Rahmen des 10. ECPGR working group meeting on forages, 30 Personen, Vorstellung der Arbeitsweise nach QMS, insbesondere Dokumentation: GBIS mit C- und E-Daten-Verwaltung (S. Hünmörder, V. Miehe, M. Oppermann, E. Willner).

30. April 2010
Besuch von Berufsberatern der Arbeitsagentur Harzkreis, 12 Personen, Überblick über Ausbildungsmöglichkeiten am IPK (Bürokauffrau/-mann, Biologielaborant/-in, Gärtner/-in, Bibliothekassistent/-in), Besichtigung eines Labors und Gewächshauses sowie der Bibliothek, Rundgang im Grünen Labor (C. Höpfner, J. Becker, Priv.-Doz. Dr. A. Börner, J. Marlow, S. Winter, S. Amme).

30. April 2010
Führung durch die Malchower Öl- und Futterpflanzen-Sortimente der IPK-Genbank im Rahmen des 10. ECPGR working group meeting on forages, 3 Personen, vertiefende Vorstellung der Arbeitsweise nach QM-Standards, insbesondere Vermehrungsstandards, Isolationen (E. Willner).

3. Mai 2010
Besuch von Fachschülern der Landesanstalt für Landwirtschaft, Forsten und Gartenbau, Fachschule für Landwirtschaft, Gartenbau und Hauswirtschaft, Quedlinburg, 9 Personen, Vorstellung des Instituts, *In vitro*-Erhaltung und Kryokonservierung von Kulturpflanzen, Besichtigung des Herbars sowie der Samensammlung, Gewächshausbesichtigung (Dr. J. Keller, Dr. K. Pistrick, J. Marlow).

5. Mai 2010
Besuch von Mitgliedern des Rotary Club aus Sandy, UK, 3 Personen, Vorstellung des Instituts, Besichtigung des Genomzentrums und der Genbank (Prof. Dr. A. Graner, Dr. habil. P. Schweizer, Priv.-Doz. Dr. A. Börner).

7. Mai 2010
Besuch des Staatssekretärs Herrn Jürgen Stadelmann und Herrn Karl-Heinz Weege vom Ministerium für Landwirtschaft und Umwelt des Landes Sachsen-Anhalt, Vorstellung des Instituts mit anschließender Diskussion, Führung Lemnatec-Anlage, Besuch Grünes Labor (Prof. Dr. A. Graner, Prof. Dr. Th. Altmann, Prof. Dr. I. Schubert, S.-A. Lorenz, Priv.-Doz. Dr. H.-P. Mock, Dr. habil. P. Schweizer, Prof. Dr. F. Schreiber, I. Mücke).

10. Mai 2010
Führung von Ph. D. Efisio Mattana, Centro Conservazione Biodiversità, Università degli Studi di Cagliari, Cagliari, Italien, Vorstellung des Instituts und der Aufgaben der Genbank, Führung durch die Genbank, Erläuterung der *In vitro*-Erhaltung und Kryokonservierung (Priv.-Doz. Dr. A. Börner, Dr. J. Keller).

11. Mai 2010
Besucher im Rahmen der Landesgartenschau (LAGA), Aschersleben, 4 Personen, Darstellung der Aufgaben einer Genbank, Führung durch die Botanischen Vergleichssammlungen zum Thema *Allium*-Taxonomie (Priv.-Doz. Dr. A. Börner, Dr. J. Keller, Dr. K. Pistrick, M.-L. Graichen).

17. Mai 2010
Besuch eines Freundeskreises aus Friedrichsaue, 8 Personen, Führung durch den Staudengarten (B. Schütze).

17. Mai 2010
Mitarbeiter der Firma Norika, 2 Personen, Führung durch die Groß Lüsewitzer Kartoffel-Sortimente der IPK-Genbank (M. Angeli).

26. Mai 2010
Besucher des Landseniorenvereins Salzwedel, 42 Personen, Vorstellung des Instituts und der Aufgaben der Genbank, Genbankführung und durch die Herbar- und Samensammlung, Führung durch die Vermehrungsflächen und Gewächshäuser der Genbank, Diskussion über Gentechnik (Dr. U. Lohwasser, Dr. K. Pistrick, Dr. J. Kumlehn).

3. Juni 2010
Teilnehmer am EXBARDIV-Meeting-Projekt, 14 Personen, Vorstellung der Aufgaben der Genbank, Genbankführung und Feldbesichtigung (Dr. U. Lohwasser, P. Schreiber).

5. Juni 2010
Führungen zum „Tag der offenen Tür" der Malchower Sortimente für Öl- und Futterpflanzen der IPK-Genbank, ca. 250 Personen, Rundgänge und Erläuterungen zum Thema „2010 – Jahr der Biologischen Vielfalt" im Schaugarten bzw. im Feldanbau und in den Arbeitsräumen (M. Hautmann, P. Hermann, S. Hünmörder, R. Rudloff, H. Schmalfeldt, E. Willner unter Mithilfe von B. Fietz, H. Weiß).

8. Juni 2010
Besuch des Freundeskreises der Fakultät für Physik und Geowissenschaften, Leipzig, 40 Personen, Vorstellung des Instituts, Besichtigung der Genbank mit Kühllager, Keimfähigkeitstestlabor und Dreschscheune (R. Schnee, Priv.-Doz. Dr. A. Börner, Dr. A. Meister).

9. Juni 2010
Besuch von Mitgliedern der GFP-Arbeitsgruppe Getreide, 50 Personen, Führung durch die Botanischen Vergleichssammlungen (Dr. K. Pistrick).

11. Juni 2010
Besuch von Studenten der Universität Rostock, Agrar- und Umweltwissenschaftliche Fakultät/ Agrobiotechnologie, 10 Personen, Führung durch die Groß Lüsewitzer Kartoffel-Sortimente der IPK-Genbank (M. Angeli, U. Behrendt, Dr. K.J. Dehmer).

12. Juni 2010
Besucher zum „Tag der offenen Tür", ca. 60 Personen, Besichtigung der Genbank, Führung durch die Botanischen Vergleichssammlungen des Bereiches Taxonomie und Evolution (Herbarium, Samen- und Fruchtsammlung sowie Ährensammlung, Präsentation der Teilsammlungen Nord der IPK-Genbank (Priv.-Doz. Dr. A. Börner, Dr. K. Pistrick, Dr. U. Lohwasser, M. Kotter, Dr. K. J. Dehmer, Dr. J. Keller, D. Büchner, G. Matzig, B. Schmidt, R. Kurch, M.-L. Graichen).

14. Juni 2010
Besuch von Studenten der Universität Hohenheim, Institut für Pflanzenzüchtung, Saatgutforschung und Populationsgenetik (350), Stuttgart, 15 Personen, Vorstellung der Genbank, Genbankdokumentation, *In vitro*-Erhaltung und Kryokonservierung von Kulturpflanzen, Führung durch die Herbarsammlungen und durch die Vermehrungsbestände der Genbank (Priv.-Doz. Dr. A. Börner, Dr. H. Knüpffer, Dr. J. Keller, Dr. K. Pistrick, P. Schreiber).

15. Juni 2010
Besucher der Landesgartenschau (LAGA) Aschersleben, 4 Personen, Darstellung der Aufgaben einer Genbank, Führung durch den Anbau des Salatsortiments (Dr. U. Lohwasser, S. Thumm, M.-L. Graichen).

16. Juni 2010
Besuch von Studenten und Mitarbeitern des Instituts für Pflanzenbau und Pflanzenzüchtung der Universität Göttingen, 27 Personen, Vorstellung des Instituts und der Aufgaben der Genbank, Genbankführung, Informationen über die Aufgaben der Genbankdokumentation sowie Führungen in der *In vitro*-Erhaltung und Kryokonservierung, Herbar- und Samensammlung, automatisierte Phänotypisierung und Feldführung (Dr. U. Lohwasser, Dr. J. Keller, Dr. H. Knüpffer, Dr. K. Pistrick).

16. Juni 2010
Besuch von Vertretern des Landwirtschaftsministeriums Mecklenburg-Vorpommern, 3 Personen, Führung durch die Groß Lüsewitzer Kartoffel-Sortimente der IPK-Genbank (Dr. K.J. Dehmer, E. Willner).

16. Juni 2010
Besuch von Mitarbeitern des Pflanzenschutzdienstes Rostock mit Gästen des Plant Protection Directorats Serbien, 5 Personen, Führung durch die Groß Lüsewitzer Kartoffel-Sortimente der IPK-Genbank (Dr. K.J. Dehmer, U. Behrendt).

18. Juni 2010
Besuch von Mitarbeitern und Kunden einer Kartoffel-Vermarktungsgesellschaft, 45 Personen, Vorstellung der Groß Lüsewitzer Kartoffel-Sortimente der IPK-Genbank (Dr. K.J. Dehmer).

24. Juni 2010
Besuch des Genbank-Beirats, 7 Personen, Führung durch die Malchower Öl- und Futterpflanzen-Sortimente der IPK-Genbank, insbesondere QM-Standards, Genbankdokumentationssystem GBIS, Vermehrungs- und Versuchsanbau (E. Willner).

25. Juni 2010
Besuch des Genbank-Beirats, 7 Personen, Führung durch die Groß Lüsewitzer Kartoffel-Sortimente der IPK-Genbank, insbesondere *in vitro*-Kultur, Wildkartoffelvermehrung und Feldanbau (Dr. K.J. Dehmer, M. Angeli, U. Behrendt, K. Diekmann, K. Göhrke, M. Vandrey).

30. Juni 2010
Besuch vom Centre for Genetic Resources (CGN), Niederlande, 3 Personen, Vorstellung der Aufgaben der Genbank, Führungen der *In vitro*-Erhaltung und Kryokonservierung, Führung im Gewächshaus und Feldbesichtigung sowie Informationen über die Herbarsammlung und das Aufgabengebiet der Dokumentation (Priv.-Doz. Dr. A. Börner, Dr. J. Keller, Dr. A. Senula, Dr. U. Lohwasser, B. Schmidt, M.-L. Graichen, S. Thumm, M. Oppermann).

1. bis 2. Juli 2010
Workshop „Bestimmung von Schlafmohn und anderen Mohnarten", Kriminalämter der BRD, 10 Personen, Vorstellung der Aufgaben der Genbank, Forschung an Schlafmohn, Einführung der Mohnarten sowie Feldbesichtigung Mohnanbau, Führung durch die Genbank (Priv.-Doz. Dr. A. Börner, Dr. U. Lohwasser, R. Kurch).

4. Juli 2010
Besuch einer Gruppe ehemaliger Agraringenieure aus Berlin, 15 Personen, Führung durch die Malchower Sortimente für Öl- und Futterpflanzen der IPK-Genbank und Erläuterung der Arbeit einer Genbank (E. Willner).

7. Juli 2010
Besuch eines Kartoffelzüchters mit Mitarbeiterin, 2 Personen, Führung durch die Groß Lüsewitzer Kartoffel-Sortimente der IPK-Genbank (U. Behrendt).

7. Juli 2010
Besuch von Studenten der Martin-Luther-Universität Halle-Wittenberg, 5 Personen, Vorstellung des Instituts, Grüne Gentechnik, Besichtigung der Arbeitsgruppe Pflanzliche Reproduktionsbiologie (R. Schnee, Dr. J. Kumlehn).

9. Juli 2010
Besuch von Interessenten der BioTech Farm GmbH & Co. KG, Üplingen, 6 Personen, Vorstellung der Genbank, Freilandversuche, Rundgang durchs Institut (R. Schnee).

10. Juli 2010
Besuch von Vorstandsmitgliedern und Aufsichtsrat der Milchtrocknung Süd-Hannover (MTS), Sitz in Harbarnsen bei Hildesheim, 15 Personen, Vorstellung des Instituts und der Aufgaben der Genbank, Genbankführung sowie Feld- und Gewächshausführung (Priv.-Doz. Dr. A. Börner).

14. Juli 2010
Vertreter des Landwirtschaftsministeriums Mecklenburg-Vorpommern, 2 Personen, Führung durch die Malchower Öl- und Futterpflanzen-Sortimente der IPK-Genbank (Dr. K.J. Dehmer, E. Willner).

20. Juli 2010
Besucher der Landesgartenschau (LAGA), Aschersleben, 6 Personen, Darstellung der Aufgaben einer Genbank, Führung durch den Anbau des Hülsenfrüchtesortiments (Dr. U. Lohwasser, M. Kotter).

22. Juli 2010
Besuch von Mitgliedern des Wirtschaftsclubs Quedlinburg, 18 Personen, Vorstellung des Instituts, Genbankführung, Führung durch das Genomzentrum (Prof. Dr. A. Graner, Dr. U. Lohwasser, Dr. habil. L. Altschmied).

30. Juli 2010
Besuch des *WGL*-Präsidenten, Prof. Karl Ulrich Mayer, und seiner Referentin, Dr. Nicola Isendahl, Berlin, Vorstellung des Instituts, Vortrag „Grüne Gentechnik am IPK", Rundgang Genbank, Genomzentrum und Staudengarten, Abschlussdiskussion (Prof. Dr. A. Graner, Prof. Dr. I. Schubert, Prof. Dr. Th. Altmann, S.-A. Lorenz, Prof. Dr. F. Schreiber, Dr. F. Blattner, Dr. U. Lohwasser, Dr. habil. P. Schweizer, Dr. J. Kumlehn, R. Schnee, N. Schmid, M. Mau, L. Gerson, K. Menzel).

3. August 2010
Besuch von Lehrern aus Staßfurt, 60 Personen, Vorstellung des Instituts und der Aufgaben der Genbank, Führung durch die Genbank sowie Feld- und Staudengartenführung (Dr. U. Lohwasser, P. Schreiber, J. Marlow).

4. August 2010
Besuch des Lehrerkollegiums der Sekundarschule „Maxim Gorki", Schönebeck, 32 Personen, Vorstellung des Instituts, Besichtigung des Genomzentrums und der Lemnatec-Gewächshausanlage (Dr. habil. L. Altschmied, I. Mücke, R. Schnee).

5. August 2010
Besuch von Herrn Veit Wolpert, Landesvorsitzender der FDP-Fraktion Sachsen-Anhalt, in Begleitung eines Referenten, einem InnoPlanta-Mitarbeiter und zwei dpa-Journalisten, Vorstellung der Aufgaben der Genbank und anschließende Genbankführung (Dr. U. Lohwasser, R. Schnee).

5. August 2010
Gast aus Japan in der Ag Genomdiversität, Vorstellung der Aufgaben der Genbank und Genbankführung (Dr. U. Lohwasser).

17. August 2010
Besucher der Landesgartenschau (LAGA) Aschersleben, 17 Personen, Darstellung der Aufgaben einer Genbank, Führung durch den Anbau des Tomatensortiments (Dr. U. Lohwasser, B. Schmidt).

18. August 2010
Besuch von Frau Prof. Dr. Ulla Bonas, MLU Halle-Wittenberg, Vorstellung der Aufgaben der Genbank und Genbankführung (Priv.-Doz. Dr. A. Börner).

23. bis 27. August 2010
Besuch von Frau L. Stimolo, Genbank Bari, Italien, Einführung in die Aufgaben der Genbank, Vorstellung des Genbankinformationssystems (GBIS) und Genbankdokumentation, Erläuterung des Qualitätsmanagementsystems der Genbank, Besichtigung der Herbar- und Samensammlung, Erläuterung der *in vitro*-Erhaltung und Kryokonservierung, Führung im Gewächshaus und auf dem Feld, Durchführung der Charakterisierung der Kürbiskollektion sowie ein Abschlussgespräch (Priv.-Doz. Dr. A. Börner, Dr. U. Lohwasser, Dr. K. Pistrick, Dr. C. Zanke, M. Oppermann, B. Schmidt).

23. August 2010
Auszubildende des Julius Kühn-Instituts Groß Lüsewitz, 7 Personen, Führung durch die Groß Lüsewitzer Kartoffel-Sortimente der IPK-Genbank (U. Behrendt, K. Göhrke, M. Vandrey).

28. August 2010
Exkursion der EGF-Tagung (European Grass Foundation), Kiel, 44 Personen, Führung durch die Malchower Sortimente für Öl- und Futterpflanzen der IPK-Genbank und Erläuterung der Arbeit einer Genbank (K. Ploen, E. Willner).

3. September 2010
Besuch von Mitarbeitern der Ag Heterosis des IPK, 12 Personen, Führung durch die Sortimente für Öl- und Futterpflanzen der IPK-Genbank und Erläuterung der Arbeit der Teilsammlungen Nord mit Schwerpunkt Ölpflanzen (K. Ploen, E. Willner).

6. September 2010
Besuch von russischen Wirtschaftsvertretern, Organisation über die Deutsche Management Akademie Niedersachsen, Celle, 18 Personen, Vorstellung des Instituts, Campusrundgang, Genbankbesichtigung, Besichtigung der Gewächshäuser Genetik und am Genomzentrum (R. Schnee).

7. September 2010
Besucher der Landesgartenschau (LAGA) Aschersleben, 25 Personen, Darstellung der Aufgaben einer Genbank, Führung im Dauergarten des Kräutersortiments (Priv.-Doz. Dr. A. Börner, R. Kurch).

8. September 2010
Besucher aus dem Institut für Spezielle Zoologie und Evolutionsbiologie, Jena, 8 Personen, Vorstellung des Instituts und der Genbank mit anschließender Führung, Vorstellung der taxonomischen Sammlungen in Vorbereitung der Sonderausstellung „Domestikation" des Phyletischen Museums (Priv.-Doz. Dr. A. Börner, Dr. K. Pistrick, M. Grau).

11. September 2010
Besuch von Mitgliedern der Freiwilligen Feuerwehr Grimma, 40 Personen, Vorstellung des Instituts und der Genbank mit anschließender Führung sowie eine Feld- und Gewächshausführung (Priv.-Doz. Dr. A. Börner).

15. September 2010
Besuch von Mitgliedern des Bundesverbandes für Teilnehmergemeinschaften e.V. (BTG), Schönebeck, 67 Personen, Vorstellung des Instituts, Bewahrung von Pflanzenschätzen, Erfassung pflanzlicher Merkmale „am laufenden Band" (R. Schnee, Dr. C. Klukas, I. Mücke).

21. September 2010
Besucher der Landesgartenschau (LAGA), Aschersleben, 25 Personen, Darstellung der Aufgaben einer Genbank, Führung durch den Anbau des Kürbissortiments (Dr. U. Lohwasser, B. Schmidt).

22. September 2010
Besuch von Mitgliedern des Vereins der Freunde des Märkischen Ausstellungs- und Freizeitzentrums (MAFZ), 26 Personen, Vorstellung der Aufgaben der Genbank und anschließende Genbankführung sowie eine Feld- und Gewächshausführung (Priv.-Doz. Dr. A. Börner).

27. September 2010
Besuch von Auszubildenden als landwirtschaftlich-technische Angestellte der Fachschule Lüneburg, 22 Personen, Vorstellung des Instituts, Genbankführung, Demonstration der Variabilität von Kulturpflanzen im Herbarium sowie in der Ähren- und Früchtesammlung, Variabilität in den Gewächshäusern der Genbank (R. Schnee, Dr. U. Lohwasser, Dr. K. Pistrick, J. Marlow).

28./29. September 2010
Besuch einer Schülergruppe der Freien Schule Neinstedt, 12 Personen, Einführende Erläuterungen zu den Grundlagen der Dokumentation von Pflanzenmaterial in Botanischen Vergleichssammlungen (Dr. K. Pistrick).

2. Oktober 2010
Besuch von Mitgliedern des Lions Club, Bad Driburg, 42 Personen, Vorstellung des Instituts und der Aufgaben der Genbank, Genbankführung, Variabilität in den Gewächshäusern der Genbank und im Tropenhaus, Molecular Ph(F)arming – eine Chance für die Landwirtschaft der Zukunft? (Priv.-Doz. Dr. A. Börner, Priv.-Doz. Dr. U. Conrad, J. Marlow).

7. Oktober 2010
Besuch von Wissenschaftlern der UC Davis, USA, 2 Personen, Vorstellung des Instituts und der Aufgaben der Genbank, anschließende Genbankführung (Prof. Dr. A. Graner, Priv.-Doz. Dr. A. Börner).

7. Oktober 2010
Besuch von Schülern der 3. und 4. Klassen der Grundschule Sanitz, ca. 80 Personen, Führung durch die Groß Lüsewitzer Kartoffel-Sortimente der IPK-Genbank (U. Behrendt, K. Göhrke).

12. Oktober 2010
Führung durch die Groß Lüsewitzer Kartoffel-Sortimente der IPK-Genbank für Kartoffel-Interessenten, 2 Personen (U. Behrendt, K. Göhrke, S. Pelikan).

13. Oktober 2010
Besuch von Teilnehmern des 1. Vergabekongresses Sachsen-Anhalt, 40 Personen, Vorstellung der Aufgaben der Genbank und Genbankführung, Warum Frost für Pflanzensamen gut ist, Bestimmung von Pflanzen: der Nutzen von Herbar-Sammlungen, Reise ins Innere der Pflanzen (Priv.-Doz. Dr. A. Börner, Dr. K. Pistrick, Dr. M. Melzer).

20. Oktober 2010
Besuch von Prof. F. Corbineau, Pierre und Marie Curie-Universität Paris, Besichtigung der Botanischen Vergleichssammlungen (Dr. K. Pistrick).

21. Oktober 2010
Teilnehmer am Begleitprogramm anlässlich der Jahreskonferenz der Ministerpräsidentinnen und Ministerpräsidenten der deutschen Bundesländer in Magdeburg, 7 Personen, Vorstellung des Instituts, Rundgang auf dem Gelände des IPK und Besichtigung der LemnaTec-Anlage im Gewächshaus der Genetik, Besichtigung der Kühllager der Bundeszentralen *Ex-situ*-Genbank für landwirtschaftliche und gartenbauliche Kulturpflanzen, Samenaufbereitung in der Genbank (R. Schnee, Priv.-Doz. Dr. A. Börner).

22. Oktober 2010
Besuch von australischen Kartoffelzüchtern, 2 Personen, Führung durch die Groß Lüsewitzer Kartoffel-Sortimente der IPK-Genbank (Dr. K.J. Dehmer).

26. Oktober 2010
Besuch von kubanischen Kartoffelzüchtern als Gäste der Agrar- und Umweltwissenschaftlichen Fakultät der Universität Rostock, 3 Personen, Führung durch die Groß Lüsewitzer Kartoffel-Sortimente der IPK-Genbank (Dr. K.J. Dehmer).

2. bis 4. November 2010
Besuch von Frau M. Stein, Head of the Evogene Seed Bank, Israel, Vorstellung der Aufgaben der Genbank und anschließende Genbankführung, Gespräche mit den Sortimentsgruppen, Informationen über das GBIS-System, *in vitro*-Erhaltung, Kryolagerung, Herbarium, Gewächshaus und Qualitätsmanagement (Priv.-Doz. Dr. A. Börner, K. Krusch, K. Bollmann, M. Oppermann, D. Dittmann, Dr. J. Keller, Dr. K. Pistrick, J. Marlow, Dr. U. Lohwasser).

8. November 2010
Besuch von Studenten des Studiengangs Agrarökologie der Universität Rostock, 6 Personen, Führung durch die Groß Lüsewitzer Kartoffel-Sortimente der IPK-Genbank (Dr. K. J. Dehmer).

10. November 2010
Besuch einer Delegation von Wissenschaftlern aus dem Königreich Jordanien, 5 Personen, Vorstellung des Instituts, Vorstellung der Forschungsinteressen der jordanischen Delegation, Diskussion möglicher Kooperationsthemen zur Saat- und Pflanzenzucht, Institutsbesichtigung (Prof. Dr. I. Schubert, Prof. Dr. G. Kunze, Dr. N. Sreenivasulu, Dr. T. Schnurbusch, Ahmad M. Alqudah, Dr. B. Kilian, R. Schnee).

11. November 2010
Besuch vom Bundessortenamt Hannover, 3 Personen, Vorstellung der Aufgaben der Genbank und Genbankführung (Priv.-Doz. Dr. A. Börner, Dr. U. Lohwasser, M. Oppermann, M. Kotter).

11. November 2010
Besuch von Schülern der 9. Klasse der ecolea, Internationale Schule Warnemünde, 25 Personen, Führung durch die Groß Lüsewitzer Kartoffel-Sortimente der IPK-Genbank (Dr. K.J. Dehmer, U. Behrendt, K. Göhrke).

12. und 18. November 2010
Besuch von Schülern anlässlich der Berufsorientierungstage des Grünen Labors Gatersleben, 40 Personen, Führung und leichte Arbeiten im Gewächshaus der Genbank, Analyse gesundheitsförderlicher Pflanzeninhaltsstoffe (J. Marlow, A. Dittbrenner).

18. November 2010
Besuch einer Seminargruppe für ein Freiwilliges Ökologisches Jahr (FÖJ), Jugendwerk Aufbau Ost e.V., Berlin, 30 Personen, Vorstellung des Instituts, Biodiversität in der Genbank, Genbankführung, Grüne Gentechnik, Nährstoffeffizienzuntersuchungen (R. Schnee, Priv.-Doz. Dr. A. Börner, Dr. J. Kumlehn, Prof. Dr. N. von Wirén).

18. November 2010
Besuch von Dr. J.P. Sampoux, Leiter der Futterpflanzengenbank des INRA-Instituts Lusignan, Frankreich, Führung durch die Malchower Öl- und Futterpflanzen-Sortimente der IPK-Genbank und anschließende Kooperationsabsprachen für 2011 (S. Nehrlich, E. Willner).

25. November 2010
Besuch einer Studentengruppe der Martin-Luther-Universität Halle-Wittenberg, 5 Personen, Vorstellung des Instituts, Besichtigung der Genbank und Campus-Führung (R. Schnee).

6. Dezember 2010
Besuch von Frau Heike Brehmer, Mitglied des Deutschen Bundestages, und Herrn Detlef Gürth, CDU-Fraktion im Landtag von Sachsen-Anhalt, Vorstellung des Instituts, Genom-basierte Ansätze in der Getreidezüchtung? Die Gerste-Genomsequenz ist in Sicht, Klimawandel und Ressourcenverknappung als Herausforderung für die Pflanzenzüchtung: Das Beispiel Hybridweizen, Rundgang und Besichtigung der LemnaTec-Anlage, Sequenzierung (Prof. Dr. Th. Altmann, Dr. N. Stein, Dr. M. Gils, R. Schnee).

14. Dezember 2010
Besuch von Studenten der Hochschule Bremen, 45 Personen, Vorstellung des Instituts sowie der Aufgaben der Genbank, Vortrag zu den Arbeiten der Taxonomie am IPK, Besichtigung der Herbar- und Samensammlung einschließlich des Samenkühllagers, Gewächshausbesichtigung (Priv.-Doz. Dr. A. Börner, Dr. F. Blattner, Dr. K. Pistrick, J. Marlow).

15. Dezember 2010
Besuch von Studenten der Fachhochschule Südwestfalen, Fachbereich Agrarwirtschaft, Soest, 15 Personen, Vorstellung des Instituts, Anwendung von Assoziationskartierung zur Verbesserung der Malzqualität bei Gerstensorten, Was ist Epigenetik?, anschließende Besichtigung der Ag Epigenetik mit einem „Blitzversuch" der GUS-Reportergenexpression, Führung durch die Kühlräume der Genbank, Vorstellung der *In vitro*-Erhaltung der Genbank (R. Schnee, Dr. M. Röder, Dr. M.F. Mette, Priv.-Doz. Dr. A. Börner, Dr. Ch. Zanke).

16. Dezember 2010
Besuch der Universität Florenz, Italien, Bereich Landwirtschaft und Pflanzengenetik, 6 Personen, Vorstellung des Instituts und der Genbank mit anschließender Besichtigung, Vorstellung der *In vitro*-Erhaltung und Besichtigung der Herbar- und Samensammlung (R. Schnee, Priv.-Doz. Dr. A. Börner, Dr. J. Keller, Dr. K. Pistrick).

2011

20. Januar 2011
Besuch von Herrn C. Ullrich im Rahmen eines Schülerpraktikums, Zarrendorf, Führung durch die Malchower Öl- und Futterpflanzen-Sortimente der IPK-Genbank (S. Nehrlich).

31. Januar 2011
Besuch von Studenten der Hochschule für Technik und Wirtschaft (HTW), Dresden, 10 Personen, Vorstellung des Instituts und der Genbank, Langzeitlagerung von Saatgut mit anschließender Führung durch die Genbank, *In vitro*-Erhaltung und Kryo-Lagerung, Führung durch die Gewächshäuser der Genbank (Dr. U. Lohwasser, Dr. J. Keller, J. Marlow).

3. Februar 2011
Besuch einer norwegischen Aktionskünstlerin, Führung durch die Groß Lüsewitzer Kartoffel-Sortimente der IPK-Genbank (U. Behrendt, K.J. Dehmer, K. Göhrke).

8. Februar 2011
Besuch von Schülern der 1. bis 4. Klasse der Grundschule Gatersleben (Hortkinder), 20 Personen, Führung durch die Genbank, Samenkühllager, Dreschhalle und durch die Gewächshäuser der Genbank (R. Schnee, J. Marlow).

10. Februar 2011
Besuch der Ministerin Prof. Birgitta Wolff in Begleitung von Herrn Detlef Gürth (CDU), MdL Sachsen-Anhalt, Vorstellung des Instituts, allgemeine Diskussion mit den Mitgliedern des Direktoriums, Vorführung der Mais-Pflanzenphänotypisierungsanlage (Prof. A. Graner, Prof. I. Schubert, Prof. T. Altmann, Prof. N. von Wirén, S.-A. Lorenz, R. Schnee).

1. März 2011
Genbankführung für Dr. Bu-Jun Shi aus Adelaide, Australien (Dr. U. Lohwasser).

2. März 2011
Besuch von Teilnehmern einer Lehrerfortbildung, 21 Personen, Vorstellung sowie Führung durch die Groß Lüsewitzer Kartoffel-Sortimente der IPK-Genbank (U. Behrendt).

14. März 2011
Führung durch die Genbank für Prof. Director Dr. Qifa Zhang, Wuhan, China (Priv.-Doz. Dr. A. Börner).

16. März 2011
Besuch von Studenten der Universität Kiel, 6 Personen, Vorstellung des Instituts und Aufgaben der Genbank, Keimfähigkeit, Saatgutaufreinigung/Ernteerfassung/Erntekontrolle mit Herbar und Samensammlung, Führung durch die Genbank (Dr. U. Lohwasser, C. Dittmann, S. Pistrick, A. Winger, M. Kotter, S. Schmidt, B. Harke, B. Schmidt. S. Eickmeier).

18. März 2011
Besuch von Schülern der Takefu High Super Highschool, Fukui, Japan, 20 Personen, Vorstellung des Instituts, Strategien zur Verbesserung der pflanzlichen Ernährung, Führung durch die Genbank und Gewächshäuser, Vorführung der automatischen Anlage zur Merkmalserfassung in Pflanzen (Prof. N. von Wirén, R. Schnee).

24. März 2011
Besuch von MinDirig'in Petra Steiner-Hoffmann, Frau Dr. Claudia Herok und Dr. Henk van Liempt vom BMBF sowie MinRat Thomas Reitmann und Frau Gisela Liepelt vom Kultusministerium des Landes Sachsen-Anhalt, Vorstellung des Instituts, Diskussionen zur Genomsequenzierung, Genidentifizierung mittels quantitativer genetischer Methoden, Analyse biologischer Prozesse/Genidentifizierung mittels systembiologischer Verfahren am Beispiel Samenfüllung, Charakterisierung von Genbankmaterial, Erfahrungen und Stand der Entwicklung der Pflanzenphänotypisierung am IPK, Zielstellungen der IPK-Beteiligung am DPPN, Deutsches Innovations-Netz zur Erschließung und Nutzung Pflanzengenetischer Ressourcen für die BioÖkonomie, Besichtigung der Kulturpflanzenbank, Labor: Biochemische Analytik, Sequenzierung, Vorführung Mais-Pflanzenphänotypisierungsanlage (Prof. Dr. A. Graner, Prof. Dr. I. Schubert, Prof. Dr. T. Altmann, Prof. Dr. N. von Wirén, Dr. P. Schweizer, Dr. N. Stein, Dr. M. Röder, Dr. W. Weschke, R. Schnee).

31. März 2011
Besuch der ECPGR Umbellifer Working Group, 15 Personen, Vorstellung des Instituts, Besichtigung der Genbank und der Herbar-, Ähren- und Fruchtsammlung, *In vitro*-Erhaltung und Cryo-Lagerung sowie der LemnaTec-Anlage und der Gewächshäuser (Priv.-Doz. Dr. A. Börner, Dr. U. Lohwasser, Dr. J. Keller, Dr. K. Pistrick, M. Oppermann, P. Schreiber, J. Marlow).

6. April 2011
Besuch von Mitarbeitern des Pfarrkonvents Salzlandkreis, 15 Personen, Vorstellung des Instituts, Diskussion zur Geschichte des IPK, zur Molekulargenetik und insbesondere zur Grünen Gentechnik (Prof. U. Wobus, R. Schnee).

8. April 2011
Besuch von Schülern der 9. Klasse der Prof. Hans Lembke-Schule, Kirchdorf, 16 Personen, Vorstellung des Instituts, Führung durch die Malchower Öl- und Futterpflanzensortimente der IPK-Genbank (S. Nehrlich).

20. April 2011
Besuch der Mitglieder des VERN, Boitzenburger Land, 4 Personen, Begrüßung und Führung durch die Groß Lüsewitzer Kartoffel-Sortimente der IPK-Genbank (U. Behrendt).

28. April 2011
Besuch von Schülern der 6. Klasse der Prof. Hans Lembke-Schule, Kirchdorf, 24 Personen, Begrüßung und Führung durch die Malchower Öl- und Futterpflanzensortimente der IPK-Genbank (S. Nehrlich).

29. April 2011
Besuch von rumänischen und deutschen Studenten im Rahmen eines Seminars „Jugendliche entdecken die Zukunft der Landwirtschaft in der EU", 15 Personen, Vorstellung des Instituts, Ährenmutationen und erhöhter Ertrag, Führung durch die Pflanzen-Samenbank, Besichtigung der LemnaTec-Anlage und der Feldflächen (R. Schnee, T. Seidensticker).

3. Mai 2011
Besuch von Absolventen, Wolfen, 11 Personen, Vorstellung des Instituts, Diskussion zur Geschichte des IPK, zur Molekulargenetik und insbesondere zur Grünen Gentechnik (R. Schnee).

4. Mai 2011
Besuch von Agraringenieurstudenten der Fachhochschule Kiel, 22 Personen, Vorstellung des Instituts, Identifizierung von Markern für den Einsatz in Kreuzungen, Genbankführung, Besichtigung der Herbar-, Ähren- und Fruchtsammlung als Vergleichsbasis für die Bestimmung von pflanzengenetischen Ressourcen (Dr. S. Kollers, Dr. U. Lohwasser, Dr. K. Pistrick, R. Schnee).

7. Mai 2011
Besuch von Wasserbauingenieuren, 50 Personen, Vorstellung des Instituts, Führung durch die Genbank und Rundgang im IPK (R. Schnee).

11. Mai 2011
Besuch der ehemaligen Leiterin Hella Brumme des Rosariums Sangerhausen mit Lehr- und Studienkollegen, 10 Personen, Vorstellung des Instituts und der Genbank, Führung durch den Staudengarten (B. Schütze, R. Schnee).

11. Mai 2011
Besucher eines Arbeitstreffens zum Projekt triploide Kamille, Vorstellung des Instituts und der Aufgaben der Genbank mit anschließender Genbankführung (Priv.-Doz. Dr. A. Börner).

17. Mai 2011
Besuch von Frau Prof. Dr. Chris-Carolin Schön, LMU München, Vorstellung der Aufgaben der Genbank mit anschließender Genbankführung (Priv.-Doz. Dr. A. Börner).

17. Mai 2011
Besuch von Mitgliedern des Plattdeutschen Vereins, Schwerin, 30 Personen, Vorstellung des Instituts, Führung durch die Malchower Öl- und Futterpflanzensortimente der IPK-Genbank (S. Nehrlich, E. Willner).

19. Mai 2011
Besuch einer Delegation aus Südkorea, 20 Personen, Vorstellung des Instituts, Besichtigung der Genbank, Rundgang durch Labore und Gewächshäuser (Priv.-Doz. Dr. A. Börner, R. Schnee).

20. Mai 2011
Besuch von Studenten der Universität Rostock, Agrar- und Umweltwissenschaftliche Fakultät/Agrobiotechnologie, 10 Personen, Führung durch die Groß Lüsewitzer Kartoffelsortimente der IPK-Genbank (Dr. K.J. Dehmer).

3. Juni 2011
Besuch von Mitgliedern des Rotary Club München, 15 Personen, Vorstellung des Instituts und der Aufgaben der Genbank, Führung durch das Genomzentrum und die Genbank (Prof. A. Graner, Dr. habil. P. Schweizer, Priv.-Doz. Dr. A. Börner).

6. Juni 2011
Besuch von Schülern der 10. Klasse des Christophorus-Gymnasiums Rostock, 17 Personen, Aufgaben der Groß Lüsewitzer Kartoffelsortimente der IPK-Genbank mit anschließender Führung (Dr. K.J. Dehmer).

6.-9. Juni 2011
Besuch von Dr. Grzegorz Gryziak, Gene Bank Manager, National Center for Plant Genetic Resources, Radzików, Polen, Vorstellung der Aufgaben der Genbank, Informationen über die Aufgaben der Ag Genbankdokumentation und der *In vitro*-Erhaltung und Cryo-Lagerung. Beseitigung der Herbar- und Samensammlung mit anschließender Genbankführung, Besichtigung LemnaTec-Anlage und Gewächshaus (Priv.-Doz. Dr. A. Börner, P. Schreiber, Dr. J. Keller, Dr. K. Pistrick, Dr. H. Knüpffer, M. Oppermann, C. Dittmann, J. Marlow, K. Krusch, K. Bollmann, M.A. Rehman Arif).

7. Juni 2011
Besuch von Kartoffelanbauern aus dem Kreis Kleve, 20 Personen, Aufgaben der Groß Lüsewitzer Kartoffelsortimente der IPK-Genbank mit anschließender Führung (Dr. K.J. Dehmer).

8. Juni 2011
Besuch von Bürgermeistern aus Sachsen-Anhalt, 25 Personen, Vorstellung des Instituts, Führung durch die Genbank und Besichtigung der Freiflächen (P. Schreiber, R. Schnee).

15. Juni 2011
Besuch von Studenten der Universität Gießen, 30 Personen, Führung durch die Botanischen Vergleichssammlungen der Genbank, Erhaltung und Nutzbarmachung pflanzengenetischer Ressourcen für künftige Pflanzenzüchtung, Assoziationsgenetik für Züchtung von Malzqualität bei Gerste, Feldführung (Dr. K. Pistrick, Priv.-Doz. Dr. A. Börner, Dr. M. Röder).

16. Juni 2011
Besuch von Studenten der Universität Hohenheim, 25 Personen, Vorstellung der Aufgaben der Genbank, Informationen über die Aufgaben der Ag Genbankdokumentation und der *In vitro*-Erhaltung und Cryo-Lagerung, Führung durch die Herbar-Sammlungen und durch die Vermehrungsbestände der Genbank (Priv.-Doz. Dr. A. Börner, Dr. H. Knüpffer, Dr. J. Keller, Dr. K. Pistrick, P. Schreiber).

16. Juni 2011
Besuch von Studenten der TU Dresden, 34 Personen, Vorstellung des Instituts und Rundgang auf dem Gelände, Besichtigung der Kulturpflanzenbank und Führung durch die Labore der Ag Hefegenetik (Prof. G. Kunze, R. Schnee).

17. Juni 2011
Besuch von Staatssekretär Marco Tullner, Ministerium für Wissenschaft und Wirtschaft des Landes Sachsen-Anhalt, Vorstellung des Instituts, Gespräch mit den Mitgliedern des Direktoriums, Besichtigung LemnaTec-Anlage (Prof. A. Graner, Prof. T. Altmann, Prof. I. Schubert, Prof. N. von Wirén, S.-A. Lorenz, K. Neumann, R. Schnee).

21. Juni 2011
Besuch von Studenten der Fachhochschule Wismar, Umwelt- und Verfahrenstechnik, 17 Personen, Führung durch die Malchower Öl- und Futterpflanzensortimente der IPK-Genbank (S. Nehrlich, K. Ploen).

23. Juni 2011
Besuch von Geisenheimer Gartenbaustudenten, 12 Personen, Vorstellung des Instituts und der Aufgaben der Genbank, Besichtigung des Samenkühllagers und der Herbar- und Samensammlung, Erläuterung der *In vitro*-Erhaltung und Cryo-Konservierung, Feldführung (Priv.-Doz. Dr. A. Börner, Dr. K. Pistrick, Dr. J. Keller, P. Schreiber).

23. Juni 2011
Besuch von Studenten der Berlin-Brandenburg School for Regenerative Therapies (BSRT), 21 Personen, Production of antibodies in plants, Introduction of IPK and tour through seedbank, Plant evolution in time and space, Epigenetics in plants, Metabolomics and Iron acquisition, and transport in plants (Priv.-Doz. Dr. U. Conrad, N. Nürk, A. Finke, T. Liiving, M. Franke, N. Schmid, R. Schnee).

27. Juni 2011
Besuch von Mitarbeitern der Ag Teilsammlungen Nord, Groß Lüsewitz und Malchow, 20 Personen, Besichtigung der Genbank, Feld- und Gewächshausführung, Besichtigung der LemnaTec-Anlage (Priv.-Doz. Dr. A. Börner, Dr. A. Senula, P. Schreiber).

29. Juni 2011
Besuch von Kindern des Hortes Immenhus Tessin, 23 Personen, Aufgaben der Groß Lüsewitzer Kartoffelsortimente der IPK-Genbank und anschließende Führung (U. Behrendt).

1. Juli 2011
Besuch einer Delegation der Academy of Agricultural Sciences, Nordkorea, 16 Personen, Vorstellung des Instituts und der Genbank, Führung durch das Samenkühllager, Vorstellung der Arbeit mit dem GBIS-System, Besichtigung der Vermehrungsflächen (Priv.-Doz. Dr. A. Börner, Dr. H. Knüpffer, M. Oppermann, P. Schreiber, R. Schnee).

1. Juli 2011
Besucher aus China, Afrika und Österreich vom Projekt Reichenstraße, Quedlinburg, 6 Personen, Vorstellung des Instituts, Besichtigung der Genbank, Forschung an resistentem Weizen (R. Schnee, Dr. N. Sreenivasulu).

4. Juli 2011
Besuch von Studenten der Universität Kassel-Witzenhausen, 6 Personen, Aufgaben der Groß Lüsewitzer Kartoffelsortimente der IPK-Genbank und anschließende Führung (Dr. K.J. Dehmer, M. Vandrey).

8. Juli 2011
Besuch von Dr. Günter Welz und Dr. Marcus Weidler, Bayer CropScience, Führung durch die Kulturpflanzenbank, Feldführung (Priv.-Doz. Dr. A. Börner, P. Schreiber).

8. Juli 2011
Besuch von Anbauberatern der Landwirtschaftskammer NRW, 30 Personen, Vorstellung des Instituts, Führung durch die Genbank und die taxonomischen Sammlungen, Feldführung (R. Schnee, P. Schreiber, M. Grau).

8. Juli 2011
Besuch von Weizenzüchtern, Institute of Food Crops, Jiangsu Academy of Agricultural Sciences, Nanjing, China, 3 Personen, Vorstellung der Aufgaben der Genbank mit anschließender Feldführung im Getreidesortiment (M. Grau).

25.-29. Juli 2011
Besuch von S. Fourtier, Mitarbeiter der Futterpflanzengenbank des INRA-Instituts Lusignan, Frankreich, Führung durch die Malchower Öl- und Futterpflanzensortimente der IPK-Genbank, Kooperationsabsprachen für 2011/2012 (S. Nehrlich, K. Ploen, E. Willner).

28. Juli 2011
Besuch von Mitarbeitern der Fa. Saaten-Union, 20 Personen, Vorstellung der Genbank und Führung, Besichtigungen Samenkühllager, Herbar- und Samensammlung (Priv.-Doz. Dr. A. Börner, Dr. K. Pistrick).

1. August 2011
Besuch von vietnamesischen Gastwissenschaftlern des JKI, 2 Personen, Führung durch die Groß Lüsewitzer Kartoffelsortimente der IPK-Genbank und Erläuterung ihrer Aufgaben (U. Behrendt, K. Diekmann).

11. August 2011
Besuch eines Wissenschaftlers der BOKU Wien, Führung durch die Groß Lüsewitzer Kartoffelsortimente der IPK-Genbank und Erläuterung ihrer Aufgaben (K. Diekmann).

3. September 2011
Besuch im Rahmen eines Klassentreffens von Dr. H. Lellbach, 8 Personen, Diedrichshagen, Führung durch die Malchower Öl- und Futterpflanzensortimente der IPK-Genbank und Erläuterung (E. Willner).

3. September 2011
Besuch von Mitgliedern des Landfrauenvereins Glasin, 15 Personen, Führung durch die Malchower Öl- und Futterpflanzensortimente der IPK-Genbank und Erläuterung (E. Willner).

5. September 2011
Besuch von Landwirten aus der oberbayerischen Region des Planungs- und Ausführungsbüros für angewandte Chaosforschung, Quantentechnologie, Geomantie und Galabau aus Baldhalm, 4 Personen, Vorstellung des Instituts und der Aufgaben der Genbank, Führung durch die Genbank und die Außenflächen (Dr. U. Lohwasser).

14. September 2011
Besuch von Lehrern im Rahmen einer themengebundenen Lehrerfortbildung des Landesinstituts für Schulqualität und Lehrerbildung Sachsen-Anhalt, Halle/S., 30 Personen, Gewächshaus-Rundgang: technische Lösungen für die Pflanzenforschung, Genbank-Führung, Besichtigung Staudengarten (Priv.-Doz. Dr. A. Börner, E. Geyer).

15. September 2011
Besuch von zwei 9. Klassen des Weinberggymnasiums Kleinmachnow, 30 Personen, Führung durch die Groß Lüsewitzer Kartoffelsortimente der IPK-Genbank und Erläuterung der Aufgaben (Dr. K.J. Dehmer).

16. September 2011
Besuch von Mitarbeitern der Mitteldeutschen Baumschulen, Reinstedt, 6 Personen, Vorstellung des Instituts, Rundgang Gewächshauskomplex Genetik und Gelände, Führung durch die Genbank: Herbar-, Ähren- und Samensammlung, Samenkühllager (R. Schnee).

24. September 2011
Besichtigung der Botanischen Vergleichssammlungen durch S. Jantassov, Kaskh Research Institute of Potato and Vegetable Production (Dr. K. Pistrick).

27. September 2011
Besuch von Fachschullehrern aus China, 7 Personen, Vorstellung des Instituts, Ug99 – Globalisierte Gefahr, Führung Genbank – insbesondere Weizenkollektion (Dr. M. Röder, Priv.-Doz. Dr. A. Börner, R. Schnee).

27. September 2011
Besuch von Mitgliedern des Landwirtschaftsausschusses im Landtag von Südtirol, 10 Personen, Vorstellung des Instituts, Grundlagen der Gentechnik, Neue Ansätze zur Züchtung ertragreicherer Weizensorten, Führung durch die Genbank (Dr. J. Kumlehn, R. Schnee).

28. September 2011
Besuch von Mitarbeitern der Justizbehörden des Landes Sachsen-Anhalt, 10 Personen, Vorstellung des Instituts, Rundgang: Campus, Felder, Genbank, Labore, Gewächshaus PGRC (R. Schnee).

28. September 2011
Besuch im Rahmen eines Klassentreffens von G. Bachler, Niendorf, 10 Personen, Führung durch die Malchower Öl- und Futterpflanzensortimente der IPK-Genbank (V. Miehe).

28.-29. September 2011
Besuch einer Mitarbeiterin des National Agriculture Institute Kairo, Ägypten, Führung durch die Malchower Öl- und Futterpflanzensortimente der IPK-Genbank (S. Nehrlich, E. Willner).

29. September 2011
Besuch von Dr. Fransisca Tan, CEO Gudang Garam, Indonesia-based cigarette producer, 2 Personen, Vorstellung des Instituts, Besichtigung der Gewächshausanlagen und Labore, Führung durch die Genbank (R. Schnee).

4.-6. Oktober 2011
Besuch von drei 4. Klassen der Grundschule „John Brinckman", Rostock, ca. 70 Personen, Vorstellungen und Führung der Groß Lüsewitzer Kartoffelsortimente der IPK-Genbank (U. Behrendt, K. Göhrke, K. Löschner, M. Vandrey).

6. Oktober 2011
Besuch von Mitarbeitern des Instituts für Geobotanik, Halle/S., 2 Personen, Vorstellung der Aufgaben der Genbank und der Arbeitsgruppe Experimentelle Taxonomie, Besichtigungen des Samenkühllagers und der Herbar- und Samensammlung (Dr. F. Blattner, Dr. U. Lohwasser).

10. Oktober 2011
Besuch von Studenten der Hochschule Bremen, 30 Personen, Vorstellung des Instituts und der Aufgaben der Genbank, Vortrag zu den Arbeiten der Taxonomie am IPK, Besichtigung der Herbar- und Samensammlung, Samenkühllager sowie Gewächshausbesichtigung (Priv.-Doz. Dr. A. Börner, Dr. F. Blattner, Dr. K. Pistrick, J. Marlow).

13. Oktober 2011
Besuch von Dr. Mirzaei, Dr. Jafari und Dr. Ashani, Research Institute for Forest and Rangelands Teheran, Iran, 4 Personen, Vorstellung des Instituts, Besichtigung der Genbank und der Botanischen Vergleichssammlungen, *In vitro*-Erhaltung und Cryo-Lagerung (Prof. Dr. A. Graner, Dr. K. Pistrick, Dr. J. Keller, R. Kurch, R. Schnee).

20. Oktober 2011
Besuch einer Praktikantin der NPZ, Führung durch die Malchower Öl- und Futterpflanzensortimente der IPK-Genbank (E. Willner).

26. Oktober 2011
Vorlesung für Mitarbeiter des IPK im Rahmen der Innerbetrieblichen Qualifizierung: „Sequenziertechniken: Methodische Grundlagen, aktuelle Anwendungen und zukünftige Entwicklungen" (Dr. L. Altschmied).

3. November 2011
Besuch von Schülerinnen im Rahmen einer Ausbildung zur biologisch-technischen Assistentin, Bad Berleburg, 2 Personen, Vorstellung des Instituts und der Arbeitsgruppe Phytoantikörper, Spinnenseidenproteine (R. Schnee, N. Weichert).

9. November 2011
Besuch von Studenten der Otto-von-Guericke-Universität Magdeburg, Fachrichtung Biosystemtechnik, 14 Personen, Vorstellung des Instituts und der Arbeitsgruppe Systembiologie, Führung durch die Genbank, die Gewächshäuser am Genomzentrum und die Genetik (Dr. B. Junker, R. Schnee).

18. und 25. November 2011
Besucher des Freiwilligen Ökologischen Jahres (FÖJ), Jugendwerk Aufbau Ost e.V., Berlin, je 30 Personen, Vorstellung des Instituts, Biodiversität in der Genbank, Grüne Gentechnik, (Priv.-Doz. Dr. A. Börner, Dr. G. Hensel, Dr. J. Kumlehn, R. Schnee).

22. November 2011
Besucher im Rahmen des Berufsorientierungstages des Grünen Labors, Gatersleben, 7 Personen, Gewächshausrundgang (E. Geyer).

1. Dezember 2011
Besuch von Schülern des John-Brinckman-Gymnasiums, Güstrow, 16 Personen, Führung durch die Groß Lüsewitzer Kartoffelsortimente der IPK-Genbank (U. Behrendt, M. Vandrey).

8. Dezember 2011
Besuch von Schülern des Käthe-Kollwitz-Gymnasiums, Rostock, 15 Personen, Führung durch die Groß Lüsewitzer Kartoffelsortimente der IPK-Genbank (U. Behrendt, Dr. K.J. Dehmer).

14. Dezember 2011
Besuch von Studenten des Kurses „Bioethik" der Martin-Luther-Universität, Halle/S., 15 Personen, Rundgang durch das Institut, Einführung zur Anwendung von Gewebekulturen in der Pflanzenanzucht, Grüne Gentechnik, Rundgang durch Labore der Arbeitsgruppen *In vitro*-Erhaltung und Cryo-Lagerung sowie Pflanzliche Reproduktionsbiologie (Dr. J. Keller, Dr. J. Kumlehn, Dr. G. Hensel, R. Schnee).

Pressemitteilungen/Press Releases

2010

20. Januar 2010
Langjähriger Administrativer Leiter des IPK Gatersleben scheidet aus dem Institut.

23. März 2010
Erster Wricke-Preis geht an Gaterslebener Forscher.

11. Mai 2010
Agrar-Staatssekretär besuchte das IPK und das Schülerlabor.

14. Juni 2010
IPK Gatersleben nun auch offiziell familienfreundlicher Arbeitgeber.

8. September 2010
3. Gaterslebener Gespräch „Globale Aspekte der Grünen Gentechnik" am 17. September.

9. September 2010
IPK Gatersleben präsentiert Kürbisse auf LAGA 2010 in Aschersleben.

4. Oktober 2010
Neue Resistenzgene gegen Weizenmehltau in alten Landrassen entdeckt.
8. Gaterslebener Forschungspreis geht an Züricher Nachwuchswissenschaftlerin.

22. November 2010
Zukunft der Pflanzenforschung im Visier. 10. Gatersleben Research Conference.

8. Dezember 2010
Mehr Schlagkraft für Forschung zur Kulturpflanze in der Region.
(Gemeinsame Pressemitteilung vom IPK Gatersleben und dem JKI Quedlinburg anlässlich der Unterzeichnung eines Kooperationsvertrages).

2011

10. Februar 2011
Erster Stopp: Leibniz-Institut für Pflanzengenetik und Kulturpflanzenforschung (IPK).
Die Kultusministerin des Landes, Frau Prof. Dr. Birgitta Wolff, besuchte Leibniz-Einrichtungen in Sachsen-Anhalt.

4. März 2011
Saat für die Zukunft. Neuer WissenschaftsCampus „Pflanzenbasierte Bioökonomie".
(Gemeinsame Pressemitteilung des Kultusministeriums des Landes Sachsen-Anhalt, der Martin-Luther-Universität Halle-Wittenberg und der Leibniz-Gemeinschaft).

15. März 2011
Feldzerstörer scheitern erneut vor Gericht.
Bundesgerichtshof bestätigt Urteil des OLG Naumburg.

13. April 2011
Einladung zur Gaterslebener Begegnung XII, vom 12. bis 14. Mai 2011, zum Thema „Wachstum und Reifung in Natur und Gesellschaft".

25. Mai 2011
Biotech-Campus Gatersleben lädt zum Tag der offenen Tür ein.

30. Mai 2011
Vier Feldzerstörer fechten mildes Urteil des Amtsgerichtes Aschersleben an.
Berufungsverhandlung vor dem Landgericht Magdeburg am 1. Juni.

14. Juni 2011
Weitere 7.000 Samen gehen auf die Reise gen Nordpol.

20. Juni 2011
Eine Woche Hybridzüchtung.
IPK Gatersleben ist Gastgeber für internationale Pflanzenzüchter.

14. Juli 2011
Weshalb die doppelte Hälfte besser ist als das ursprüngliche Ganze.
Pflanzenforscher entdecken Geheimnis zur Eliminierung von Chromosomen.

22. Juli 2011
Berufung der Feldzerstörer von Gatersleben scheitert vor dem Magdeburger Landgericht.
Strafkammer des Landgerichts Magdeburg verurteilt Feldzerstörer in Revisionsverfahren.

5. Dezember 2011
Forschungspreise gehen an Daniela Christiane Dieterich, Gotthard Kunze und Niels Angermüller.

Presse- und Medienarbeit/Contributions in Press and Media

soweit erfasst/as registered

2010

25. Januar 2010
Mitteldeutsche Zeitung Aschersleben, „Wechsel an der Führungsspitze" – Langjähriger Administrativer Leiter des IPK geht in den Ruhestand (B. Eise, S.-A. Lorenz).

28. Januar 2010
Mitteldeutsche Zeitung, „Forscher warten auf EU-Entscheidung" - CDU-Landtagsabgeordneter Detlef Gürth besucht den Biotechnologiestandort Gatersleben (Prof. Dr. A. Graner).

24. März 2010
Volksstimme, „Wricke-Forschungspreis erstmals verliehen" (Dr. N. Stein).

22. April 2010
DIE ZEIT, Nr. 17, „Mendels Kinder" – Junge Pflanzenforscher haben es oft mit Gentechnik zu tun, aber nur wenige bauen transgene Pflanzen (T. Guse, Prof. Dr. A. Graner).

1. Mai 2010
Mitteldeutsche Zeitung, Aschersleben, „Erster Wricke-Preis geht an Gaterslebener Forscher" (Dr. N. Stein, R. Schnee).

4. Mai 2010
Mitteldeutsche Zeitung, Magdeburg, „Genweizen-Prozess: Neue Vorwürfe vor neuer Runde" – Gentechnik-Gegner sehen Versuchsgenehmigung als Farce (Prof. Dr. A. Graner).

17. Mai 2010
Deutschlandfunk Magdeburg, Interview, „Rechtsstreit Feldzerstörung" (Prof. Dr. A. Graner).

22. Mai 2010
HARZER Kreisblatt, Nr. 5, „Tag der offenen Tür im Institut für Pflanzengenetik" (N. Wahle).

23. Mai 2010
Generalanzeiger, „Agrar-Staatssekretär besuchte das IPK und das Schülerlabor" (Prof. Dr. A. Graner).

26. Mai 2010
NDR Hamburg, Interview für W. wie Wissen, „Biodiversität in Kleingärten am Beispiel der Kulturpflanzen" (Prof. Dr. A. Graner).

31. Mai 2010
MZ-Marktplatz, Nr. 22, „IPK wird für seine Personalpolitik geehrt" (R. Schnee).

9. Juni 2010
Mitteldeutsche Zeitung, „Wissenschaft gibt tiefe Einblicke" - Tag der offenen Tür und Fest der Begegnung laden am Sonnabend ein (R. Schnee).

14. Juni 2010
Mitteldeutsche Zeitung, Aschersleben, „Die Welt der Wissenschaft zum Anfassen und Probieren" – Zahlreiche Besucher kamen zum Tag der offenen Tür und zum Begegnungsfest (Prof. Dr. A. Graner, R. Schnee).

22. Juni 2010
Mitteldeutsche Zeitung, Aschersleben, „Leibniz-Institut erhält offiziell familienfreundliches Prädikat" – Vereinbarkeit von Familie und Beruf stehen im Mittelpunkt (Prof. Dr. A. Graner).

6. Juli 2010
ARD/MDR, Interview, „Forschung am IPK" (R. Schnee).

8. Juli 2010
Zeitschrift „K+S Information", Kassel, „Die Welt braucht unsere Düngemittel" (anlässlich Fachtagung „Megatrend Agrarrohstoffe") (Prof. Dr. A. Graner).

20. Juli 2010
Mitteldeutsche Zeitung, Halle/S., Interview, „Bedeutung der Züchtung, Landwirtschaft und Biodiversität" (R. Schnee).

20. Juli 2010
Mitteldeutsche Zeitung, „Junge Wissenschaftler machen sich auf die Spur der Nabelschnur" – Doktoranden des Gaterslebener Leibniz-Instituts gehen auf Exkursion und untersuchen ungewöhnliche Firmengeschichten in der Region (M. Mau, L. Gerson, H. Wolf von der BIO Mitteldeutschland GmbH).

21. Juli 2010
Mitteldeutsche Zeitung, „Kritik an Patent auf Brokkoli" (Prof. Dr. A. Graner).

22. Juli 2010
nufan-Film, Berlin, Beiträge für biotechnologie.tv, Interview, „Zehn Jahre *Arabidopsis*-Genom; Genbank Gatersleben; Gerste-Genom: Erstmals deutsche Koordinierung einer Kulturpflanzensequenzierung" (Prof. Dr. Th. Altmann, Prof. Dr. A. Graner, Dr. N. Stein).

22. Juli 2010
Mitteldeutsche Zeitung, „Kleine Bauarbeiter probieren sich auf neuer Baustelle aus" – Die Gaterslebener Kindertagesstätte überrascht mit neuem Angebot (S.-A. Lorenz).

19. August 2010
Mitteldeutsche Zeitung, „Globale Aspekte der Gentechnik" (R. Schnee).

26. August 2010
WDR, „Das Wunder von Köln", Materialbereitstellung für Filmaufnahmen (Dr. K. Pistrick).

3. September 2010
dapd Nachrichtenagentur GmbH, Fotoaufnahmen von Forschungsarbeiten am IPK anlässlich des Gründungsjubiläums des InnoPlanta e.V. (R. Schnee).

14. September 2010
Mitteldeutsche Zeitung, Aschersleben, „Leibniz-Institut zeigt Kürbisse" (R. Schnee).

14. September 2010
Mitteldeutsche Zeitung, Aschersleben, „Sportler setzen Zeichen gegen Gewalt" – Traditionelles Fußballspiel findet in Gatersleben bereits seit zehn Jahren statt (R. Schnee).

14. September 2010
Mitteldeutsche Zeitung, Aschersleben, „Prozessauftakt gegen Feldzerstörer" (R. Schnee).

15. September 2010
Mitteldeutsche Zeitung, Aschersleben, „Die Grüne Gentechnik aus globaler Sicht" – Morgen Abend beginnt das 3. Gaterslebener Gespräch (R. Schnee).

16. September 2010
Mitteldeutsche Zeitung, Aschersleben, „Kürbisse mit Feigenblatt und Warze" – Gaterslebens Leibniz-Institut präsentiert Halloweenklassiker in allen Formen und Farben (B. Schmidt).

17. September 2010
MDR Figaro, Das Kulturradio des Mitteldeutschen Rundfunks, Interview, „Die positiven Seiten der Grünen Gentechnik und welche rationalen Argumente gibt es" (R. Schnee, Prof. Dr. A. Graner).

18. September 2010
Mitteldeutsche Zeitung, Aschersleben, „Knorrige Bäume und leuchtende Weizenähren" – Eine Kunstausstellung eröffnet das Gaterslebener Gespräch (Prof. Dr. Anna M. Wobus, Prof. Dr. U. Wobus, Prof. Dr. A. Graner, R. Schnee, K. Menzel).

1. Oktober 2010
Mitteldeutsche Zeitung, Aschersleben, „Glaubt an Aufrichtigkeit" – Zusammenhalten – Zukunft gewinnen (Dr. N. Sreenivasulu).

15. Oktober 2010
Mitteldeutsche Zeitung, Aschersleben, „Verhandlung geht in eine dritte Runde" – Feldzerstörer-Angeklagte lehnen eine Verurteilung mit einer geringen Geldstrafe ab (Dr. W. Weschke).

27. Oktober 2010
mdr aktuell, Interview, „Fragen zu Untersuchungen und Experimenten am IPK, Potenziale für die Ernährungssituation bei uns und möglicherweise in der ganzen Welt" (Dr. J. Kumlehn, R. Schnee).

24. November 2010
Mitteldeutsche Zeitung, Aschersleben, „Pflanzenforscher aus 22 Nationen" – Die Gaterslebener Research Conference beschäftigt sich mit Genomforschung (R. Schnee, Dr. N. Stein).

8. Dezember 2010
WDR Köln, Interview, „Welche Methoden werden eingesetzt, um Getreidesorten auf neue klimatische Bedingungen vorzubereiten und welche Erfolge man mit herkömmlichen Züchtungsmethoden haben kann, wenn es um Resistenzen gegen Pilze o.ä. geht? Welche Rolle wird die Gentechnik in den nächsten Jahren in der Getreidezucht einnehmen?" (Prof. Dr. A. Graner, Dr. M. Röder).

2011

25. Januar 2011
MDR, LexiTV, Leipzig, Dreharbeiten über das IPK zum Thema „Vererbung" (Priv.-Doz. Dr. A. Börner, Dr. U. Lohwasser, P. Schreiber, J. Marlow, R. Schnee).

3. Februar 2011
radioeins, Telefoninterview, „Archivierung von Pflanzen" (Prof. Dr. A. Graner).

9. Februar 2011
Mitteldeutsche Zeitung, Aschersleben, „Zwölfte Auflage der Gaterslebener Begegnung" (R. Schnee).

12. Februar 2011
Mitteldeutsche Zeitung, Aschersleben, „Kultusministerin besucht das Leibniz-Institut" (Prof. Dr. A. Graner).

7. März 2011
Mitteldeutsche Zeitung, Aschersleben, „Kultureller Atem der Region". Der Gaterslebener Kulturverein ist 20 Jahre alt und schaut auf über 100 Veranstaltungen zurück (Dr. H. Knüpffer, K. Menzel).

11. März 2011
Leipzig School of Media, Telefoninterview, „Kommunikation und Akzeptanz grüner Gentechnik" (R. Schnee).

17. März 2011
Mitteldeutsche Zeitung, Aschersleben, „Schicksal der Partner geht nah". Das IPK sorgt sich um japanische Institute (Prof. Dr. A. Graner, Prof. Dr. N. von Wirén).

15. April 2011
Mitteldeutsche Zeitung, Aschersleben, „Wachstum in Natur und Gesellschaft". Die zwölfte Gaterslebener Begegnung vereint Wissenschaftler, Künstler und Politiker (R. Schnee).

14. Mai 2011
Mitteldeutsche Zeitung, Aschersleben, „Blumiger Schatz aus der Kantine". Leibniz-Institut eröffnete Ausstellung (Prof. Dr. U. Wobus).

Mai 2011
Poeler Inselblatt, „Tag der offenen Tür – Der Wissenschaftsstandort Malchow öffnet seine Tore" (S. Nehrlich).

18. Mai 2011
LaborJournal, Telefoninterview „Pflanzenvielfalt aus dem Tiefkühlschrank" (Prof. Dr. A. Graner).

25. Mai 2011
Mitteldeutsche Zeitung, Aschersleben, „Pflanzenvielfalt zum Staunen, Anfassen und zum Verkosten". Gaterslebens Biotechnologie-Campus lädt Sonnabend zum Tag der offenen Tür ein (R. Schnee).

27. Mai 2011
Mitteldeutsche Zeitung, Aschersleben, „Hefen, die zum Backen nicht taugen". Zum Tag der offenen Tür (Prof. Dr. G. Kunze, R. Schnee).

31. Mai 2011
Mitteldeutsche Zeitung, Aschersleben, „Das Ei der Pflanzen unter dem Mikroskop gesehen". Im Gaterslebener Institut für Pflanzengenetik und Kulturpflanzenforschung konnten die Gäste so einiges sehen, schmecken und fühlen (Dr. H. Bäumlein, Dr. U. Lohwasser, I. Mücke).

8. Juni 2011
Bayerisches Fernsehen, Redaktion Unser Land, Beitrag über die Genbank in Gatersleben, Sortenvielfalt und Möglichkeiten der grünen Gentechnik, Fragen zu GVO (Priv.-Doz. Dr. A. Börner, Prof. Dr. T. Altmann).

10. Juni 2011
Mitteldeutsche Zeitung, Aschersleben, „Hefe entpuppt sich als vielseitiges Talent". Gaterslebener Wissenschaftler entwickeln Tests für Östrogen und Hormone (Prof. Dr. G. Kunze, Dr. K. Florschütz, Dr. M. Giersberg).

15. Juni 2011
Mitteldeutsche Zeitung, Aschersleben, „Neue Samen für Genbank am Nordpol" (R. Schnee).

17. Juni 2011
Volksstimme, „Gatersleber Genbank geht auf Nummer sicher". Pflanzensamen werden zusätzlich auf Spitzbergen eingelagert (Priv.-Doz. Dr. A. Börner).

21. Juni 2011
Mitteldeutsche Zeitung, Aschersleben, „Leibniz-Institut beherbergt Züchter aus aller Welt". In dieser Woche veranstaltet amerikanische Universität in Gatersleben ein Fortbildungsprogramm (R. Schnee).

21. Juni 2011
Prof. Dr. H. Spohler, Hochschule für Technik und Wirtschaft, Berlin, Fotoaufnahmen vom IPK zum Buch- und Ausstellungsprojekt „Der dritte Tag" (Priv.-Doz. Dr. A. Börner, S. Pistrick, A. Winger, I. Mücke, Dr. J. Kumlehn, R. Schnee).

24. Juni 2011
Mitteldeutsche Zeitung, Aschersleben, „Von Adler-Imitat, Handarbeit und Unkrautbildern". Gaterslebener Institut ist Gastgeber für Pflanzenzüchter-Weiterbildung (Priv.-Doz. Dr. A. Börner).

29. Juni 2011
Volksstimme, „Gentechnik und Erhalt der Vielfalt gehen Hand in Hand" (R. Schnee).

1. Juli 2011
Volksstimme, „Auf Vermehrungsflächen der Genbank beginnt Getreideernte" (Priv.-Doz. Dr. A. Börner).

7. Juli 2011
Mitteldeutsche Zeitung, Aschersleben, „Wenn Gene einfach blaumachen". IPK-Arbeitsgruppe betreibt Grundlagenforschung für die Pflanzenzucht (Dr. M.F. Mette, Dr. M. Kuhlmann).

8. Juli 2011
Mitteldeutsche Zeitung, Aschersleben, „Sichere Impfstoffe aus der Region". IPK-Nachwuchskräfte sind auf Fachexkursion (S. Witter vom PhD Student Board, U. Pigla von BIO Mitteldeutschland GmbH).

15. Juli 2011
Frau im Spiegel, Telefoninterview „Ist Genfood gefährlich?" (Prof. Dr. A. Graner).

26. Juli 2011
Mitteldeutsche Zeitung, Aschersleben, „Berufung der Feldzerstörer scheitert" (R. Schnee).

12. Oktober 2011
Mitteldeutsche Zeitung, Aschersleben, „Wissenschaft trifft wieder auf Kultur". Konzert und Vernissage im IPK (K. Menzel).

15. Oktober 2011
Mitteldeutsche Zeitung, Aschersleben, „Zwischen Lichtjahren und Nanometern". Illustratorin Svetlana Kilian stellt im Leibniz-Institut aus (K. Menzel).

13. November 2011
Frankfurter Allgemeine Sonntagszeitung, Wissenschaft, Nr. 45, „Saatgut für die Urenkel" (Priv.-Doz. Dr. A. Börner).

5. Dezember 2011
Mitteldeutsche Zeitung, Aschersleben, „Gaterslebener wird mit Forschungspreis geehrt" (R. Schnee).

Messen und Ausstellungen/Fairs and Exhibitions

2010

23. bis 26. März 2010
Das IPK beteiligte sich im Rahmen des Gemeinschaftsstandes „Forschung für die Zukunft" mit einem Exponat zum Thema „Biosensoren zum Nachweis östrogen wirksamer Substanzen" (Dr. M. Giersberg, T. Gerlach) an der ANALYTICA 2010 in München.

8. Mai 2010
Mitarbeiter der Teilsammlungen Malchow der IPK-Genbank präsentierten sich auf dem 8. Landesrapsblütenfest in Sternberg, Mecklenburg-Vorpommern, mit einem Ausstellungsstand „Pflanzenvielfalt – Anbau und Erhaltung in der Genbank". Die Veranstaltung wurde von etwa 1000 Gästen besucht (V. Miehe, S. Hünmörder).

7. bis 8. Juni 2010
Beteiligung des IPK an der NAROSSA 2010 (Nachwachsende Rohstoffe und Pflanzenbiotechnologie) in Magdeburg zum Thema „Plant breeding for non food application" (Dr. K. Florschütz).

9. Juni 2010
Das IPK war auf der Landesgartenschau 2010 (LAGA) in Aschersleben vertreten und gestaltete einen Stand zu Doldengewächsen (Dr. U. Lohwasser, B. Schmidt, R. Kurch, M.-L. Graichen, Priv.-Doz. Dr. A. Börner, F. Schröder).

12. bis 13. August 2010
Das IPK beteiligte sich an einer gemeinsamen Veranstaltung von Lehr- und Forschungseinrichtungen in Sachsen-Anhalt, die vom Julius Kühn-Institut in Quedlinburg unter dem Motto „Biologische Vielfalt bei Pflanzen" durchgeführt wurde. Mitarbeiter präsentierten zum Thema „Biodiversität zum Probieren" Doldenblütler mit einer anschließenden Teeverkostung (Dr. U. Lohwasser, B. Schmidt, R. Kurch, M.-L. Graichen).

29. August 2010
Auf der Ausstellung BioErleben 2010 in Warnemünde präsentierte die Arbeitsgruppe Teilsammlungen Nord des IPK das Groß Lüsewitzer Kartoffel-Sortiment (Dr. K.J. Dehmer, U. Behrendt).

15. September 2010
Das IPK war auf der Landesgartenschau 2010 (LAGA) in Aschersleben vertreten und gestaltete mit einer Präsentation von zahlreichen Kürbissen das Thema „Die bunte Welt der Kürbisse" anschaulich (Dr. U. Lohwasser, B. Schmidt, S. Eickmeier).

16. bis 19. September 2010
Mitarbeiter der Teilsammlungen Nord nahmen an der Mecklenburger Landwirtschaftsausstellung (MeLa) teil und präsentierten sich auf dem Gemeinschaftsstand des Rates für Agrarwissenschaften Mecklenburg-Vorpommern mit der Ausstellung „Teilsammlungen Nord der IPK-Genbank" (U. Behrendt, Dr. K.J. Dehmer, K. Göhrke, S. Pelikan, K. Ploen, E. Willner).

5. bis 7. Oktober 2010
Mitarbeiter des IPK präsentierten sich erneut im Rahmen des Gemeinschaftsstandes „Forschung für die Zukunft" mit einem Exponat zum Thema „Auf den Spuren von Viren und Pilzen" auf der BIOTECHNICA 2010 in Hannover (Dr. K. Florschütz).

14. Oktober 2010
Bereits zum dritten Mal riefen der Wirtschaftsclub Aschersleben e.V. und die Stadt Aschersleben zu einem Berufsorientierungstag auf, an dem auch das Institut teilnahm. Es wurde vor allem den Sekundarschülern die Möglichkeit gegeben, sich beruflich zu orientieren und über Praktikums- und Ausbildungsplätze zu informieren (J. Marlow).

2011

21. bis 30. Januar 2011
Grüne Woche Berlin: Beteiligung der Arbeitsgruppe Teilsammlungen Nord/Standort Groß Lüsewitz der IPK-Genbank am Ausstellungsstand des BMBF (insgesamt ca. 415.000 Besucher; Dr. K.J. Dehmer, K. Diekmann).

7. Mai 2011
9. Landes-Rapsblütenfest in Sternberg: Beteiligung der Arbeitsgruppe Teilsammlungen Nord/Standort Malchow der IPK-Genbank mit einem Ausstellungsstand „Pflanzenvielfalt – Anbau und Erhaltung in der Genbank" (ca. 1.000 Besucher; K. Ploen, S. Nehrlich).

14. Mai 2011
5. Poeler Rapsblütenfest in Kirchdorf: Beteiligung der Arbeitsgruppe Teilsammlungen Nord/Standort Malchow der IPK-Genbank mit einem Ausstellungsstand „Pflanzenvielfalt – Anbau und Erhaltung in der Genbank" (ca. 1.000 Gäste; V. Miehe, E. Willner).

16. März 2011
Das Institut beteiligte sich am Tag der Berufe, der im Biotech-Gründerzentrum durchgeführt wurde. In diesem Zusammenhang wurden die Ausbildungsberufe Biologielaborant/-in und Gärtner/-in vorgestellt.

7. bis 9. Juni 2011
An der Veranstaltung Sensor + Test 2011, die in Nürnberg stattfand, beteiligten sich Mitarbeiter des IPK mit einem Poster „On-Chip-Nachweis von phytopathogenen RNA-Viren und miRNA mittels Oberflächenplasmonenresonanz" (Dr. K. Florschütz, A. Schröter, Prof. Dr. G. Kunze).

28. August 2011
Präsentation der Groß Lüsewitzer Kartoffel-Sortimente auf der Ausstellung BioErleben 2011 in Warnemünde (über 25.000 Besucher; U. Behrendt).

4. September 2011
Tag der offenen Tür am Standort Groß Lüsewitz der Arbeitsgruppe Teilsammlungen Nord der IPK-Genbank mit Führungen und Erläuterungen zu den Groß Lüsewitzer Kartoffel-Sortimenten im Rahmen des Park- und Seefestes Groß Lüsewitz.

15.-18. September 2011
Mitarbeiter der Arbeitsgruppe Teilsammlungen Nord der IPK-Genbank beteiligten sich auf der Mecklenburger Landwirtschaftsausstellung (MELA) am Gemeinschaftsstand des Rates für Agrarwissenschaften Mecklenburg-Vorpommern. Diese Veranstaltung verzeichnete etwa 66.000 Besucher (U. Behrendt, Dr. K.J. Dehmer, K. Diekmann, K. Löschner, S. Nehrlich, S. Pelikan, K. Ploen, E. Willner).

11. bis 13. Oktober 2011
Mitarbeiter aus dem IPK beteiligten sich am Gemeinschaftsstand „Forschung für die Zukunft" mit Exponaten zum Thema „Biologische Sensorsysteme" auf der BIOTECHNICA 2011 in Hannover (Dr. K. Florschütz, Dr. M. Giersberg).

Gremien und Mitarbeiter/-innen in speziellen Funktionen/
Boards of the IPK and Employees with Special Responsibilities

Der Stiftungsrat überwacht die Geschäftsführung des Direktoriums, überprüft die Wirtschaftsführung, genehmigt die Jahresrechnung und erteilt Entlastung für das jeweils abgelaufene Haushaltsjahr.

Mitglieder des Stiftungsrates

MinDirig Dr. Joachim Welz, MK LSA, Magdeburg, (Vorsitz bis November 2011),
RD Peter Hassenbach. BMBF, Bonn, (stellv. Vorsitz bis September 2010),
Dr. Henk van Liempt, BMBF, Bonn, (stellv. Vorsitz seit März 2011),
Martin Köhler, BMELV, Bonn, (bis Oktober 2010),
MinRat Thomas Reitmann, MK LSA bis April 2011; MW LSA seit April 2011, Magdeburg,
MinRat Friedel Cramer, BMELV, Bonn, (seit Oktober 2011),
Prof. Dr. Wulf Diepenbrock, Martin-Luther-Universität Halle-Wittenberg, (bis Februar 2011),
Prof. Dr. Birgit Dräger, Martin-Luther-Universität Halle-Wittenberg, (seit März 2011),
Prof. Dr. Lothar Willmitzer, Max-Planck-Institut für Molekulare Pflanzenphysiologie Potsdam-Golm,
Prof. Dr. Christian Jung, Christian-Albrechts-Universität zu Kiel, (Vorsitz Wissenschaftlicher Beirat)
Prof. Dr. Ralph Bock, Max-Planck-Institut für Molekulare Pflanzenphysiologie Potsdam-Golm, (stellv. Vorsitz Wissenschaftlicher Beirat).

Das Direktorium ist ein Kollegialorgan, zusammengesetzt aus den Leitern der wissenschaftlichen Abteilungen und dem Administrativen Leiter. Der Stiftungsrat bestellt einen der wissenschaftlichen Abteilungsleiter für drei Jahre zum Geschäftsführenden Direktor. Dieser bildet gemeinsam mit dem Administrativen Leiter die Geschäftsführung, die die Stiftung nach Maßgabe der Geschäftsordnung gerichtlich und außergerichtlich vertritt.

Mitglieder des Direktoriums

Prof. Dr. Andreas Graner, Geschäftsführender Direktor und Leiter der Abteilung Genbank,
Sybille-Andrea Lorenz, Administrative Leiterin und Leiterin der Abteilung Verwaltung und Zentrale Dienste,
Prof. Dr. Ingo Schubert, Leiter der Abteilung Cytogenetik und Genomanalyse,
Prof. Dr. Thomas Altmann, Leiter der Abteilung Molekulare Genetik,
Prof. Dr. Nicolaus von Wirén, Leiter der Abteilung Physiologie und Zellbiologie.

Der Wissenschaftliche Beirat berät den Stiftungsrat und das Direktorium in wissenschaftlichen und technischen Fragen. Er ist verantwortlich für die Bewertung der wissenschaftlich-technischen Arbeiten und fördert die Verbindung mit Einrichtungen des In- und Auslandes.

Mitglieder des Wissenschaftlichen Beirates

Prof. Dr. Christian Jung, Kiel, (Vorsitz),
Prof. Dr. Ralph Bock, Potsdam-Golm, (stellv. Vorsitz),
Prof. Dr. George Coupland, Köln,
Prof. Dr. Thomas Dandekar, Würzburg,
PD Dr. Christiane Gebhardt, Köln, (Vorsitz Genbank-Beirat),
Prof. Dr. Marcus Koch, Heidelberg,
a.o. Univ. Prof. Dr. Josef Loidl, Wien,
Prof. Dr. Jerzy Paszkowski, Genf,
Prof. Dr. Dierk Scheel, Halle,
Prof. Dr. Dietmar Schomburg, Braunschweig, (seit November 2011),
Dr. Ralf-Michael Schmidt, Ludwigshafen, (bis Oktober 2011),
Prof. Dr. Chris-Carolin Schön, München.

Aufgrund der Sonderstellung der Genbank im Servicebereich und um den mit der globalen Erhaltung genetischer Ressourcen verbundenen Fragestellungen gesondert Rechnung zu tragen, verfügt die Genbank satzungsgemäß über einen **Genbank-Beirat**, der dem Wissenschaftlichen Beirat beratend zur Seite steht.

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Dr. Theo J. L. van Hintum, Wageningen, (stellv. Vorsitz) (bis November 2011),
Prof. Dr. Heiko Becker, Göttingen,
Dir. und Prof. Dr. Frank Ordon, Quedlinburg,
Dr. habil. Heiko Kurt Parzies, Stuttgart-Hohenheim,
(† August 2011),
Dr. habil. Hans Günter Welz, Wolfenbüttel.

Mitglieder des IPK-Personalrates

Thomas Kruse (Vorsitzender),
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Melanie Ruff,
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Evelin Willner, Teilsammlungen Nord, Malchow/Poel,
Dagmar Böhmert (Ersatzmitglied),
Ute Riedel (Ersatzmitglied).

Mitarbeiter/-innen des IPK in speziellen Funktionen

Dr. Ulrike Lohwasser (Qualitätsmanagement-Beauftragte),
Thomas Lüttge (Qualitäts-Beauftragter für die Abteilung VZD),
Dr. Winfriede Weschke und Dr. Jochen Kumlehn (Beauftragte für Biologische Sicherheit),
Dr. Hans-Peter Mock (Beauftragter für Betäubungsmittel und Gefahrstoffe),
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[1)] Management

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