Forschungsbericht
Scientific Report
2008/2009

Leibniz-Institut für Pflanzengenetik
und Kulturpflanzenforschung

IPK
GATERSLEBEN

Leibniz
Gemeinschaft

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

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As of 1 January 2008

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Bioinformatics	Coordinator: Prof. Falk Schreiber

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Gatersleben, März 2010

Leibniz Gemeinschaft

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Gesamtherstellung: Halberstädter Druckhaus GmbH

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Vorwort

Im Jahr 2009 starb der große amerikanische Wissenschaftler und Pflanzenzüchter Norman Borlaug. Die von ihm ins Leben gerufene „Grüne Revolution" bildete die Grundlage für die weltweite Bekämpfung des Hungers in den vergangenen Jahrzehnten. Leider kann sich die Menschheit nicht auf seinen Erkenntnissen und Errungenschaften ausruhen, für die er 1970 mit dem Friedensnobelpreis ausgezeichnet wurde. Damals lebten 3,7 Milliarden Menschen auf der Erde, im Jahr 2009 waren es bereits 6,8 Milliarden und in 40 Jahren werden es voraussichtlich 9 Milliarden Menschen sein. Dementsprechend wird der Bedarf an Nahrungsmitteln, erneuerbaren Energien und nachwachsenden Rohstoffen weiter wachsen, während das durch die „Grüne Revolution" geschaffene Guthaben aufgebraucht ist.

Ohne Zweifel ist die Sicherung der Lebensgrundlagen der Menschen an die weitere Verbesserung der Leistungsfähigkeit unserer Kulturpflanzen gebunden. Sie erfordert die Aufklärung der genetischen, biochemischen und zellbiologischen Prozesse, die an der Ausprägung der Leistungsmerkmale von Pflanzen beteiligt sind und welche ihre Anpassung an unterschiedliche Umweltbedingungen bewirken. Vor diesem Hintergrund reiht sich das IPK mit seinen Forschungsarbeiten unter die großen internationalen Zentren für Pflanzenforschung ein, in denen Beiträge zur Sicherung der zukünftigen Lebensgrundlagen erarbeitet werden.

Leistungsfähige, ausschließlich an wissenschaftlicher Exzellenz orientierte Grundlagenforschung ist der Nährboden für die Erarbeitung von Lösungen, die im Jahr 2050 verfügbar sein müssen. Auf diesem Weg gilt es auch, den Erkenntnisgewinn aus der Grundlagenforschung so rasch wie möglich in Anwendungen zu überführen. Entlang dieser zwei Handlungsstränge erstreckt sich das Spektrum der am IPK durchgeführten Forschungsarbeiten: Von reiner Grundlagenforschung, bis hin zur Bearbeitung angewandter Forschungsthemen aus den Bereichen Biotechnologie, Pflanzenernährung und züchtungsorientierter Genetik.

Ein wichtiges Ziel ist hierbei die Entwicklung von Strategien zur verbesserten Nutzung der in der Genbank erhaltenen pflanzengenetischen Ressourcen. Ein Thema, das im Jahr 2010, welches von den Vereinten Nationen zum ‚Internationalen Jahr der Biodiversität' ausgerufen wurde, von besonderer Aktualität sein wird. Biodiversität lässt sich nur gezielt nutzen, wenn wir Anstrengungen unternehmen, sie zu erhalten und zu erforschen. Dementsprechend erstrecken sich entsprechende Forschungsthemen am Institut über das gesamte Spektrum von der Erhaltung pflanzengenetischer Ressourcen über die Er-

Foreword

The great American scientist and plant breeder Norman Borlaug died in the year 2009. He was the founder of the "Green Revolution" which has been the fundament for the worldwide combat against hunger during the last decades. Unfortunately humankind cannot rest on his findings and achievements for which he also received the Nobel Peace Prize in 1970. Back then 3.7 billion people lived on Earth, in the year 2009 it was already 6.8 billion and in 40 years it is estimated to be 9 billion. Accordingly the need for food, regenerative energy and renewable resources will grow, while the created balance of the "Green Revolution" will be depleted.

Without doubt the assurance of natural resources towards the livelihood of humankind is tied to continued improvements in the performance of our crop plants. This will require knowledge of the genetic, biochemical and cell-biological processes that define the performance and ability of plants to adapt to diverse environmental conditions. Against this background IPK places itself among the great international plant research centres, where contributions are being developed towards safeguarding the livelihood for future generations.

While being exclusively orientated towards scientific excellence, fundamental research is indispensible towards developing solutions that must be available in the year 2050. This requires also that the gain of knowledge through fundamental research needs to be converted as rapidly as possible over into implementation. The spectrum of research at the IPK is aligned along these two strands: from pure fundamental research to the implementation of applied research topics in biotechnology, plant nutrition and applied genetics.

The most important goal is the development of strategies to make better use of the Plant Genetic Resources preserved in the Federal *ex situ* Genebank. This theme fits to 2010 which has been declared by the United Nations as 'International Year of Biodiversity'. Biodiversity can only be selectively used if we make efforts regarding its research and conservation. Thus the research themes at our institute comprise a wide spectrum, including the conservation of Plant Genetic Resources, research into the evolution of genetic diversity and to the valorization of Genetic Resources for the genetic improvement of agricultural and horticultural crop plants.

Overwhelming technological progress in the chemical analysis of biological molecules together with the exponential increase of the corresponding data has resulted in shift of emphasis in the experimental sciences: from data generation in the laboratory, to analysing the

forschung der Evolution genetischer Vielfalt und ihrer Funktion bis hin zu ihrer Nutzbarmachung für die züchterische Verbesserung landwirtschaftlicher und gärtnerischer Nutzpflanzen.

Der rasche technische Fortschritt in der chemischen Analytik von Biomolekülen und das damit verbundene exponentielle Anwachsen der Datenmengen hat in den vergangenen Jahren zu einer Schwerpunktverschiebung in den Experimentalwissenschaften geführt: Von der Datengenerierung im Labor, hin zur Datenanalyse und der darauf aufbauenden Modellierung biologischer Prozesse. Dieser Entwicklung wurde am IPK vor mehr als 10 Jahren mit der Etablierung einer leistungsfähigen Bioinformatik Rechnung getragen, welche in den vergangenen Jahren kontinuierlich ausgebaut wurde.

Vor diesem Hintergrund wurden in den vergangenen beiden Jahren wieder eine Reihe interessanter und wichtiger Forschungsergebnisse erzielt und Entwicklungen eingeleitet, mit denen das IPK gut gerüstet ist, um wesentliche Beiträge zur Beantwortung wichtiger Zukunftsfragen zu erarbeiten. Einzelheiten hierzu und zu vielen weiteren Themen finden Sie in dem vorliegenden Forschungsbericht.

Andreas Graner
Geschäftsführender Direktor

data and subsequent modelling of biological processes. This development was met more than 10 years ago with the establishment of a comprehensive program in Bioinformatics that saw continuous expansion over the past years.

With this background, a range of highly interesting and significant research results were achieved in the past two years and a series of developments were initiated, to sustain continued excellence of our research. More details on these and many other topics can be found in the following research report.

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. Es ist Mitglied der Leibniz-Gemeinschaft und firmiert seit Januar 2006 als Leibniz-Institut für Pflanzengenetik und Kulturpflanzenforschung. Sein Zuwendungsbedarf wird gemäß Artikel 91b 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 den Kultusminister.

„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)

Stiftungsorgane, Funktionsträger und Organisationsstruktur des IPK

Organe der Stiftung sind der **Stiftungsrat**, das **Direktorium** und der **Wissenschaftliche Beirat** sowie als Unterausschuss des Wissenschaftlichen Beirates der **Genbank-Beirat**. Die personelle Zusammensetzung der Beiräte im Berichtsjahr ist in einer Übersicht auf S. 171 dargestellt. Die Übersicht führt zudem die IPK-Mitarbeiterinnen und Mitarbeiter auf, die mit speziellen Funktionen innerhalb des IPK betraut waren und sind.
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. Organigramme, innere Umschlagseiten). Als abteilungsübergreifender Verbund mit spezieller Aufgabenstellung fungiert das **Pflanzengenom-Ressourcen-Centrum (PGRC; S. 146)**. Darüber hinaus werden die Forschungs- und Entwicklungsarbeiten im Be-

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 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 the Ministry of Education and Cultural Affairs 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 relevant 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)

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** with its subcommittee, the **Genebank Advisory Board**. Members of these bodies are listed on p. 171. In addition, the list includes all IPK staff members with specific responsibilities.

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. 146**)** performs tasks relevant to all departments. Regarding Bioinformatics, research and service activities in the different departments are coordinated via the **IPK-Bioinformatics-Platform**. Extramural funding contributes

reich **Bioinformatik** abteilungsübergreifend koordiniert (s. S. 148). Die Einwerbung von Drittmitteln resultiert in einer wesentlichen Aufstockung der Personal- und Forschungsmittelausstattung (s. Drittmittelübersicht im Addendum S. 72–104).

Forschungskonzept

Die strategische Ausrichtung der Forschungsarbeiten am Institut ist 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, gleichzeitig aber auch das Verständnis evolutiver Vorgänge fördert, um aus beiden Erkenntnissträngen 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

(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 substantially to the implementation of the research programme (cf. survey on p. 72–104).

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, while at the same time an understanding of evolutionary processes is being promoted. Insights from these two threads 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 multi-disciplinary investigation, incorporating a strong component of bioinformatics with aiming at modelling of metabolic processes, i.e. pursuing a Systems Biology approach.

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. Flowing from a strategic decision taken in 1997 barley (*Hordeum vulgare*) has been developed as a model system for the Triticeae cereals owing to its agronomic importance and the major commitment of many IPK researchers to this species. After having established the technical and bioinformatic infrastructure to perform

ten in erster Linie auf landwirtschaftlich bedeutsame Pflanzenarten. Die im Jahr 1997 mit der Gründung des Pflanzengenom-Ressourcen-Centrums eingeleitete Fokussierung auf die Gerste als Modellsystem für die Genomanalyse für Getreide wurde in den vergangenen Jahren auf Weizen, Mais und Raps ausgeweitet. Hierbei können nach der erfolgreichen Etablierung einer leistungsfähigen technischen und bioinformatischen Infrastruktur für die Genomforschung methodenorientierte Forschungs- und Entwicklungsansätze zunehmend durch die Bearbeitung biologischer Fragestellungen untersetzt werden. Spezielle Fragen zur Samenentwicklung werden seit vielen Jahren an Leguminosen untersucht. Die Bearbeitung einer Reihe grundlegender Problemstellungen erfolgt an Modellpflanzen wie *Arabidopsis, Nicotiana tabacum* und *Hypericum*. Ergänzend hierzu werden ausgewählte Forschungsthemen an Hefe (Abteilung Physiologie und Zellbiologie) und Säugerstammzellen (Abteilung Cytogenetik und Genomanalyse) 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 hinausgehende 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 die integrierte Forschungs- und Dienstleistungsplattform für die Genomforschung, insbesondere an Gerste. Weitere Informationen zum PGRC finden sich auf Seite 146.

Die aus dem ursprünglich vom BMBF geförderten Bioinformatik-Centrum Gatersleben-Halle hervorgegangene **IPK-Bioinformatik-Plattform** wird von einem im Rahmen einer gemeinsamen Berufung mit der Martin-Luther-Universität (MLU) Halle-Wittenberg berufenen Koordinator geleitet. Im Berichtszeitraum wurde der Bereich Bioinformatik durch Etablierung einer weiteren durch das BMBF geförderten Projektgruppe „Systembiologie" verstärkt. Weitere Einzelheiten sind auf Seite 148 zu finden.

Das 2003 gegründete **Europäische Genomforschungs-Netzwerk für Gerste (BarleyGenomeNet, BGN)** ist ein Zusammenschluss von Forschungseinrichtungen, welche sich schwerpunktmäßig mit der Genomforschung an dieser Art befassen. Neun Forschungseinrichtungen aus fünf europäischen Ländern kooperieren gegenwärtig im Rahmen verschiedener EU-Verbundprojekte, die im Rahmen der ERA-PG (European Research Area-Plant Genomics) und COST gefördert werden. Weitere Einzelheiten sind unter www.barleynet.org zu finden.

systematic genome research on this species the research portfolio of the Institute has been expanded in a stepwise manner 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 tabacum* and *Hypericum* are employed to study fundamental questions in plant biology. Two research groups work on non-plant organisms. Yeast is being used as a cellular expression system to study the molecular basis of particular metabolic pathways and to develop biosensors. Mammalian cell systems are used to study regulatory mechanisms of *in vitro* differentiation as well as their reprogramming potential.

Integrative Structures and Networks

The Institute has established platforms for internal services and scientific cross section activities. Above 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 the attraction of young scientists.

The **Plant Genome Resources Centre (PGRC)**, established in 1997, continues to provide an integrated research and service platform for genome research, with special emphasis on barley (see p. 146).

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-Wittenberg. In the reporting period the research group "Systems Biology", which is funded by the BMBF, has been established and now forms an integral constituent of the Platform (see p. 148).

The **European Barley Genomic Research Network** (BarleyGenomeNet, 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, which are funded through the ERA-PG (European Research Area-Plant Genomics) and COST. 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. The corresponding research activities performed within the Institute are funded by BMBF (GABI-

Das **„International Barley Sequencing Consortium"** (IBSC, http://barleygenome.org) wurde im Dezember 2006 gegründet. Das Ziel ist die Totalsequenzierung des Gerstengenoms. Basierend auf einer unter den neun Mitgliedsinstitutionen aus sieben Ländern abgestimmten Forschungsagenda werden gegenwärtig Forschungsprojekte durch das BMBF (GABI-FUTURE), die DFG (ERA-PG) und aus Mitteln des „Pakts für Forschung und Innovation" der *WGL* gefördert.

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 (s. dazu die Abschnitte „Collaboration" in den Berichten der Arbeitsgruppen). Ergänzend zu der bestehenden Kooperation mit der Martin-Luther-Universität Halle-Wittenberg wurden durch den Abschluss von Kooperationsverträgen mit der Christian-Albrechts-Universität zu Kiel und dem National Institute for Agrobiological Sciences (NIAS) in Tsukuba, Japan, die Beziehungen zu Forschungseinrichtungen im In- und Ausland intensiviert.

FUTURE), DFG (ERA-PG) and the *WGL* "Pakt für Forschung und Innovation".

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, as detailed in the individual reports of the research groups under the heading "Collaborations". In addition to ongoing cooperation with the University of Halle-Wittenberg, national and international relationships were further strengthened in 2009 by entering cooperation agreements with the Christian-Albrechts-University at Kiel and the National Institute for Agrobiological Sciences (NIAS) in Tsukuba, Japan.

Das Institut in den Jahren 2008 und 2009

Die vergangenen zwei Jahre waren gekennzeichnet durch eine Fülle interessanter Forschungsergebnisse, wichtige personelle Veränderungen, die Weiterentwicklung der technischen Infrastruktur im Hinblick auf Gebäude, Großgeräte und Gewächshausanlagen, umfangreiche Drittmitteleinwerbung und fortgesetzte nationale und internationale Kooperation. Nachfolgende Abschnitte sollen dem Leser einen Überblick zu den wichtigsten Entwicklungen aus diesem Zeitraum vermitteln. Weitere Informationen zu den Forschungsarbeiten sind den Berichten der Abteilungen und der einzelnen Arbeitsgruppen zu entnehmen.

Organisatorische Veränderungen

Im April 2008 übernahm Prof. Thomas Altmann von Prof. Ulrich Wobus die Leitung der Abteilung Molekulare Genetik. Zuvor hatte Prof. Altmann die Professur für Genetik an der Universität Potsdam inne und leitete parallel dazu eine Arbeitsgruppe am Max-Planck-Institut für Molekulare Pflanzenphysiologie in Golm.

Ebenfalls im Jahr 2008 nahmen zwei durch das BMBF geförderte Projektgruppen, *Pflanzliche Baupläne* (Leiter Dr. Thorsten Schnurbusch) und *Systembiologie* (Leiter Dr. Björn Junker) ihre Arbeit am IPK auf.

Nachdem Prof. Uwe Sonnewald Ende 2004 einen Ruf an die Universität Erlangen angenommen hatte, wurde die Abteilung Molekulare Zellbiologie über mehrere Jahre hinweg kommissarisch von Prof. Gotthard Kunze weitergeführt. Im April 2009 übernahm Prof. Nicolaus von Wirén die Leitung der Abteilung. Zuvor war Prof. von Wirén Lehrstuhlinhaber am Institut für Pflanzenernährung an der Universität Hohenheim. Die verstärkte Ausrichtung auf pflanzenphysiologische Themen spiegelt sich auch in der Umbenennung der Abteilung in *Physiologie und Zellbiologie* wider.

Im März 2008 nahm Dirk Koschützki einen Ruf an die Hochschule Furtwangen an, wo er an der Fakultät Computer & Electrical Engineering als Professor für Angewandte Informatik tätig ist.

Im April 2008 folgte der Leiter der Arbeitsgruppe *Quantitative Evolutionsgenetik*, Dr. Karl Schmid, einem Ruf an die Universität in Uppsala, Schweden. Von dort wechselte er als erster Inhaber der F. Wolfgang Schnell-Stiftungsprofessur für Nutzpflanzenbiodiversität und Züchtungsinformatik zum 1. Dezember 2008 an die Universität Hohenheim.

The Institute in 2008 and 2009

The past two years have been marked by a plethora of interesting research outcomes, critical changes in personnel, the ongoing development of the technical infrastructure related to buildings, large equipment and plant growth facilities, the attraction of many sources of financial support and the cementing of current national and international collaborations. In the summary which follows, an overview of the most important developments over this period is given. More detailed information regarding the research programmes is provided in the reports produced by the departments and working groups.

Organisational Changes

In April 2008, Prof. Thomas Altmann succeeded Prof. Ulrich Wobus as head of the "Molecular Genetics" Department. Prior to this, Prof. Altmann held the post of professor of Genetics at the University of Potsdam, while at the same time leading a working group based at the Max Planck Institute at Golm. Two new project groups were initiated in 2008, as recommended by BMBF (the Federal Ministry of Education and Research): these were *Plant Architecture* (led by Dr. Thorsten Schnurbusch) and *Systems Biology* (led by Dr. Björn Junker).

Following the appointment of Prof. Uwe Sonnewald to the University of Erlangen at the end of 2004, the "Molecular and Cell Biology" Department was for several years led on an acting basis by Prof. Gotthard Kunze. In April 2009, Prof. Nicolaus von Wirén took over as formal head of the Department. His prior position was Chair of the Plant Nutrition Institute at the University of Hohenheim. The re-focussed emphasis on plant physiological themes was reflected by renaming of the Department as "*Physiology and Cell Biology*".

In March 2008, Dirk Koschützki accepted a post at the Furtwangen Hochschule, where he is now active as a professor of Applied Informatics within the faculty of Computer & Electrical Engineering.

In April 2008, the leader of the *Quantitative Evolutionary Genetics* research group Dr. Karl Schmid left for an appointment at the University of Uppsala in Sweden. On 1st December 2008, he moved on to become the first holder of the F. Wolfgang Schnell Professorship of Crop Biodiversity and Breeding Informatics at the University of Hohenheim.

Die Arbeitsgruppe Mustererkennung wurde nach dem Fortgang des Leiters Dr. Udo Seiffert zum 28. Februar 2008 geschlossen.

Ende November 2009 verabschiedete sich der langjährige Administrative Leiter des IPK, Bernd Eise, in den Ruhestand. Er hinterlässt seiner Nachfolgerin Sybille-Andrea Lorenz, die ihr Amt zum 1. Januar 2010 antrat, ein wohlorganisiertes und geordnetes Haus. Die Entwicklung, die der Gaterslebener Campus seit 1991 genommen hat, ist untrennbar mit seiner Tätigkeit verbunden.

Entwicklungen von zentraler Bedeutung

(1) Nachdem sich das Institut in verschiedenen Programmen, allen voran dem BMBF GABI-FUTURE Programm, sehr erfolgreich um die Einwerbung von Drittmitteln bemüht hat, überstieg die Mitarbeiterzahl des Instituts im Sommer 2009 die Marke von 500. In diesem Zusammenhang konnte das IPK im Jahr 2009 zum fünften Mal in Folge mit einem Forschungsantrag zur Sequenzierung von Gerste Fördermittel aus dem Pakt für Forschung und Innovation der Leibniz-Gemeinschaft einwerben. Mit einem Forschungsprojekt zur Stresstoleranz bei Getreide ist das IPK in einem der vom BMBF geförderten Kompetenznetzwerke in der Agrarforschung vertreten. Ein vollständiger Überblick zur Drittmitteleinwerbung kann der Aufstellung im Addendum auf den Seiten 72-104 entnommen werden.

(2) Die Forschungsergebnisse wurden in den vergangenen beiden Jahren in 249 Artikeln in referierten Fachzeitschriften veröffentlicht. Hinzu kommen 77 Publikationen, die als Buchbeiträge erschienen sind. Eine detaillierte Aufstellung der jeweiligen Referenzen ist in den Berichten der einzelnen Arbeitsgruppen zu finden.

(3) In den Jahren 2008/2009 wurden wichtige Schritte zum weiteren Ausbau der wissenschaftlichen und technischen Infrastruktur unternommen. Mit dem Neubau eines Labor- und Bürogebäudes am Standort Groß Lüsewitz konnten die dortigen Arbeitsbedingungen erheblich verbessert werden.
Mit dem weiteren Ausbau der Gewächshausinfrastruktur wurden wichtige Voraussetzungen für die systematische Phänotypisierung von Pflanzenmaterial geschaffen. Die vorhandene Gewächshausfläche wird um insgesamt 400 m² Nutzfläche erweitert. Um die automatische Erfassung verschiedenster Wachstumsparameter von Pflanzen zu ermöglichen, wurden zwei Gewächshäuser mit modernsten Anlagen zur automatischen Erfassung phänotypischer Parameter ausgestattet. Parallel zur Gewächshausfläche wurden die Klimakammerkapazitäten um 80 m² Nutzfläche erweitert. Auch hier wurde auf einer Teilfläche eine automatische Phänotypisierungseinheit installiert.

The research group *Pattern Recognition* was closed on 28th February 2008 following the departure of Dr. Udo Seiffert.

The end of November 2009 marked the retirement of Bernd Eise, the long-standing head of IPK Administration. His successor, Sybille-Andrea Lorenz, who succeeded him on January 1st 2010, inherited a well-organised and orderly site. The development of the Gatersleben campus in the years since 1991 is very much associated with his sound management.

Developments of Central Importance

(1) Thanks to the success of the Institute in winning funding from a range of providers, in particular the BMBF GABI-FUTURE programme, the number of staff employed at the site had risen by the summer of 2009 to over 500. As a result, for the fifth time in succession, IPK in 2009 was able to successfully submit a proposal in the Leibniz Society Research and Innovation Consortium (Pakt für Forschung und Innovation) and obtain funding for the barley sequencing programme. IPK is also a partner in the BMBF Agricultural Research programme (Kompetenznetzwerke in der Agrarforschung) to work on stress tolerance in cereals. A comprehensive overview of our funding achievements can be viewed on pages 72-104 (Addendum).

(2) IPK research outcomes have been published over the past two years in the form of 249 peer-reviewed articles in academic journals. In addition there have been 77 contributions in the form of book chapters. A detailed listing of these papers can be found in the reports of the relevant research groups.

(3) The years 2008 and 2009 saw further important progress in the expansion of our scientific and technical infrastructure. The new construction of a laboratory and office block at the Groß Lüsewitz site has markedly improved the working conditions there. The expansion of the plant growth facilities has improved our capacity for the systematic phenotyping of plant materials. The usable area in the facility has been expanded by 400 m². To allow for the automatic control of various plant growth parameters, two new modern glasshouses have been equipped to provide automated phenotyping. In parallel with the expansion of glasshouse space, the area of growth chamber space has been increased by around 80 m², part of which includes a facility for the automized capture of phenotype.

(4) After just a single year in construction, the new IPK communications centre was inaugurated in June 2008. With this, the Institute has now acquired a custom-built and fully equipped lecture theatre in a central position on the campus, next to the canteen. The communica-

(4) Nach nur einjähriger Bauzeit wurde im Juni 2008 das IPK-Kommunikationszentrum eingeweiht. Damit verfügt das IPK neben einem zentral auf dem Campus angesiedelten Casino über einen völlig neu gestalteten und hervorragend ausgestatteten Tagungssaal. Das Kommunikationszentrum stellt einen zentralen Anlaufpunkt für die Mitarbeiter der über den Campus verteilten Abteilungen sowie der Mitarbeiter der Firmen am Standort dar. Es bietet darüber hinaus die Infrastruktur für die Durchführung von Tagungsveranstaltungen mit bis zu 200 Teilnehmern.

(5) Im Rahmen von zwei externen Audits in den Jahren 2008 und 2009 wurde der Zertifizierungsstatus des Qualitätsmanagements nach ISO 9001:2000 der Genbank und der Abteilung Verwaltung und Zentrale Dienste bestätigt. Im globalen Wettbewerb um die besten Mitarbeiter/-innen und Köpfe ist eine familienfreundliche Personalpolitik ein wichtiges Heraushebungsmerkmal für das Institut. Um diese weiter zu verbessern und nach innen und außen zu kommunizieren, wurde das Institut Ende 2009 von der *berufundfamilie* gGmbH auditiert.

(6) Trotz Aufklärungsarbeit zu dem auf dem IPK-Gelände durchgeführten Freisetzungsversuch für transgenen Weizen und umfangreicher Sicherungs- und Bewachungsmaßnahmen wurde der Freisetzungsversuch auf dem IPK-Gelände im zweiten Versuchsjahr (2008) von Mitgliedern der Gruppierung „Gendreck weg" zerstört. Zur Wiedergutmachung des entstandenen Schadens hat das Institut beim Landgericht in Magdeburg eine Schadenersatzklage eingereicht. Ein rechtskräftiges Urteil steht gegenwärtig noch aus.

Die Arbeit der Gremien

Wie in den vergangenen Jahren trafen sich der Wissenschaftliche Beirat und der Genbank-Beirat anlässlich des Institutstages zu ihrer Begutachtung. Im Jahr 2008 (29. September bis 1. Oktober) befasste sich der Wissenschaftliche Beirat mit den Abteilungen Genbank sowie Cytogenetik und Genomanalyse, im Jahr 2009 (12. bis 14. Oktober) lag der Schwerpunkt der Begutachtung auf den Forschungsarbeiten in der Abteilungen „Molekulare Genetik" und „Physiologie und Zellbiologie". Parallel hierzu besuchte der Genbank-Beirat in beiden Jahren die Genbank.

Der Stiftungsrat tagte am 1. Oktober 2008 und am 14. Oktober 2009 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, die Nachbesetzung der Stelle des Administrativen Leiters sowie der im Jahr 2012 anstehenden Nachbesetzung der Stelle des Leiters der Abteilung Cytogenetik und Genomanalyse.

tions centre location represents a convenient meeting place for staff from the various departments, as well as for those employed in the companies sited on campus. It has sufficient facilities to organize meetings of up to 200 participants.

(5) As an outcome of two external audits held in 2008 and 2009, both the Genebank and the Administration and Central Services won quality management certification (ISO 9001:2000). The Institute recognizes that in the face of global competition to attract the best staff and leadership, family-friendly policies are an important asset. In an effort to further improve this area, and to enhance both internal and external communications, the Institute arranged to be audited at the end of 2009 by the *berufundfamilie* gGmbH organization.

(6) Despite an intensive programme of education and a heavy investment in security and patrolling, the second season's (2008) transgenic wheat field trial carried out on IPK property was destroyed by members of the "Gendreck weg" ("Away with Genetic Filth") movement. The Institute has filed for indemity with the regional court in Magdeburg. The outcome of the claim is currently pending.

The Activities of the Advisory Boards

As in previous years, the Scientific Advisory Board and the Genebank Advisory Board met for their deliberations on the Institute Day. In 2008 (29th September - 1st October), the Scientific Advisory Board concentrated its evaluation on the Genebank and the "Cytogenetics and Genome Analysis" Department; while in 2009 (12th October - 14th October), the focus was on the research programmes carried out in the "Molecular Genetics" and "Physiology and Cell Biology" Departments. In parallel, the Genebank Advisory Board visited the Genebank in both years.

The Trustees met on 1st October 2008 and 14th October 2009 under the chairmanship of the Ministerialdirigent (Department Head of Ministry) Dr. Joachim Welz. The major topics for discussion were the programme budget, plans to expand glasshouse and growth cabinet capacity, the acquisition of large equipment, the replacement for the Administrative Director, and the replacement for the head of the "Cytogenetics and Genome Analysis" Department, anticipated for 2012.

Symposia and Conferences

Several symposia, workshops and seminars were organised during the reporting period at IPK. An overview can be found on page 151.

Supplementing purely scientific symposia and workshops, events aiming at both the scientific community and the

Symposien und Tagungen

Im Berichtszeitraum wurden verschiedene Tagungsveranstaltungen sowie Seminare und Workshops am Institut ausgerichtet. Eine Übersicht ist auf S. 151 zu finden.

Neben rein wissenschaftlich orientierten Tagungen und Workshops haben am Institut Veranstaltungen, die sowohl Wissenschaftler als auch die breite Öffentlichkeit ansprechen, eine lange Tradition. So organisierten die Professoren Anna M. und Ulrich Wobus zusammen mit der Sommerakademie der Evangelischen Akademie Sachsen-Anhalt e.V. am **11. und 12. September 2008 das 2. Gaterslebener Gespräch zum Thema „Programmierung und Reprogrammierung – Potentialität auf zellulärer und organismischer Ebene"**. Im Mittelpunkt des Symposiums standen naturwissenschaftliche, rechtliche und ethische Fragen der Stammzellforschung. Vom **7. bis 10. Mai 2009 fand die XI. Gaterslebener Begegnung „Der Begriff der Natur – Wandlungen unseres Naturverständnisses"** statt (s. Fig. 1). Diese wurde ebenfalls von Anna M. und Ulrich Wobus gemeinsam mit der Leopoldina, der Nationalen Akademie der Wissenschaften, organisiert. Mit 140 Teilnehmern aus ganz Deutschland fand das Thema regen Zuspruch nicht nur im wissenschaftlichen Umfeld. In hochrangig besetzten Vorträgen wurde das Thema aus dem Blickwinkel von Naturwissenschaftlern, Publizisten, Philosophen und Künstlern erörtert und in einer abschließenden Podiumsdiskussion vertiefend betrachtet. Umrahmt wurde das Symposium von einer an das Thema angelehnten Ausstellung von Künstlern aus Halle und Dessau. Die Vortragsabende wurden jeweils mit Schriftstellerlesungen beschlossen.

broad public have a longstanding tradition at IPK. The **2nd Gatersleben Discourse** has been organised by Profs. Anna M. and Ulrich Wobus together with the Summer Academy of the Evangelische Akademie Sachsen-Anhalt from **11th to 12th September 2008**. The topic was **"Programmierung und Reprogrammierung – Potentialität auf zellulärer und organismischer Ebene"** and covered **scientific, legal, and ethical questions of stem cell research**. The **Gatersleben Encounters XI** on **"Der Begriff der Natur – Wandlungen unseres Naturverständnisses"** were also organised by Anna M. and Ulrich Wobus, and the Leopoldina, the German National Academy of Sciences, from **May 7th - 10th, 2009 (see Fig. 1)**. 140 registered participants from Germany reflect the broad interest in such a venue. High-ranking invited speakers discussed Nature and its different facettes from the view of **natural scientists, publicists, philosophers and artists**. A panel discussion at the end of the symposium made the attempt to combine those views and derive solutions for endangered nature. The exhibition by artists from Halle and Dessau made a nice contribution to the talks. Every evening closed with readings by writers.

Two other events worth mentioning did not take place at IPK but were co-organised by IPK scientists.
One, the **German Conference on Bioinformatics '09** took place at **Martin Luther University Halle-Wittenberg** from 28th to 30th September 2009. Prof. Falk Schreiber and Dr. Uwe Scholz from IPK were members of the Local Organising Committee for the annual international conference. With approximately 250 participants it reached a peak attendance. A smaller workshop on **"Cereal Diversity, Plant Domestication and Human History in the Fertile**

Fig. 1
Die Teilnehmer der Podiumsdiskussion der XI. Gaterslebener Begegnung am 9. Mai 2009: Dr. Norbert Wiersbinski (Moderation), Prof. Ernst-Peter Fischer, Prof. Jens Reich, Dr. Andreas Weber und Dr. Reinhard Piechocki; v.l. (Foto: B. Schäfer)./ Participants of the panel discussion of XI. Gatersleben Encounters on 9th May 2009: Dr. Norbert Wiersbinski (Moderator), Prof. Ernst-Peter Fischer, Prof. Jens Reich, Dr. Andreas Weber and Dr. Reinhard Piechocki; from left (Photo: B. Schäfer).

Zwei weitere erwähnenswerte Veranstaltungen fanden zwar nicht am IPK selbst statt, wurden aber maßgeblich von IPK-Wissenschaftlern mitorganisiert. Dabei handelt es sich um die internationale Bioinformatik-Konferenz, **German Conference on Bioinformatics**, die vom **28. bis 30. September 2009** an der **Martin-Luther-Universität Halle-Wittenberg** stattfand. Seitens des IPK beteiligten sich Prof. Falk Schreiber und Dr. Uwe Scholz an der Organisation der Tagung, zu der mit etwa 250 Teilnehmern die seit langem größte Beteiligung an der jährlich stattfindenden Konferenz verzeichnet werden konnte. Ein Workshop mit etwa 20 Teilnehmern wurde von Dr. Benjamin Kilian aus der Arbeitsgruppe Genomdiversität und Prof. Hakan Özkan (Universität Çukurova, Adana, Türkei) organisiert. Das Thema des Workshops lautete „**Cereal Diversity, Plant Domestication and Human History in the Fertile Crescent**". Die Veranstaltung fand vom **10. bis 15. Mai 2009** in der Türkei statt und brachte Wissenschaftler der Fachrichtungen **Genetik, Botanik, Archäobotanik, Archäologie und Pflanzenzüchtung** zusammen.

Im Rahmen des XX. Internationalen Congress of Genetics vom **12. bis 17. Juli 2008** in Berlin organisierte und leitete am 15. Juli Prof. Ingo Schubert den Workshop „**Plant Artificial Minichromosomes: Potential Vectors for Gene Transfer**" mit den international führenden Wissenschaftlern auf diesem Gebiet als geladenen Sprechern.

Die **Plant Science Student Conference,** von Doktoranden des Instituts initiiert, fand in den Jahren 2008 bzw. 2009 in 4. bzw. 5. Auflage statt. Einzelheiten können dem Bericht des „PhD Student Board (PSB)" auf S. 149 entnommen werden.

Ausbildung, Zusammenarbeit mit Universitäten und das IPK-Doktorandenprogramm

Im Zuge der weiteren Intensivierung der Zusammenarbeit der Martin-Luther-Universität Halle-Wittenberg mit den in der Region angesiedelten außeruniversitären Forschungseinrichtungen wurde im November 2008 das an der Universität angesiedelte und vom Land Sachsen-Anhalt geförderte Interdisziplinäre Zentrum für Nutzpflanzenforschung (IZN) etabliert. In dem Zentrum sollen in erster Linie Kooperationsprojekte bearbeitet werden, die sich mit der Reaktion von Pflanzen auf biotische und abiotische Stressfaktoren befassen. Darüber hinaus ist die Etablierung einer unabhängigen Nachwuchsgruppe geplant.
Zur weiteren Verbesserung der nationalen und internationalen Vernetzung des IPK sowie zur Gewinnung von wissenschaftlichem Nachwuchs wurden im Dezember 2009 Kooperationsabkommen mit der Christian-Albrechts-Universität zu Kiel sowie mit dem National Institute of Agrobiological Sciences in Tsukuba (Japan) abgeschlossen.
Wissenschaftler des Instituts führten Lehrveranstaltungen an oder in Zusammenarbeit mit den Universitäten

Crescent" with about 20 participants was organised by Prof. Hakan Özkan (University of Çukurova, Adana, Turkey) and Dr. Benjamin Kilian, Genome Diversity group. Scientists from various disciplines, **Genetics, Botany, Archeobotany, Archeology, and Plant Breeding** met in Turkey from **10th to 15th May 2009**. Following the various lectures by the participating scientists, the participants had the opportunity for visiting excavations sites and naturally occuring wildforms of barley and wheat.

During the XX International Congress of Genetics from **July 12th to 17th, 2008** in **Berlin** Prof. Ingo Schubert organised and chaired a Workshop on "**Plant Artificial Minichromosomes: Potential Vectors for Gene Transfer**" (July 15, 2008) with the internationally leading researchers in the field as invited speakers.

The **Plant Science Student Conference** initiated by the student programme at IPK, saw its fourth and fifth recurrence in 2008, in 2009 respectively. These are described in more detail in the section of the PhD Student Board (PSB), p. 149.

Training, Cooperation with Universities, and the IPK PhD Programme

In the context of the ongoing intensification of collaboration between Martin Luther University at Halle-Wittenberg and non-university sector research establishments in the region, November 2008 saw the founding of the Interdisciplinary Centre for Crop Research (IZN), sited at the University and funded by the Saxony-Anhalt regional government. Its priority will be to support collaborative projects concerned with the reaction of plants to biotic and abiotic stress. In addition, there are plans to establish an independent Junior Research group. As part of a continuing effort to improve the national and international connections of the Institute, and to enhance our scientific development, collaboration agreements were signed with both Christian-Albrechts-University at Kiel and the National Institute of Agrobiological Sciences, Tsukuba (Japan). IPK scientists have given lectures at, or collaborated with colleagues at the Universities of Halle-Wittenberg, Potsdam, Kassel, Kiel, Jena, Greifswald, Western Australia (Perth), as well as at the Hochschule Anhalt in Bernburg and Köthen. In addition, our scientists have offered courses and workshops to the Institute's students. A total of 45 Masters/Diploma and 26 PhD candidates graduated during 2008 and 2009. The IPK PhD programme was actively led by the "PhD Student Board". Among the activities organized were a series of student seminars, invited lectures given by external scientists, the staging of a "Plant Science Student Conference" and the provision of various special training events designed for PhD students. Further details of the IPK PhD programme can be found on page 149.

Halle-Wittenberg, Potsdam, Kassel, Kiel, Jena, Greifswald und der University of Western Australia, Perth, sowie der Hochschule Anhalt an den Standorten Bernburg und Köthen fort. Daneben boten Wissenschaftler Kurse und Praktika für Studierende am IPK an. In den Jahren 2008 und 2009 wurden insgesamt 45 Master-/Diplomarbeiten und 26 Doktorarbeiten abgeschlossen.
Das am IPK etablierte Doktorandenprogramm wird durch das „PhD Student Board" aktiv geführt. 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. Weitere Details zum Doktorandenprogramm sind auf S. 149 zu finden.

Öffentlichkeitsarbeit und öffentliche Wirkung

Die Wissenschaftler/-innen präsentierten ihre Ergebnisse in einer Vielzahl von Vorträgen, auf Postern sowie über das Internet. Neben diesen wissenschaftlichen Veröffentlichungen wurde die breite Öffentlichkeit mit 15 (2008: 7; 2009: 8) Presseinformationen über aktuelle Entwicklungen am Institut und dem Biotechnologie-Campus informiert.

Im Rahmen der Öffentlichkeitsarbeit wurden die Arbeiten am Institut in insgesamt **152 Führungen** (2008: 94; 2009: 58) mehr als 2.400 Besuchern, darunter Wissenschaftler, Schüler- und Studentengruppen, Politiker sowie Vertreter der Wirtschaft, vorgestellt. Darüber hinaus war das Institut ein gefragter Ansprechpartner für die Politikberatung. So informierten sich am 28. März 2008 die Mitglieder der Arbeitsgruppe „Infrastruktur, Landwirtschaft und Umweltschutz" der SPD-Fraktion des Landtages von Sachsen-Anhalt über Anforderungen zur Freisetzung von gentechnisch veränderten Pflanzen (GVO) und zu den Zulassungsvoraussetzungen zum Inverkehrbringen von GVO.
Zusätzlich informierte Prof. Andreas Graner im Jahr 2008 Parlamentarier der CDU- bzw. SPD-Fraktion des Bundestages zur Grünen Gentechnik und zur Pflanzenforschung im Allgemeinen. Hierfür war von der Leibniz-Gemeinschaft das Konzept „**Science Meets Parliament**" entworfen worden, bei dem Wissenschaftler die Parlamentarier in ihren Büros aufsuchen und dort in Vier-Augen-Gesprächen zu deren Fragen Stellung nehmen.

Großen Anklang in der Bevölkerung fand der am 7. Juni 2008 veranstaltete **Tag der offenen Tür** bzw. das anschließende **Fest der Begegnung**, das zusammen mit der Gemeinde veranstaltet wurde. Etwa 2.000 Gäste konnten an dem Tag auf dem Campus begrüßt werden. Den Einführungsvortrag zum Thema „Mit Hilfe der Modellpflanze *Arabidopsis* dem genetischen Phänomen der Hybridwüchsigkeit (Heterosis) auf der Spur" hielt der neue Leiter der Abteilung Molekulare Genetik, Prof. Thomas Altmann.

Public Relations and Public Impact

Scientists presented their results in a variety of oral presentations, in poster presentations, as well as via the internet. In addition to these scientific publications, the wider public was informed of recent developments at the Institute and the Biotechnology Campus through 15 (2008: 7; 2009: 8) press releases.

In the course of the public relation activities of the Institute more than **2,400 guests** were partaking in **152 guided tours** (2008: 94; 2009: 58) among them scientists, student and pupil groups, politicians and firm representatives. For instance, the members of the workgroup "Infrastructure, Agriculture and Environmental Protection" of the SPD party in Saxony-Anhalt seeked first-hand information about field trials of genetically modified plants (GMO) and the requirements for the market approval of GMO on 28th March 2008.

The Open House Day and the Multicultural Event jointly organised with the municipality of Gatersleben on 7th June 2008 have been very well received. About 2,000 guests crowded the campus and made it a lively festival with many attractions. Prof. Thomas Altmann, new head of the Department of Molecular Genetics, gave the opening lecture on "Mit Hilfe der Modellpflanze *Arabidopsis* dem genetischen Phänomen der Hybridwüchsigkeit (Heterosis) auf der Spur", illustrating research on heterosis with results gained in *Arabidopsis*.
In 2009, the Open House Day at the Biotech Campus Gatersleben took place on 6th June where local and regional guests got information on latest developments and results in plant research and biotechnology at IPK. Also the neighbouring institutions and firms presented an interesting and diverse programme. Prof. Joachim Schiemann of the Julius Kühn-Institute, Quedlinburg held the opening lecture "Sicherheitsbewertung und weltweite Nutzung gentechnisch veränderter Pflanzen", presenting an overview on safety research and worldwide application of GMO that was followed with great interest.
Prof. Graner met with six Members of Parliament of the CDU, and the SPD respectively, in May 2008. For this purpose the central PR of the Leibniz Association developed the concept of "**Science Meets Parliament**", where Scientists meet with Members of Parliament in their offices for individual discussions.

The Institute contributed to the Students Week that was organised by the "**Grüne Labor**" in both years. During one week, students from primary and secondary schools of the region had the opportunity to get first-hand information about education and studying in the fields of life sciences and the nutritional sector.

As in previours years, the Institute continued its engagement at seleceted national fairs. In both years, the Research Group Yeast Genetics presented its system for the

Im Jahr 2009 fand der Tag der offenen Tür am Biotechnologie-Campus Gatersleben am 6. Juni statt. Hier wurde die lokale und regionale Bevölkerung wieder über die neuesten Entwicklungen und Ergebnisse der Pflanzenforschung und Biotechnologie am Institut informiert. Auch die ansässigen Einrichtungen und Unternehmen hielten ein interessantes und abwechslungsreiches Programm bereit. Prof. Joachim Schiemann vom Julius Kühn-Institut, Quedlinburg hielt den Einführungsvortrag zum Thema „Sicherheitsbewertung und weltweite Nutzung gentechnisch veränderter Pflanzen", der mit großer Aufmerksamkeit verfolgt wurde.

Das Institut beteiligte sich in beiden Jahren an der vom „Grünen Labor" organisierten Schüleraktionswoche, in der Schülern aus Realschulen und Gymnasien Berufs- und Studienfelder in den Lebenswissenschaften bzw. der Nahrungsmittelwirtschaft nähergebracht werden sollen.

Wie in den vorangegangenen Jahren beteiligte sich das Institut ebenfalls mit Exponaten an ausgewählten deutschlandweiten Messen. So stellte die Arbeitsgruppe Hefegenetik in beiden Jahren ihr **System zur Detektion von mykorrhizierten Wurzeln** auf der **BIOTECHNICA** in Hannover aus bzw. im April 2008 auf der **ANALYTICA** in München das **Assay zum Nachweis von Östrogen-wirkenden Substanzen**.

An dem vom 24. April bis 24. November 2009 durch Deutschland rollenden **Wissenschaftszug „Expedition Zukunft"** wirkte das IPK mit einem **Exponat zur Evolution des Weizens** mit. Der vom BMBF initiierte und von der Max-Planck-Gesellschaft konzipierte Zug stoppte in 62 deutschen Städten und zog 260.000 Besucher an.

Vom 12. bis 15. März 2009 wurde die **„EcoGerma"** als erste deutsch-brasilianische Messe für Nachhaltigkeit und Umwelttechnologie in Wirtschaft und Industrie in **São Paulo** veranstaltet. Das IPK war auf einem Stand des BMBF im Rahmen des **Agrarforschungsnetzwerkes „AgriResearch plus"** der Leibniz-Gemeinschaft mit einer Präsentation des **BMBF-geförderten Projektes „Hybrid-Wheat"** (Dr. M. Gils) vertreten.

Innerhalb der öffentlichkeitswirksamen Veranstaltungen der Leibniz-Gemeinschaft war das Institut in beiden Jahren auf den **Parlamentarischen Abenden in Berlin** vertreten. Im Jahr 2008 stand der Abend unter dem Motto „Biodiversität" und fand in den Räumlichkeiten des Naturkundemuseums in Berlin statt (s. Fig. 2). Das IPK beteiligte sich mit Exponaten zur Vielfalt von Getreide bzw. präsentierte durch Dr. Patrick Schweizer ein System zum Nachweis der basalen Resistenz von Gerste gegen Mehltau. Technologie- bzw. Wissenstransfer war das Thema des Parlamentarischen Abends 2009, auf dem sich die Firma *SunGene* als ehemaliges Joint Venture zwischen der BASF AG und dem IPK präsentierte.

detection of mycorrhiza in roots at BIOTECHNICA in Hannover. Prof. Kunze's group also exhibited an assay for the **proof of estrogenic substances in waste water** at **ANALYTICA** in Munich in April 2008.

With a showcase illustrating the **evolution of today's wheat** the Institute contributed to the **Science Express "Expedition Zukunft"** touring through Germany from 24th April to 24th November 2009. The train initiated by the Federal Ministry of Education and Research (BMBF) and concepted by the Max Planck Society stopped in 62 German cities and attracted about 260,000 visitors.

EcoGerma, the first German-Brazilian fair for sustainability and environmental technologies was organised from 12th to 15th March 2009 in **São Paulo**. The **BMBF-funded project "Hybrid Wheat"** (Dr. M. Gils) presented a new system for developing hybrid wheat at a booth of the BMBF within the course of the **Leibniz Association agricultural research network "AgriResearch plus"**.

The Institute participated at both **Parliament Nights in Berlin** organised as central PR activities of the **Leibniz Association**. In 2008 "Biodiversity" was the central theme. Accordingly, the Parliament Night had been organised in the Museum of Natural History in Berlin (see Fig. 2). IPK demonstrated the natural diversity of cereals, and Dr. Patrick Schweizer presented a system to detect basal resistance against mildew in barley. The focus of 2009's Parliament Night was on technology and knowledge transfer, highlighting *SunGene* GmbH as former joint venture between BASF and IPK.

Fig. 2
Im Gespräch mit Frau Dr. Christel Happach-Kasan, MdB, Prof. Andreas Graner (M.) und Dr. Patrick Schweizer (r.) während des Parlamentarischen Abends am 16. Mai 2008 im Naturhistorischen Museum in Berlin (Foto: R. Günther/Leibniz-Gemeinschaft)./ Communication with Dr. Christel Happach-Kasan, MoP, Prof. Andreas Graner (c.) and Dr. Patrick Schweizer (r.) during the Parliament Night on 16th May 2008 in the Museum of Natural History in Berlin. (Photo: R. Günther/Leibniz-Association).

On 30th September 2008 **Dr. Hans Peter Maurer, University of Hohenheim** received the seventh Gatersleben Research Award of the **Gemeinschaft zur Förderung der Kulturpflanzenforschung and the Leibniz Institute of Plant**

Am 30. September 2008 wurde **Dr. Hans Peter Maurer**, **Universität Hohenheim**, von der **Gemeinschaft zur Förderung der Kulturpflanzenforschung und dem Leibniz-Institut für Pflanzengenetik und Kulturpflanzenforschung** der siebente **Gaterslebener Forschungspreis** verliehen. Im Jahr 2009 erhielt die **Agrarbiologin Judith Jäger**, ebenfalls von der **Universität Hohenheim**, für ihre Arbeit „Eine systematische Methode geographische Herkünfte genetischer Ressourcen zu analysieren, am Beispiel Perlhirse [*Pennisetum glaucum* (L.) R. Br.] in der Genbank von ICRISAT-Niger" den achten **Rudolf-Mansfeld-Preis** der Gemeinschaft.

Ende **Februar 2008** wurde in Svalbard auf Spitzbergen der so genannte **Global Seed Vault** eröffnet. Zielstellung dieses „Eisbunkers" ist die Erhaltung von Kulturpflanzen weltweit, insbesondere aus Entwicklungsländern und Krisenregionen. Die Genbank des IPK beteiligt sich an dieser Anstrengung und nimmt das Angebot der norwegischen Genbank und des Global Crop Diversity Trust gern an, um dort im Permafrost die **Sicherheitsduplikate der eigenen Sammlungen** deponieren zu lassen. Dies ist auf ein breites öffentliches und mediales Interesse gestoßen und mehrere nationale Zeitungen und Sender berichteten ausführlich über deren Eröffnung und die Einbindung der Gaterslebener Genbank. Bereits mehrere Monate vor dem Termin und auch im Nachgang hierzu waren beispielsweise zwei Kamera-Teams für mehrere Tage am Institut, um Aufnahmen für das 3sat-Wissenschaftsmagazin „hitec" und das ZDF-Magazin „Umwelt" zu machen. Beide Sendungen wurden mehrfach von der Senderfamilie des ZDF ausgestrahlt.

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. Die Zusammenarbeit mit verschiedenen am Standort angesiedelten Firmen erfolgt in erster Linie durch die Bearbeitung gemeinsamer Forschungsprojekte.

Um das Interesse Jugendlicher an Lebenswissenschaften zu wecken, hat das auf dem Campus angesiedelte **„Grüne Labor"** ein breites Kursangebot entwickelt, welches in erster Linie auf den schulischen Bereich abzielt. Das Angebot stößt auf stetig zunehmendes Interesse. Mehr als 6.000 Schüler, Auszubildende und Lehrer nahmen in den vergangenen beiden Jahren an den Kursen und Veranstaltungen teil.

Genetics and Crop Plant Research. In 2009 **agrar biologist Judith Jäger**, **University Hohenheim** received the eighth Rudolf Mansfeld Award for her Diploma Thesis "A systematic approach to analyze the eco-geographical origin of germplasm exemplified for pearl millet [*Pennisetum glaucum* (L.) R. Br.] in the genebank of ICRISAT-Niger".

The so-called **Global Seed Vault** was opened in Svalbard on the isle of Spitzbergen at the end of **February 2008**. Aim of this "icy vault" is the preservation of crop plants worldwide, and especially those originating in Least Developed Countries and crisis regions of the world. **IPK's Genebank** uses this opportunity of the Norwegian Genebank and the *Global Crop Diversity Trust* to deposit its **safety duplicates in permafrost**. The opening received a broad public and media interest. Therefore, several newspapers and broadcasts extensively informed about this event and IPK's participation. Even several months before the opening and after the opening, two teams of German TV stations 3sat and ZDF came for a few days for filming. Both 30-minute features had multiple air times in national German television.

Gatersleben as a Biotechnology Centre

As a scientific centre, the Institute is engaged in many ways in the local initiative "Green Gate Gatersleben", and supports the further development of the Biotechnology Centre. Collaborations with various of the companies established on site are primarily performed in the context of joint research projects.

To awaken young people's interest in biology, the "Grüne Labor" ("Green laboratory") has developed a wide curriculum, targeted mainly at a school audience. This has attracted increasing interest, with over 6,000 school students, teachers and trainee teachers having taken part in the various courses and events of the past two years.

Verwaltung und technische Infrastruktur/ Administration and Technical Infrastructure

Personal und Finanzierung der Stiftung/Human Resources and Foundation Funding

Personal/Staff

Erfreulicherweise hat sich der Gesamtpersonalbestand in den beiden Berichtsjahren 2008 und 2009 gegenüber dem Jahr 2007 (Stichtag: 31. Dezember 2009) von 449 über 486 auf 500 Personen erhöht. Darunter befanden sich am Stichtag 264 Mitarbeiter/-innen auf Planstellen. Neben 157 (2008: 117; 2007: 105) Drittmittelbeschäftigten waren 57 (2008: 89; 2007: 57) Mitarbeiter/-innen über Annexstellen angestellt.

Auch im Bereich der Berufsausbildung kann das Institut mit insgesamt 22 Ausbildungsplätzen in verschiedenen Berufen, darunter zwei Bürokaufleute, 15 Biologielaborant(en)/-innen, zwei Fachinformatiker Systemintegration, eine Fachangestellte für Medien- und Informationsdienste und zwei Gärtner/-innen für Gemüsebau, einen Beitrag zur Qualifikation in der Region leisten.
Die Entwicklung der letzten fünf Jahre ist nachfolgend in Fig. 3 dargestellt.

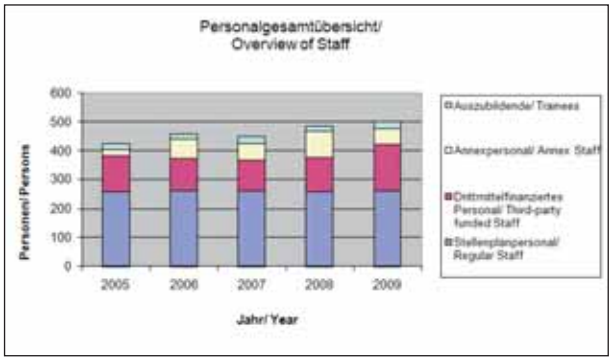

Fig. 3
Personalentwicklung/Development of staff

Zum 31. Dezember 2009 waren 297 Personen in einem befristeten Arbeitsverhältnis tätig. Von den 181 Wissenschaftler/-innen waren insgesamt 149 und von den 58 im Planstellenbereich 26 befristet beschäftigt.

Die Verteilung der Stellen auf die jeweiligen Programme zeigt Fig. 4:

Programm 1	Management, Analyse und Evolution pflanzengenetischer Ressourcen
Programm 2	Cyto-molekulare Genomanalyse
Programm 3	Molekulare Entwicklungsphysiologie
Programm 4	Angewandte Physiologie und Zellbiologie
Programm 5	Administration.

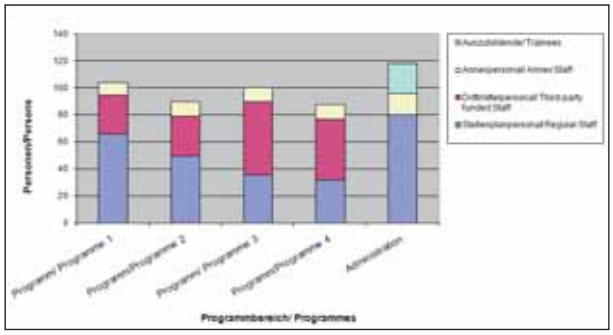

Fig. 4
Beschäftigte nach Programmen (Stand 31. Dezember 2009)/ Staff per programme (as of 31st December 2009)

Die Personalstruktur stellte sich 2009 wie folgt dar: Ein relativ hoher Anteil im technischen Bereich und in der Infrastruktur ist auf das Hauptforschungsobjekt „Pflanze" zurückzuführen, das einen hohen gärtnerischen und technischen Betreuungsaufwand verursacht.
Die Struktur im Einzelnen verdeutlicht Fig. 5.

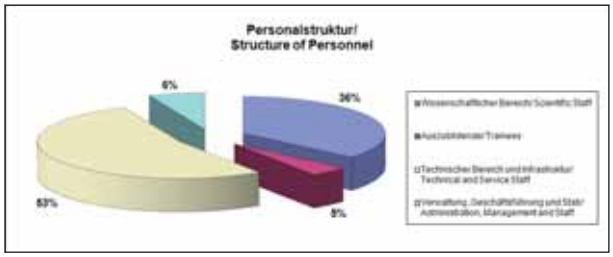

Fig. 5
Personalstruktur (Stand 31. Dezember 2009)/ Personnel structure (as of 31st December 2009)

Programmbudget 2008, 2009/Budget 2008, 2009

Seit der Einführung der Programmbudgets an Stelle der Wirtschaftspläne werden die Einnahmen und Ausgaben für die Programme ungeachtet der Mittelherkunft betrachtet. Dem IPK standen 2009 insgesamt 40.132 TEUR (2008: 36.989 TEUR) für eigene Ausgaben, d. h. ohne Einnahmen für Partner und ohne Einbehalte für Baumaßnahmen, zur Verfügung.
In 2009 betrugen die Zuwendungen im Rahmen der Grundfinanzierung 25.461 TEUR (2008: 25.909 TEUR). Darin enthalten waren 692 TEUR Betriebsmittel für die Projekte im wettbewerblichen Verfahren der Leibniz-Gemeinschaft (2008: 974 TEUR). Ab 2009 erhält das IPK zusätzliche Mittel vom Bund und vom Land für Maßnahmen aus dem Konjunkturpaket II der Bundesregierung (KP II)

in Höhe von 7.337 TEUR (2009: 1.007 TEUR). Die Einnahmen 2009 wurden zu je 50 % für Geräteinvestitionen und Baumaßnahmen verwendet. Für das IPK gesamt ergibt sich folgende Einnahmen- und Ausgabenstruktur:

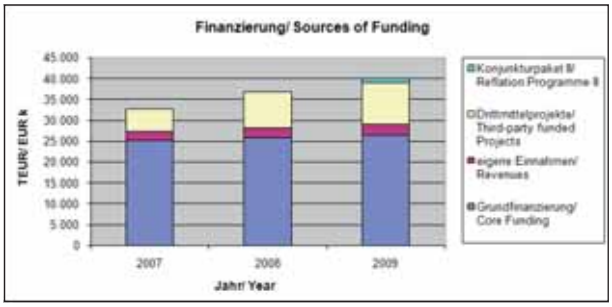

Fig. 6
Entwicklung der Gesamteinnahmen/ Development of total revenues

Auf der Seite Mittelverwendung entfielen rund 50 % der Gesamtausgaben auf den Personalbereich. Der gestiegene Anteil des Sachmittelbudgets war auf das erhöhte Drittmittelvolumen zurückzuführen. Einen Überblick über die Gesamtausgabenentwicklung 2007 bis 2009 ergibt das folgende Diagramm in Fig. 7:

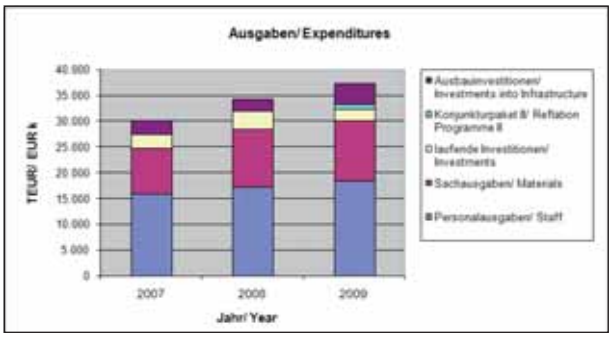

Fig. 7
Entwicklung der Gesamtausgaben/ Development of total expenditure

Drittmittelentwicklung 2008, 2009/ Third Party Funding 2008, 2009

In 2009 wurden für 127 Projekte (2008: 123) Einnahmen (ohne Partner) in Höhe von insgesamt 9.960 TEUR (2008: 8.604 TEUR) erzielt. Hauptzuwendungsgeber sind das Bundesministerium für Bildung und Forschung (BMBF), die Deutsche Forschungsgemeinschaft (DFG) und das Land Sachsen-Anhalt. Die Einnahmen vom BMBF resultierten überwiegend aus dem Programm „GABI-FUTURE", an dem das IPK mit 13 Projekten und einer Gesamtzuwendungssumme von 16.443 TEUR partizipiert.

Mit 1.087 TEUR Einnahmen im Rahmen der Auftragsforschung (2008: 623 TEUR) waren die Kooperationen ausschließlich mit Wirtschaftsunternehmen wieder zunehmend. Daneben waren in einer Vielzahl der BMBF- und EU-Projekte Betriebe der Wirtschaft als Partner involviert, ebenfalls mit steigender Tendenz. Außerdem erhielt das IPK Mittel von sonstigen Zuwendungsgebern in Höhe von 164 TEUR (Vorjahr 122 TEUR). Neben den Einnahmen für das IPK wurden 254 TEUR (Vorjahr 124 TEUR) für Partner eingenommen und weitergereicht. Die Entwicklung der Einnahmen für Projekte von 2007 über 2008 bis 2009 ist in Fig. 8 dargestellt.

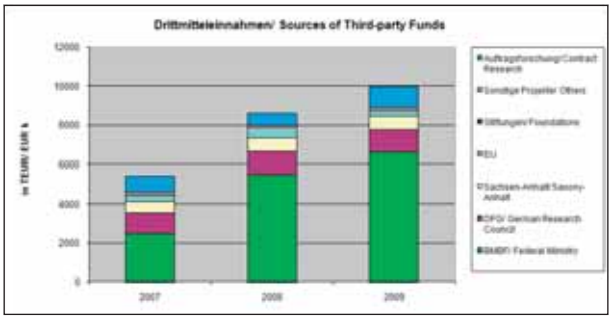

Fig. 8
Entwicklung der Drittmitteleinnahmen nach Mittelherkunft ohne Anteil für Partner/ Development of third-party funds excl. partner shares (source of funds).

Kostenrechnung/Cost Calculation

Für das IPK wird die Kostenstellenrechnung in Tabelle 1, S. 21, auf Programmebene zusammengefasst dargestellt. Zu den Forschereinzelkosten (FEK) zählen die Personalkosten, die Reisekosten und die Dienstleistungen Dritter in den wissenschaftlichen Arbeitsgruppen, einschließlich Ausgaben für Partner in Projekten. Die Gemeinkosten im Verhältnis zur Summe der Einzelkosten ergeben den Gemeinkostensatz. Gegenüber den Vorjahren ist ein Ansteigen der Gemeinkosten, speziell bei den Abschreibungen, zu verzeichnen. Die umfangreichen Sanierungsmaßnahmen in den Gebäuden und der technischen Infrastruktur wirken sich jetzt kostenseitig aus.

Tabelle 1/Table 1: Komprimierte Kostenstellenrechnung nach Programmen für 2008 (Angaben in TEUR)/Consolidated Cost Calculation for Programmes in 2008 (in EUR k)

	Wissenschaftliche Programme gesamt	Management, Analyse und Evolution pflanzengenetischer Ressourcen	Cytomolekulare Genomanalyse	Molekulare Entwicklungsphysiologie	Angewandte Zellbiologie
Summe FEK[1)]	14.684,9	4.623,4	3.780,0	3.579,7	2.701,8
Verbrauchsmaterial	2.262,9	695,1	624,3	470,7	472,8
Summe Einzelkosten	**16.947,8**	**5.318,5**	**4.404,3**	**4.050,4**	**3.174,6**
Gemeinkosten direkt gebucht	1.437,8	598,9	261,4	264,6	312,9
Abschreibungen	4.412,8	1.036,7	1.019,4	793,4	1.563,3
Zwischensumme	**5.850,6**	**1.635,6**	**1.280,8**	**1.058,0**	**1.876,2**
Summe Umlagen	6.301,2	2.787,6	1.257,7	1.095,2	1.160,7
Summe Forschergemeinkosten	**12.151,8**	**4.423,2**	**2.538,5**	**2.153,2**	**3.036,9**
Materialgemeinkosten	1.021,8	251,2	235,8	340,5	194,3
Verwaltungsgemeinkosten	2.919,6	968,1	696,0	634,4	621,1
Gemeinkosten gesamt	**16.093,2**	**5.642,5**	**3.470,3**	**3.128,1**	**3.852,3**
Selbstkosten	**33.041,0**	**10.961,0**	**7.874,6**	**7.178,5**	**7.026,9**
Gemeinkostensatz	**95 %**	**106 %**	**79 %**	**77 %**	**121 %**

[1)] FEK = Forschereinzelkosten

Technologietransfer/Technology Transfer

Zum Jahresende 2009 verfügte das IPK über 17 Betriebsgeheimnisse (2008: 16) und war alleiniger oder Mitanmelder an 25 Patentfamilien (2008: 23) mit Anmeldungen in Deutschland und im Ausland. Die Zahl der industriegeführten Patentanmeldungen mit Beteiligung von IPK-Erfindern beläuft sich auf 27 Patentfamilien und war in beiden Jahren konstant. Im Jahr 2009 wurden sechs Erfindungen (2008: 9) durch Wissenschaftler des IPK gemeldet. Diese wurden vom Institut vollumfänglich (2008: 4) in Anspruch genommen. Im gleichen Zeitraum wurden fünf neue Patentanmeldungen (2008: 3) durch das Institut vorgenommen.

Das Institut ging im Jahr 2009 insgesamt 23 Kooperations- und Konsortialverträge, darunter zwei Unteraufträge (2008: 18 Kooperationsverträge, darunter drei Unteraufträge und zwei Werkverträge) ein. Es wurden 8 Forschungs- und Entwicklungsverträge inklusive zwei Vertragsverlängerungen, (2008: 6), vier Verträge zur Ressourcennutzung und Projektimplementierung sowie zwei Beratungsverträge und eine Verwertungsvereinbarung (2008: 2) geschlossen. Daneben ging das IPK im Jahr 2009 einen Lizenzvertrag, eine Übertragungsvereinbarung sowie drei Memoranda of Understanding ein und schloss insgesamt 74 Materialtransfer- und Geheimhaltungsvereinbarungen (2008: 73) ab. Bereits 2008 hat das IPK die exklusiven Nutzungsrechte an einem neuen Antikörperformat der Firma Novoplant i.L. erworben.

Abteilung Genbank/
Department of Genebank

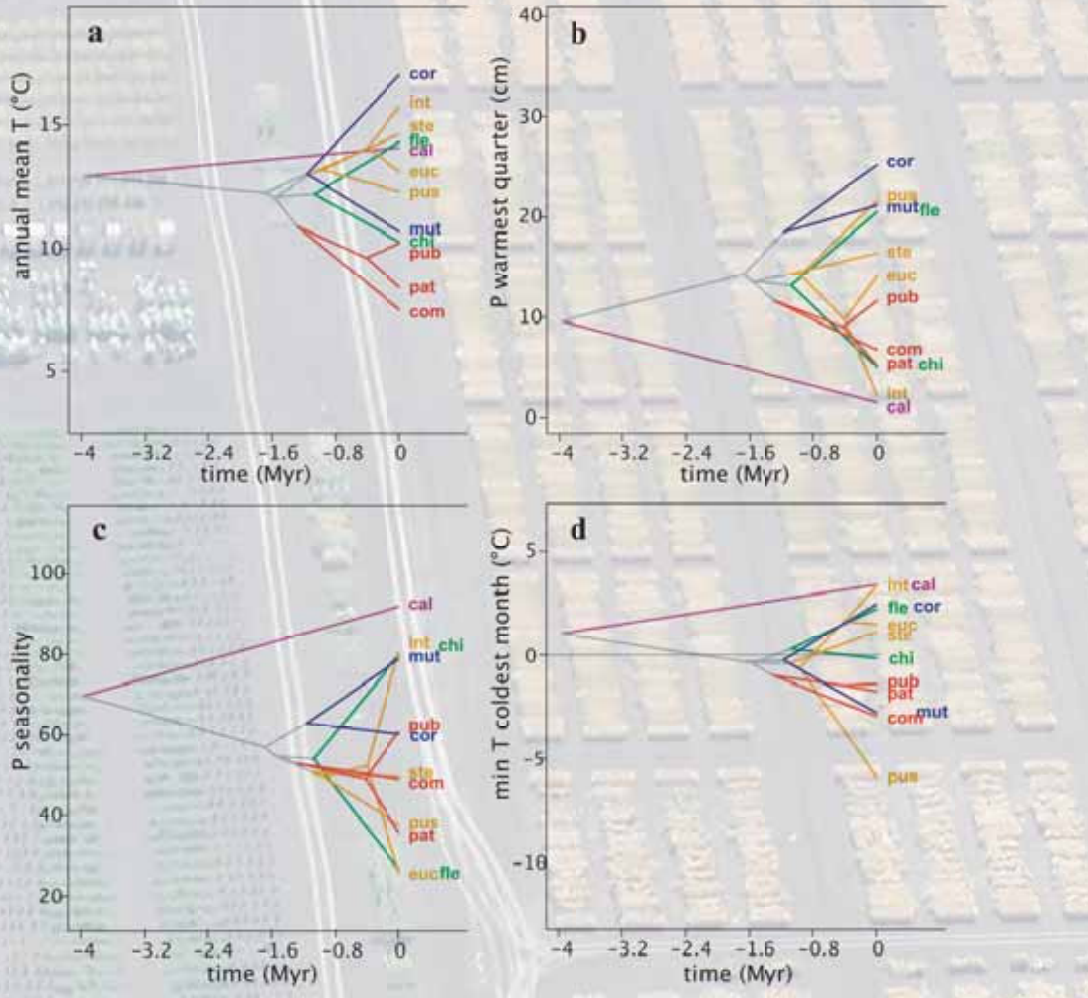

Fig. 9
Differenzierung der klimatischen Ansprüche einzelner Entwicklungslinien während der Evolution von Arten der Gerstengattung *Hordeum* in Amerika.
Wenn Arten sich aufspalten, verändern sie häufig ihre ökologischen Ansprüche und vermeiden so Konkurrenz mit ihren nächsten Verwandten. Durch die Integration der Information von Verwandtschaftsbäumen mit relevanten klimatischen Parametern lässt sich das Ausmaß dieser Veränderungen der ökologischen Nische quantifizieren. In der Abbildung sind für vier ökologische Parameter (a – Jahresdurchschnittstemperatur, b – Niederschläge während des wärmsten Quartals, c – Saisonalität der Niederschläge, d – niedrigste Temperatur im kältesten Monat) die Veränderung der Ansprüche diploider amerikanischer *Hordeum*-Arten während der letzten vier Millionen Jahre dargestellt. Nahe verwandte Artengruppen sind durch gleiche Farben im Stammbaum gekennzeichnet, die klimatischen Mittelwerte für die Arten durch die ersten drei Buchstaben des Artepithetons markiert. Die Daten zeigen, dass nahe verwandte Arten sich meist stark für zumindest einige Klimaparameter unterscheiden. Diese Differenzierung in engen Verwandtschaftskreisen führt dazu, dass Arten aus unterschiedlichen Gruppen dann wieder ähnliche ökologische Ansprüche entwickeln können (sich kreuzende Äste im Stammbaum). Dies scheint ein typisches Muster zu sein wenn schnelle Artbildung auf engstem Raum stattfindet (S. Jakob et al.).

Differentiation of climatic niches during the evolution of *Hordeum* species in the Americas.
When species split they often change their ecological niches, thus preventing competition with their closest relatives. Via combination of phylogenetic information (species trees) with the relevant climatic parameters of species it is possible to quantify the amount of niche change. In this figure, ecological changes that took place during the last four million years in the evolution of American diploid *Hordeum* species are shown for four climate parameters (a – mean annual temperature, b – precipitation during the warmest quarter, c – seasonality of precipitation, d – minimum temperature during the coldest month). Closely related species are given in identical colors in the phylogenetic tree, average parameter values through the first three letters of the species epithet. The analysis shows that close relatives evolved pronounced differences for at least some climate parameters. This differentiation resulted in a niche filling pattern, which means that species from different groups evolved into similar climatic niches for some parameters (indicated by crossing branches in the phylogenetic trees). This seems to be a typical pattern for rapid species radiations (S. Jakob et al.).

Abteilung Genbank

Leiter: Prof. Dr. Andreas Graner

Allgemeine Forschungsziele

Die Bundeszentrale *ex situ*-Genbank für landwirtschaftliche und gartenbauliche Kulturpflanzen zählt zu den weltweit größten Sammlungen und leistet einen Beitrag zur Erhaltung der biologischen Vielfalt. Ihre zentrale Aufgabe besteht in dem Erhalt und der Charakterisierung des Sammlungsmaterials sowie in der Erarbeitung von Strategien für die verbesserte Nutzung pflanzengenetischer Ressourcen.

Vor dem Hintergrund des *Internationalen Übereinkommens über die biologische Vielfalt* aus dem Jahr 1993 und des im Jahr 2004 in Kraft getretenen *Internationalen Vertrags über Pflanzengenetische Ressourcen für Ernährung und Landwirtschaft* ist die Genbank fester Bestandteil der *Nationalen Strategie zur Biologischen Vielfalt*. In diesem Zusammenhang ist sie an der Umsetzung des *Nationalen Fachprogramms zur Erhaltung und nachhaltigen Nutzung pflanzengenetischer Ressourcen* sowie am *European Co-operative Programme on Genetic Resources* (ECPGR) beteiligt. Im Rahmen der internationalen Aufgabenteilung trägt die Genbank die Verantwortung für die Erhaltung des europäischen Teils der internationalen *Barley Core Collection* und die Bereitstellung und Pflege der europäischen Datenbanken für Gerste und *Poa*.

Entwicklungen im Berichtszeitraum

Die in der Abteilung durchgeführten Arbeiten sind strukturbestimmender Bestandteil des in der Programmplanung festgelegten Themas „Management, Analyse und Evolution pflanzengenetischer Ressourcen".
Im Zentrum des Sammlungsmanagements steht die Fortführung und Weiterentwicklung der Bundeszentralen *ex situ*-Genbank, welche im Jahr 2003 aus der Fusion der Sammlungen des IPK und der ehemaligen Bundesanstalt für Züchtungsforschung an Kulturpflanzen (BAZ) Braunschweig hervorging. Sie umfasst zum gegenwärtigen Zeitpunkt 146.966 Akzessionen aus 2.649 Arten und 779 Gattungen. Neben den genannten Lebendsammlungen unterhält die Genbank als Referenzzentrum für taxonomische Arbeiten ein umfassendes Herbarium mit über 400.000 Belegen sowie über 140.000 Referenzmuster von Getreideähren und Früchten.

Die Erhaltung der Sammlung erfolgt in Gatersleben (126.837 Akzessionen) und an den beiden Außenstandorten Groß Lüsewitz (Kartoffelsortiment, 6.013 Akzessionen) und Malchow (Öl- und Futterpflanzen,

Department of Genebank

Head: Prof. Andreas Graner

Research Goals

The Federal *ex situ* Genebank for agricultural and horticultural crops is one of the largest collections worldwide and contributes to the global effort regarding conservation of biological diversity. Its main goal is the preservation and the characterisation of its accessions as well as the development of strategies aiming at an improved utilization of Plant Genetic Resources.

In conjunction with the *International Convention on Biological Diversity* from 1993 and the *International Treaty on Plant Genetic Resources for Food and Agriculture* that came into effect in 2004, the Genebank also represents a major component regarding implementation of the *National Strategy on Biological Diversity.* In this context the Genebank is involved in the *National Expert Programme for Conservation and Sustainable Use of Plant Genetic Resources (BEKO)* and the *European Co-operative Programme on Genetic Resources* (ECPGR). As to international responsibilities, the Genebank maintains the European part of the *International Barley Core Collection* and maintains the European databases for barley and *Poa.*

Developments in the Reporting Period

The central objective of the collection management is the continuation and advancement of the Federal Centre *ex situ* Genebank which was formed in 2003 through fusion of the collections of the IPK and those of the former Federal Centre for Breeding Research on Cultivated Plants (BAZ) Braunschweig. It comprises at present 146,966 accessions from 2,649 species and 779 genera. Besides this living collection the Genebank maintains a comprehensive herbarium which serves as reference centre for taxonomical studies and holds more than 400,000 voucher specimen as well as a collection representing 140,000 reference samples of spikes and fruits.

The collection is maintained in Gatersleben (126,837 accessions) and two satellite stations located at the Baltic Sea, Groß Lüsewitz (potato assortment, 6,013 accessions) and Malchow (oil and forage crops, 14,116 accessions). About 3,100 accessions are preserved *in vitro*, including 2,700 potato accessions. As a safety backup of this living collection a cryo-collection of potato is continuously extended and currently comprehends 1.140 accessions.

14.116 Akzessionen). Etwa 3.100 Akzessionen werden *in vitro* erhalten, hierunter befinden sich 2.700 Kartoffelakzessionen. Zur Absicherung der Lebendsammlung wird die Cryo-Sammlung von Kartoffeln kontinuierlich ausgebaut und umfasst gegenwärtig 1.140 Akzessionen.

Der Feld- und Gewächshausanbau wurde im Jahr 2008 von 13.126 auf 15.929 Akzessionen erhöht. Hierunter befinden sich 4.360 Akzessionen, die ausschließlich zur vegetativen Erhaltung sowie 2.710 Akzessionen, die zur wissenschaftlichen Bearbeitung/Evaluierung angebaut wurden. Die verbliebenen 8.859 Akzessionen wurden zur Samenvermehrung angebaut. Dies entspricht einer Vermehrung von ca. 6 % der Samenträger. Mit der vorübergehenden Anhebung des Vermehrungsanbaus soll in den kommenden Jahren das durchschnittliche Reproduktionsintervall in bestimmten Sortimenten verkürzt werden. Sortimentsumfänge und Anbauzahlen sind Tabelle 2, S. 25 zu entnehmen.

Zur Absicherung der weltweit in Genbanken gelagerten Saatgutbestände eröffnete der *Global Crop Diversity Trust* im Jahr 2008 im Permafrostboden von Spitzbergen ein Langzeitlager. Das IPK nutzt diese Möglichkeit zur Einlagerung von Sicherheitsduplikaten und hat seit der Eröffnung des **Global Seed Vault** über 22.000 Samenmuster nach Spitzbergen geschickt. Parallel hierzu wurden zur Absicherung der Cryo-Sammlung von Kartoffel Sicherheitskopien aller eingefrorenen Muster von der Deutschen Sammlung für Mikroorganismen und Zellkulturen (DSMZ) in Braunschweig übernommen.

In den beiden vergangenen Jahren wurden 18.480 bzw. 22.799 Muster abgegeben. Dies bedeutet einen erheblichen Anstieg gegenüber den Vorjahren. Die durchschnittliche Bearbeitungsdauer für Bereitstellung und Versand des Materials beträgt nach Eingang der unterzeichneten Standard Materialtransfer Vereinbarung (sMTA) 8,5 Tage. Forschungsinstitute stellten wie in den Vorjahren die weitaus größte Nachfragergruppe dar. Über die Hälfte der Anfragen kommt aus dem Ausland. In den vergangenen zwei Jahren wurden Muster in 55 Länder abgegeben. Eine Aufschlüsselung der im Jahr 2009 abgegebenen Muster nach Sortimenten und Nutzergruppen ist der Tabelle 2, S. 25 und Fig. 10 zu entnehmen.

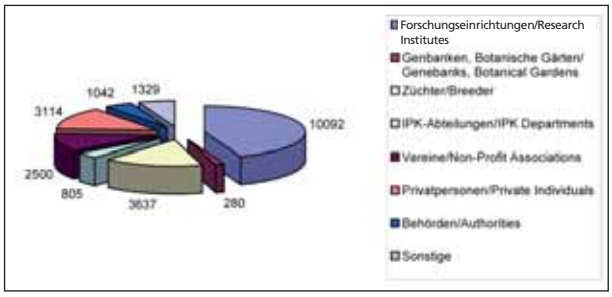

Fig. 10
Materialabgabe im Jahr 2009, aufgeschlüsselt nach Nutzergruppen (insgesamt 22.799 Muster)/ Material transfer in 2009, according to user groups (totaling 22,799 samples).

The number of accessions grown in the field or greenhouse was increased from 13,126 to 15,929. Among these 4,360 accessions were cultivated for vegetative maintenance/propagation and 2,710 accessions were cultivated for phenotypic evaluation (previous year 2,100). The remaining 8,859 accessions, corresponding to about 6 % of the total collection, were grown for seed multiplication. By transiently increasing the number of field/greenhouse multiplications for selected assortments the average interval of seed reproduction will be shortened aiming at improved seed viability for these species. Further information on the collection and its multiplication are presented in table 2, p. 25.

In order to increase the safety of the 6 million-odd seed samples maintained in genebanks across the world the *Global Diversity Trust* opened up in 2008 a long term storage facility sunk into the perma-frost soil of the island of Svalbard. IPK followed the invitation to store safety duplicates in the **Global Seed Vault**. Since then some 22,000 seed samples have been transferred to Svalbard. The Genebank will continue this effort in the years to come, until the whole collection will be mirrored in this way. In a parallel activity, safety duplicates of the complete cryo-collection of potato were taken over by the German Collection of Microorganisms and Cell Cultures (DSMZ).

In the last two years 18,480 and 22,799 samples were distributed, respectively. In comparison to previous years this represents a substantial increase. The average handling time has been further reduced and now amounts to 8.5 days from receipt of the signed standardised Material Transfer Agreement (sMTA) until dispatchment of the seeds/tubers/plants. As in previous years, research institutes represented the major user group. Also, more than 50 % of the requests are from abroad. In the last two years, material was shipped to 55 countries. A break down of the seed distribution in 2009 according to assortments and user groups is provided in table 2, p. 25 and Fig. 10.

The Genebank is spearheading internationals efforts towards the development and establishment technical standards for the conservation management. In 2007 a Quality Management System (QM) according to DIN EN ISO 9001:2000 was established. 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 2009 the ISO certificate was confirmed by an external audit.

Research within the Genebank is structured into three programmes: **"Management and Evaluation"**, **"Characterization and Documentation"** as well as **"Taxonomy and Evolution"**. The research within the department mainly applies to the priority theme **"Conservation and**

Tabelle/Table 2: Kennzahlen zur Genbank gegliedert nach Sortimentsgruppen. Für die einzelnen Sortimente sind die jeweils größten Teilsammlungen aufgeführt (Stand 1.7.2009)./Inventory of the *ex situ* collection as of July 1, 2009. For the individual assortments the largest collections are listed.

Sortimente	Assortments	Bestand/Accessions	Anbau/Cultivation	Abgaben/Distribution
Getreide und Gräser	***Cereals and Grasses***	***62720***	***2124***	***5917***
Weizen	wheat	26887	842	1847
Gerste	barley	21834	679	2639
Hafer	oat	4811	122	144
Roggen	rye	2395	66	200
Triticale	Triticale	1581	36	14
Aegilops	*Aegilops*	1527	52	249
Mais	maize	1513	94	224
Hirsen	millets	835	37	276
Gräser	grasses	1337	196	324
Leguminosen	***Legumes***	***27348***	***1474***	***2406***
Phaseolus	*Phaseolus*	8739	409	377
Erbsen	pea	5306	211	767
Ackerbohnen	field beans	3299	71	61
Lupinen	lupins	2454	96	51
Wicken	vetches	1881	69	79
Kleearten	clover species	1710	247	180
Sojabohnen	soybeans	1513	18	50
Bohnen-Sonderkulturen	other beans	647	65	207
Lathyrus	*vetchling*	533	46	545
Kichererbsen	chickpea	531	62	12
Linsen	lentils	471	74	39
Sonstige	others	264	106	38
Cucurbitaceae	***Cucurbitaceae***	***2654***	***106***	***1284***
Kürbisse	pumpkins	1078	40	406
Melonen	melons	725	21	719
Gurken	cucumbers	696	27	110
Sonstige	others	155	18	49
Gemüse (+Rüben)	***Vegetables***	***18229***	***2546***	***5026***
Tomaten	tomatoes	3358	110	656
Allium	*Allium*	3023	1210	254
Beta	*Beta*	2314	156	1041
Brassica	*Brassica*	2151	264	815
Paprika	pepper	1523	46	694
Salat	lettuce	1133	236	194
Quinoa	quinoa	958	52	44
Raphanus	*Raphanus*	742	38	68
Zichorie	chicory	692	62	177
Möhren	carrots	486	70	125
Sellerie	celery	247	32	123
Spinat	spinach	214	8	107
Eierfrüchte	eggplants	114	10	135
Sonstige	others	1274	252	593
Öl-, Faser-, Farbpflanzen	***Oil, Fibre, Dye Plants***	***5545***	***619***	***1228***
Lein	flax	2323	95	166
Sonnenblumen	sunflower	708	125	111
Ölpflanzen	oil plants	548	127	647
Farbpflanzen	dye plants	482	105	90
Faserpflanzen	fibre plants	134	29	36
Sonstige	others	1350	138	178
Arznei-, Gewürzpflanzen	***Medicinal, Spice Plants***	***8281***	***2471***	***3131***
Mohn	poppy	1155	902	1699
Tabak	tobacco	590	131	78
Sonstige	others	6536	1438	1354
Mutanten	***Mutants***	***2060***	***715***	***54***
Soja	soybean	850	603	5
Tomaten	tomato	744	15	31
Antirrhinum	*Antirrhinum*	466	97	18
Kartoffeln	***Potatoes***	***6013***	***3919***	***1647***
Öl- und Futterpflanzen	***Oil and Forage Crops***	***14116***	***1955***	***2106***
Gräser	grasses	10366	1461	536
Raps und Futterkohl	rapeseed and feeding kale	2472	359	1394
Rotklee und Luzerne	red clover and alfalfa	1278	135	176
Gesamt/Total		Err:522	15929	22799

Seit 2007 verfügt die Genbank über ein Qualitätsmanagementsystem nach DIN EN ISO 9001:2000. 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. Darüber hinaus wurde im Frühjahr 2009 ein externes Wiederholungsaudit zur Aufrechterhaltung des Zertifizierungsstatus durchgeführt.

Forschung

Eine wichtige Voraussetzung für die weitere Optimierung des Erhaltungsmanagements sowie die zukünftige Nutzung pflanzengenetischer Ressourcen ist die enge Verflechtung mit der Forschung sowohl innerhalb der Genbank als auch über die Abteilungsgrenzen hinweg. Aufgrund der Größe der Abteilung und der Breite der bearbeiteten Forschungs- und Erhaltungsarbeiten ist die Abteilung in drei Forschungsbereiche gegliedert: *Management und Evaluierung*, *Charakterisierung und Dokumentation* sowie *Taxonomie und Evolution*. Die Forschungsthemen sind überwiegend dem IPK-Schwerpunkt *Erschließung, Erhaltung und Nutzung genetischer Diversität* zugeordnet. Grundsätzlich lassen sich die Forschungsarbeiten in sammlungsbezogene und nutzungsbezogene Forschung differenzieren. Das Ziel der sammlungsbezogenen Forschung ist ein verbessertes Erhaltungsmanagement sowie die Bearbeitung von Fragestellungen zur Evolution und Artbildung. Die nutzungsbezogenen Forschungsarbeiten konzentrieren sich auf die Inwertsetzung pflanzengenetischer Ressourcen für die züchterische Verbesserung von Kulturpflanzen. Hierbei stehen molekulargenetische Ansätze bei Getreide im Vordergrund.

Im Zentrum des Forschungsbereichs **Taxonomie und Evolution** steht die Bearbeitung von Fragestellungen der Kulturpflanzenevolution, wobei Artbildungsprozesse sowie die Beziehung von Artbildung, Anpassung und Ausbreitung untersucht werden. Einen Schwerpunkt bilden Arbeiten zur phylogenetischen Analyse innerhalb der Gattung *Hordeum*. Ziel ist es hierbei, detaillierte Erkenntnisse zur Verwandtschaft, Ökologie und Populationsgeschichte zu erarbeiten und *Hordeum* als Modell für temperate Gräser zu etablieren. Beispiele für die differenzierte Angepasstheit verschiedener *Hordeum*- Arten sind auf dem Titelblatt der Abteilung dargestellt (Fig. 9, S. 22). Für drei eng miteinander verwandte diploide südamerikanische *Hordeum*-Arten (*H. comosum*, *H. patagonicum* und *H. pubiflorum*) der patagonischen Steppe wurde eine phylogeografische Analyse abgeschlossen. Darüber hinaus konnten am Beispiel von *Hordeum murinum* Alloploidisierungsereignisse als wesentliches Element der

Utilization of Genetic Diversity". Activities can be further differentiated into research related to the maintenance and management of the collection and research that targets utilization of Plant Genetic Resources. The first aims at improving management of the collection as well as research into evolution and speciation, while the latter aims at valorization of Plant Genetic Resources for the genetic improvement of crop plants. Here major emphasis on implementation of molecular genetics approaches for cereal species.

Research

The programme "**Taxonomy and Evolution**" deals with questions regarding the evolution of crop plants and related species. Specific focus is being put on the investigation of speciation as well as the relationship between speciation, adaptation and radiation. The genus *Hordeum* is used as a model for temperate grasses to gain insight into phylogenetic relationships, ecology and demographic history. Examples for the differential adaptation of different *Hordeum* species are presented on the cover page of the department (see Fig. 9, p. 22). A phylogenetic analysis was completed for three closely related, diploid *Hordeum* species of the Patagonian steppe (*H. comosum*, *H. patagonicum* und *H. pubiflorum).* Is was exemplified for *Hordeum murinum*, polyploidization represents the major driving force for speciation within this genus. Specific questions regarding evolution and speciation are being investigated within additional genera including *Macaranga* and *Crocus*.

Research within the programme "**Management and Evaluation**" centers on further optimization 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. Results on seed longevity for *Hordeum*, *Secale*, *Brassica* and *Linum* confirmed previous observations in wheat regarding intraspecific varibility of this trait. To further scrutinize the genetic basis of seed longevity, analysis of segregating populations was initiated in barley resulting in the identification of several quantitative trait loci (QTL). In addition to research into seed longevity further optimization of cryo conservation of vegetatively propagated species was continued for potato, *Allium* and mint. A project on the taxonomic, morphological and biochemical characterization and evaluation of *Papaver* was completed.
The programme "**Characterization and Documentation**" comprises the structural and functional characterization of genetic resources at the DNA level as well as the development and curation of databases for storage and provision of genebank-related data. The latter mainly includes passport data, geographic references and information on the characterization of genebank accessions. The centerpiece of these effort is the ongoing development of the Genebank Information System (GBIS).

Artbildung innerhalb der Gattung *Hordeum* nachgewiesen werden. Spezielle Fragestellungen zur Evolution und Artbildung werden an *Macaranga*, *Crocus* sowie einigen weiteren Gattungen bearbeitet.

Die Forschungsarbeiten im Bereich **Management und Evaluierung** konzentrieren sich in erster Linie auf die Verbesserung des Erhaltungsmanagements. Hierbei stellt die maximale Lagerdauer von Saatgut eine wichtige Kenngröße für die Wirtschaftlichkeit des Erhaltungsmanagements dar. In diesem Zusammenhang bestätigten die Ergebnisse zur Langlebigkeit von Saatgut bei *Hordeum*, *Secale*, *Brassica* und *Linum* die beim Weizen aufgefundene intraspezifische Variabilität. Bei Gerste wurden erste genetische Untersuchungen initiiert. Mit Hilfe von DNA-Markern wurden QTLs (Quantitative Trait Loci) identifiziert, die für das Merkmal ‚seed longevity' verantwortlich sind. Daneben wurden Arbeiten zur taxonomischen, morphologischen und biochemischen Charakterisierung und Evaluierung von *Papaver* abgeschlossen. Komplementär zu den Arbeiten zur Langlebigkeit von Saatgut wurden die Arbeiten zur Optimierung der Cryo-Konservierung vegetativ zu erhaltender Arten bei Kartoffel, *Allium* und Minze fortgeführt.

Der Bereich **Charakterisierung und Dokumentation** befasst sich mit der strukturellen und funktionellen Charakterisierung von Genbankmaterial auf DNA-Ebene sowie mit der Entwicklung und Pflege von Datenbanken zur Speicherung und Bereitstellung von genbankbezogenen Daten. Letztere umfassen in erster Linie Passportdaten, geografische Referenzierungen sowie Charakterisierungsdaten.

Die laufenden Forschungsarbeiten zur Kartierung agronomischer Merkmale und zur Genklonierung wurden durch die in 2008 gegründete und über einen Zeitraum von fünf Jahren durch das BMBF finanzierte **Nachwuchsgruppe Pflanzliche Baupläne** verstärkt. Im Mittelpunkt des Interesses steht die Aufklärung der genetischen Grundlagen von Schlüsselmerkmalen zur Ährenausbildung und des Blühzeitpunkts bei Weizen sowie deren Beziehung zur Ertragsbildung.

Neben spaltenden Nachkommenschaften aus bi-parentalen Kreuzungen werden in verstärktem Umfang „natürliche" Populationen zur Assoziationskartierung quantitativ vererbter Merkmalskomplexe genutzt. Grundlage für die systematische Erforschung und Nutzung der genetischen Diversität einer Art ist die Kenntnis der Genomsequenz. Die Arbeiten im Bereich der Genomanalyse konzentrieren sich daher auf die Entwicklung einer physischen BAC-contig-Karte des Gerstengenoms sowie auf die genomische Sequenzierung. Entsprechende Arbeiten sind Teil einer internationalen Initiative zur Sequenzierung des Gerstengenoms (http://barleygenome.org). Weitere Einzelheiten hierzu sowie zu den oben angeführten Forschungsaktivitäten sind den Berichten der einzelnen Arbeitsgruppen zu entnehmen.

Andreas Graner, Januar 2010

Regarding the characterization of genetic resources at the DNA level, research into genetic mapping of agronomic traits and cloning of the corresponding genes was further enforced by the establishment of a new research group (Plant Architecture) that is being funded by BMBF over a period of five years. The group has started to investigate the genetic basis of variation in spike morphology and flowering time in wheat and to explore the relationship of these traits with yield formation.
In addition to segregating progenies derived from bi-parental crosses, "natural" populations are increasingly used for genetic analysis of quantitative traits by association mapping. In addition to mapping individual loci, availability of the entire genomic sequence allows for the systematic exploration and utilization of the genetic diversity of a given species. Hence, research efforts regarding genome analysis focus on the construction of a physical BAC-contig map of the barley (*Hordeum vulgare*) genome and the generation of a coherent genomic sequence of this crop species. The corresponding activities are imbedded in an international initiative to sequence the barley genome (http://barleygenome.org).

Further details of these and many other research activities will be found in the subsequent reports of the individual groups.

Andreas Graner, January 2010

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, till 31.12.2008)
Athmer, Benedikt (0,25 Annex, 01.02.-30.09.2009; 0,5 P, since 01.10.2009)
Kilian, Benjamin, Dr. (P, since 01.03.2008)
Rizvi, Reshma (0,5 Annex, 01.09.-30.11.2008)
Rizvi, Syed Masood Hasan, Dr. (P, 01.10.2008-31.05.2009)
Schulte, Daniela, Dr. (Pakt für Forschung und Innovation, till 31.12.2008)
Vu, Thi Ha Giang, Dr. (0,5 Annex, till 10.02.2008)

Grant Positions
Ariyadasa, Ruvini Tharanga, Dr. (BMBF, since 01.01.2009)
Athmer, Benedikt (0,5 Saxony-Anhalt, till 31.12.2008; 0,5 Overhead, 01.01.-31.01.2009)
Gottwald, Sven, Dr. (BMBF, till 28.02.2009)
Pasam, Raj Kishore (0,5 BMBF, since 01.07.2008)
Pietsch, Christof, Dr. (BMBF, 15.03.-31.08.2008)
Poursarebani, Naser (0,5 BMBF, since 01.02.2008)
Rizvi, Syed Masood Hasan, Dr. (BMBF, till 30.09.2008)
Schmutzer, Thomas (0,5 BMBF, since 15.02.2009)
Schulte, Daniela, Dr. (BMBF, since 01.01.2009)
Shahinnia, Fahimeh, Dr. (DFG)
Sharma, Rajiv (0,5 DFG, since 01.01.2009)
Zhou, Ruonan, Dr. (0,5 BMBF; 0,5 EU, since 26.01.2009)

Visiting Scientists/Scholars
Barabaschi, Delfina, Dr. (CRA-Scholarship, till 10.02.2008)
Gottwald, Sven, Dr. (self-financed, since 02.03.2009)
Große, Ivo, Prof. (Martin Luther University Halle-Wittenberg, till 31.03.2008)
Komatsuda, Takao, Dr. (self-financed, 18.08.-27.08.2008)
Montemurro, Cinzia (University of Bari, 12.05.-23.05.2008)
Perovic, Dragan, Dr. (BAZ Quedlinburg till 31.12.2008; JKI Quedlinburg since 01.02.2009)
Rizvi, Reshma (self-financed, 01.01.-31.03.2009)
Sabetta, Wilma (University of Bari, till 30.06.2008)
Sharma, Shailendra, Dr. (self-financed, 27.10.-06.12.2008)
Vu, Thi Ha Giang, Dr. (self-financed, 19.07.-30.09.2008)

Goals

Understanding the selective forces that shape the genome of barley (*Hordeum vulgare*) and identification of agriculturally important genes to study their function and to develop approaches for the exploitation of allelic diversity in genebank collections.

Research Report

Our programme focuses on two major areas of genome research to facilitate both hypothesis-driven as well as explorative research on biological and genetic problems: (i) the continued **development of resources** for structural and functional genome analysis including the development of a physical BAC contig map and a genomic sequence of selected regions of the barley genome; (ii) **structural and functional genetic analysis** of qualitative and quantitative traits applying meiotic mapping and association analysis including the isolation of genes by map-based cloning and transcript profiling.

Embedded into the research agenda of the International Barley Sequencing Consortium (IBSC, http://barleygenome.org) the **construction of a physical map** represents a key resource for map-based sequencing of the barley genome along a minimal tiling path. Completion of high information content fingerprinting (HICF) of over 600,000 BACs corresponding to ~14-genome equivalents now provides the basis for the identification of overlapping BAC clones and the subsequent assembly of a contig map. Assignment of individual contigs to the barley genetic map has been initiated by correlating genetically mapped markers with BAC clone addresses using two complementary approaches. On the one hand PCR-based markers derived from expressed gene information (EST, cDNA) are utilised to screen multidimensional pools of BAC clone DNA. On the other hand such DNA pools are screened by microarrays representing highly multiplexed marker information (i.e. DArT markers). So far, both approaches revealed genetic anchoring information for 3,000 BAC addresses (D. Schulte, R. Ariyadasa, R. Zhou, N. Poursarebani).

In parallel to the attempt of building a physical map of the barley genome "second generation" sequencing technologies are under evaluation for their usefulness in the context of **sequencing the barley genome**. Whole genome shotgun sequencing datasets covering

1 % to 10 % of the barley genome in the format of short read sequences (35 - 100 nucleotides) were exploited to statistically assess the characteristics of barley genome composition. Such information is instrumental for the annotation of contigous genomic sequences especially for the prediction of repetitive DNA. Using the Roche/454 platform for shotgun sequencing and assembly of barley BAC clones 48 BACs were "barcoded" and sequenced as a pool to 20-fold coverage. The resulting sequences could be assembled reaching phase I quality (less than 10 gaps, non-ordered contigs). Over 2,000 BAC clones have been sequenced by this approach providing insight into sequence composition of close to 5 % of the barley genome. The possibility to sequence purified mitotic chromosomes has been explored on the Roche/454 platform using barley chromosome 1H. 10,000 chromosomes were amplified and shotgun sequenced to ~1.3-fold coverage.

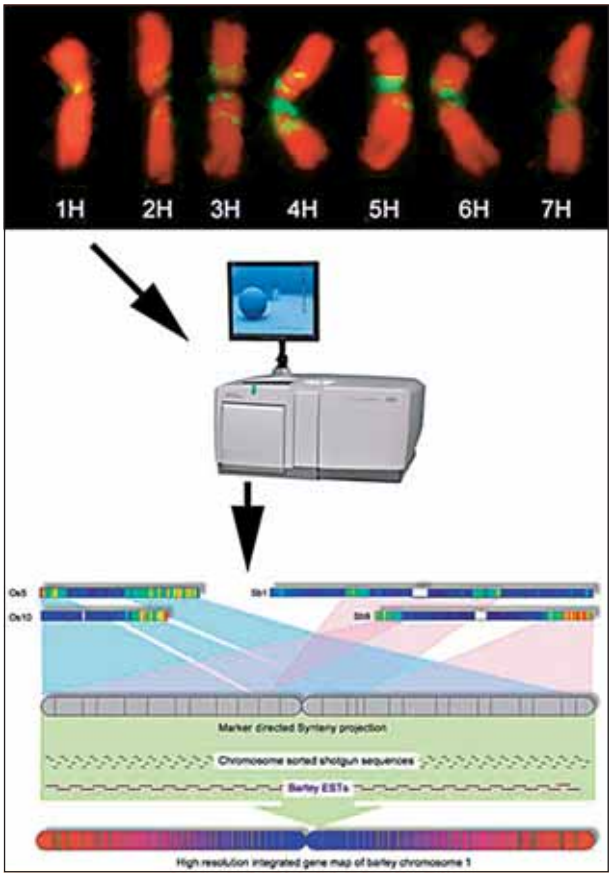

Fig. 11
Virtual gene maps of barley chromosomes can be generated by next generation sequencing of flow sorted chromosomes.
Flow-sorting of chromosome suspensions obtained from synchronised root tip tissue of wheat-barley addition lines allows the purification of individual barley chromosomes at over 90 % purity. Such DNA can be amplified to microgram quantities by whole genome amplification procedures (Genomiphi, GE Healthcare). After mechanical shearing, this DNA sample can be subjected to next generation sequencing, i.e. 454 Roche GS FLX (Titanium), resulting in millions of 250 - 400 bp. After applying repeat masking, the low-copy or gene-containing reads of the sample can be integrated with information derived from EST-based markers of barley and grass reference genome sequences as virtual gene order model of a barley chromosome. (Image of fluorescent *in situ* hybridisation of barley chromosomes is courtesy of Dr. A. Houben, IPK Gatersleben. The synteny and shotgun sequence integration model is taken from Mayer et al. 2009, Plant Physiology 151: 496-505).

This dataset allowed prediction of around 5,000 genes for this barley chromosome. Furthermore, via the integration of information from sequenced model grass genomes (rice, sorghum, *Brachypodium*) a virtual gene order map of over 2,000 genes was developed for chromosome 1H (see Fig. 11). The combination of chromosome shotgun and BAC sequence information allowed to assign a chromosomal position for ~1,500 of the above mentioned BAC clones (D. Schulte).

To develop genome-based strategies for the utilisation of plant genetic resources the value of **association mapping** in a diverse set of 225 spring barley accessions has been explored for the dissection of quantitative traits. SNPs within transcription factors GaMYB, BPBF, BLZ1, BLZ2 were investigated for association with *thousand grain weight*, *starch content* and *crude protein content*. Interestingly, only SNPs in the gene BPBF revealed highly significant associations accounting for up to 12 % and 5 % of the phenotypic variation in *crude protein content* and *starch content*, respectively (G. Haseneyer, TU Munich). Because only a minor fraction of the observed phenotypic variation could be explained by SNPs within the candidate genes, the study was expanded to investigate the feasibility of whole genome association based on 1037 DArT and 918 ILLUMINA markers, respectively. Averaged across all seven chromosomes, intrachromosomal LD decays within about 5 centiMorgans to $r^2 < 0.15$. Analyses of marker-trait associations were based on mixed models accounting for population structure and kinship. Each marker system identified more than 20 significant associations with each QTL only explaining a minor portion of the overall genetic variance (R. Pasam, R. Sharma, B. Kilian). Future work will focus on increasing the marker density around the most prominent QTLs and their verification in biparental mapping populations and the isolation of the underlying genes. To increase the genetic resolution available for association analysis, further populations are being developed that are characterised by a more rapid decay of LD.

In addition to the identification marker trait associations at the DNA level **correlations between quantitative traits and transcript abundance** of selected genes were investigated. To this end mRNA levels in germinating seeds were analysed in a panel of 56 spring barley cultivars that showed phenotypic differences in malting quality. RNA abundance was determined by interrogating a customised cDNA array comprising more than 12.000 ESTs, known to be expressed during seed formation and germination. Based on the hypothesis that the expression of a quantitative trait is a function of the expression-level of the underlying gene(s), mRNA abundance in the 56 cultivars was correlated with the level of expression of 12 parameters which are commonly used to assess malting quality. With this approach, 1,607 genes were identified that showed a difference in transcript abundance of > 2 between at least 2 cultivars.

121 of these showed an expression pattern across the 56 cultivars that was correlated ($p < 0.001$) to at least one malting quality parameter at a FDR of 5 %. This tally on the one hand comprises a substantial number of genes already known to be involved in the expression of malting quality. On the other hand a number of novel genes were detected, which are of prime interest for plant breeding and therefore will be further validated in QTL studies (M. Rizvi).

Using a similar approach, genes involved in the **regulation of freezing tolerance** in barley, wheat and rye were identified. The overall level of freezing tolerance is significantly different between the three species. Generally, analysis of transcript abundance during cold acclimation revealed down-regulation of genes belonging to the light reaction of photosynthesis. Key-genes of the sugar metabolism were activated as well as several enzymes of amino acid metabolism. Notwithstanding these commonalities in gene regulation, the cold acclimation response also affected diverse sets of genes in each species, and even within a given species functional diversity of genes recruited for cold acclimation response was observed (B. Athmer).

Collaborations (selection)

Within the Institute:

Dept. of Cytogenetics and Genome Analysis, Research Group Chromosome Structure and Function; Dr. A. Houben;

Dept. of Cytogenetics and Genome Analysis, Research Group Transcriptome Analysis; Dr. P. Schweizer;

Dept. of Cytogenetics and Genome Analysis, Research Group Bioinformatics and Information Technology; Dr. U. Scholz, Dr. B. Steuernagel.

Outside the Institute:

Julius Kühn-Institute (JKI), Federal Research Centre for Cultivated Plants, Institute for Resistance Research and Stress Tolerance, Quedlinburg; Prof. F. Ordon, Dr. A. Habekuss;

Helmholtz-Centre Munich, Munich Information Centre of Protein Sequences (MIPS), Neuherberg; Dr. K.F.X. Mayer;

Leibniz Institute for Age Research/Fritz Lipmann Institute (FLI), Jena; Dr. M. Platzer;

University of Olomouc, Olomouc, Czech Republic; Prof. J. Doležel;

Scottish Crop Research Institute (SCRI), Dundee, UK; Prof. R. Waugh;

Center of Life and Food Sciences Weihenstephan, Technical University Munich, Plant Breeding, Freising; Dr. E. Bauer, Dr. G. Haseneyer;

University of Udine, Udine, Italy; Prof. M. Morgante;

INRA, Clermont-Ferrand, France; Dr. C. Feuillet;

University of Helsinki, Institute of Biotechnology, Plant Genomics Laboratory, Helsinki, Finland; Prof. A. Schulman;

University of Dundee at SCRI, Plant Science, Invergowrie, Dundee, UK; Prof. A. Flavell;

University of Zurich, Institute of Plant Biology, Zurich, Switzerland; Prof. B. Keller, Dr. T. Wicker.

Publications

Peer Reviewed Papers

2008

Altintas, S., F. Toklu, S. Kafkas, B. Kilian, A. Brandolini & H. Özkan: Estimating genetic diversity in durum and bread wheat cultivars from Turkey using AFLP and SAMPL markers. Plant Breed. 127 (2008) 9-14.

Castillo, A., H. Budak, R.K. Varshney, G. Dorado, A. Graner & P. Hernandez: Transferability and polymorphism of barley EST-SSR markers used for phylogenetic analysis in *Hordeum chilense*. BMC Plant Biol. 8 (2008) 97.

Chabane, K., R.K. Varshney, A. Graner & J. Valkoun: Generation and exploitation of EST-derived SSR markers for assaying molecular diversity in durum wheat populations. Genet. Resour. Crop Evol. 55 (2008) 869-881.

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Kota, R., R.K. Varshney, M. Prasad, H. Zhang, N. Stein & A. Graner: EST-derived single nucleotide polymorphism (SNP) markers for assembling genetic and physical maps of the barley genome. Funct. Integr. Genomics 8 (2008) 223-233.

Sreenivasulu, N., A. Graner & U. Wobus: Barley genomics: an overview. Int. J. Plant Genomics (2008) 13 pp, doi:10.1155/2008/486258.

Sreenivasulu, N., B. Usadel, A. Winter, V. Radchuk, U. Scholz, N. Stein, W. Weschke, M. Strickert, T.J. Close, M. Stitt, A. Graner & U. Wobus: Barley grain maturation and germination: metabolic pathway and regulatory network commonalities and differences highlighted by New MapMan/PageMan profiling tools. Plant Physiol. 146 (2008) 1738-1758.

Sretenovic-Rajicic, T., T. van Hintum, A. Lebeda & K.J. Dehmer: Analysis of wild *Lactuca* accessions: conservation and identification of redundancy. Plant Genet. Res. 6 (2008) 153-163.

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Varshney, R.K., T. Thiel, T. Sretenovic-Rajicic, M. Baum, J. Valkoun, P. Guo, S. Grando, S. Ceccarelli & A. Graner: Identification and validation of a core set of informative genic SSR and SNP markers for assaying functional diversity in barley. Mol. Breed. 22 (2008) 1-13.

Wicker, T., A. Narechania, F. Sabot, J. Stein, G.T. Vu, A. Graner, D. Ware & N. Stein: Low-pass shotgun sequencing of the barley genome facilitates rapid identification of genes, conserved non-coding sequences and novel repeats. BMC Genomics 9 (2008) 518.

2009

Bolot, S., M. Abrouk, U. Masood-Quraishi, N. Stein, J. Messing, C. Feuillet & J. Salse: The 'inner circle' of the cereal genomes. Curr. Opin. Plant Biol. 12 (2009) 119-125.

Close, T.J., P.R. Bhat, S. Lonardi, Y. Wu, N. Rostoks, L. Ramsay, A. Druka, N. Stein, J.T. Svensson, S. Wanamaker, S. Bozdag, M.L. Roose, M.J. Moscou, S. Chao, R. Varshney, P. Szucs, K. Sato, P.M. Hayes, D.E. Matthews, A. Kleinhofs, G.J. Muehlbauer, J. DeYoung, D.F. Marshall, K. Madishetty, R.D. Fenton, P. Condamine, A. Graner & R. Waugh: Development and implementation of high-throughput SNP genotyping in barley. BMC Genomics 10 (2009) 582.

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Guo, P., M. Baum, S. Grando, S. Cecarelli, G. Bai, R. Li, M. von Korff, R.K. Varshney, A. Graner & J. Valkoun: Differentially expressed genes between drought-tolerant and drought-sensitive barley genotypes in response to drought stress during the reproductive stage. J. Exp. Bot. 60 (2009) 3531-3544.

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Mayer, K.F., S. Taudien, M. Martis, H. Simkova, P. Suchankova, H. Gundlach, T. Wicker, A. Petzold, M. Felder, B. Steuernagel, U. Scholz, A. Graner, M. Platzer, J. Dolezel & N. Stein: Gene content and virtual gene order of barley chromosome 1H. Plant Physiol. 151 (2009) 496-505.

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Steuernagel, B., S. Taudien, H. Gundlach, M. Seidel, R. Ariyadasa, D. Schulte, A. Petzold, M. Felder, A. Graner, U. Scholz, K.F.X. Mayer, M. Platzer & N. Stein: *De novo* 454 sequencing of barcoded BAC pools for comprehensive gene survey and genome analysis in the complex genome of barley. BMC Genomics 10 (2009) 547.

Stracke, S., G. Haseneyer, J.B. Veyrieras, H.H. Geiger, S. Sauer, A. Graner & H.P. Piepho: Association mapping reveals gene action and interactions in the determination of flowering time in barley. Theor. Appl. Genet. 118 (2009) 259-273.

Thiel, T., A. Graner, R. Waugh, I. Grosse, T.J. Close & N. Stein: Evidence and evolutionary analysis of ancient whole-genome duplication in barley predating the divergence from rice. BMC Evol. Biol. 9 (2009) 209.

Toklu, F., T. Karaköy, E. Hakli, T. Bicer, A. Brandolini, B. Kilian & H. Özkan: Genetic variation among lentil (*Lens culinaris* Medik.) landraces from Southeast Turkey. Plant Breed. 128 (2009) 178-186.

Vaccino, P., H.A. Becker, A. Brandolini, F. Salamini & B. Kilian: A catalogue of *Triticum monococcum* genes encoding toxic and immunogenic peptides for celiac disease patients. Mol. Genet. Genomics 281 (2009) 289-300.

Wicker, T., S.G. Krattinger, E.S. Lagudah, T. Komatsuda, M. Pourkheirandish, T. Matsumoto, S. Cloutier, L. Reiser, H. Kanamori, K. Sato, D. Perovic, N. Stein & B. Keller: Analysis of intraspecies diversity in wheat and barley genomes identifies breakpoints of ancient haplotypes and provides insight into the structure of diploid and hexaploid Triticeae gene pools. Plant Physiol. 149 (2009) 258-270.

Wicker, T., S. Taudien, A. Houben, B. Keller, A. Graner, M. Platzer & N. Stein: A whole-genome snapshot of 454 sequences exposes the composition of the barley genome and provides evidence for parallel evolution of genome size in wheat and barley. Plant J. 59 (2009) 712-722.

Books and Book Chapters

2008

Goncharov, N.P., K.A. Golovnina, B. Kilian, S. Glushkov, A. Blinov & V.K. Shumny: Evolutionary history of wheats - the main cereal of mankind. In: Dobretsov, N., N. Kolchanov, A. Rozanov & G. Zavarzin (Eds.): Biosphere origin and evolution. Springer-Verlag GmbH, Heidelberg (2008) 407-419.

Graner, A.: Genetische Diversität als Grundlage der Pflanzenzüchtung. In: Röbbelen, G. (Ed.): Die Entwicklung der Pflanzenzüchtung in Deutschland (1908-2008). Saatgut-Treuhandverwaltungs-GmbH, Bonn (2008) 501-509.

Sretenovic-Rajicic, T. & K.J. Dehmer: Analysis of wild *Lactuca* genebank accessions and implication on wild species conservation. In: Maxted, N., B. Ford-Lloyd, S.P. Kell, J. Iriondo, E. Dulloo & J. Turok (Eds.): Crop wild relative conservation and use. CABI Publishing, Wallingford (2008) 429-436.

2009

Eversole, K., A. Graner & N. Stein: Wheat and barley genome sequencing. In: Feuillet, C. & G. Muehlbauer (Eds.): Genetics and Genomics of the Triticeae. Plant Genetics/Genomics, Vol. 7. Springer Publishers, New York (2009) 713-742.

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Stein, N.: Physical mapping in the Triticeae. In: Feuillet, C. & G. Muehlbauer (Eds.): Genetics and Genomics of the Triticeae. Plant Genetics/Genomics, Vol. 7. Springer Publisher, New York (2009) 317-335.

Varshney, R.K., D.A. Hoisington, S.N. Nayak & A. Graner: Molecular plant breeding: methodology and achievements. In: Gustafson, J.P., P. Langridge & D.J. Somers (Eds.): Plant Genomics, Methods and Protocols (Methods Mol. Biol. 513). Humana Press (2009) 283-304.

Research Group: Genebank Documentation

Head: Dr. Helmut Knüpffer

Scientists

IPK financed
Narang, Ram, Dr. (P, till 31.10.2008)
Oppermann, Markus (P)
Stephanik, Andreas (Annex, 01.05.-31.10.2008; P, since 01.11.2008)

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 focussed on the further development and extension of the **Genebank Information System (GBIS)**.

(1) **GBIS/M**, the internal genebank management software, offers numerous functions supporting the day-to-day genebank activities (see Fig. 12). The taxonomy module developed in 2007 was subsequently integrated into GBIS/M in 2008 (M. Oppermann). The module for handling characterisation and evaluation (C&E) data of genebank accessions was largely finished in end of 2009. 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).
The developers' (technical) documentation for GBIS/M was compiled in 2008, and the user manual completed in May 2009. Bug fixing, the implementation of change requests, and improving the user-friendliness of GBIS were continuously carried out. The data were further consolidated, and their quality was improved. Geo-referenced data of ca. 16,000 accessions were added to the database.
(2) **GBIS/I**, the internet portal for searching and ordering genebank accessions (http://gbis.ipk-gatersleben.de/gbis_i/), provides online access to more than 147,000 accessions of the IPK Genebank collections at Gatersleben, Malchow and Groß Lüsewitz. It is being used by more than 50 % 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), the European Central PGR Search Catalogue (EURISCO), and numerous ECPGR European Central Crop Databases. The web service enabling GBIF (Global Biodiversity Information Facility) to access IPK's passport data was re-configured.
The group is maintaining the **European Barley Database** (EBDB) (H. Knüpffer, M. Oppermann) as well as the **European *Poa* Database** of the European Cooperative Pro-

Fig. 12
Top left: Entry screen of GBIS/I. Top right: Botanical ranks database TaxCat2 on the Mansfeld Server. Centre: Entry screen of GBIS/M. Bottom left: Pocket PC used for characterisation and evaluation data recording in the field or greenhouse (GBIS/B). Top right: Entry screen of the Mansfeld Database (Photo: M. Oppermann).

gramme for Plant Genetic Resources (ECPGR), the latter together with E. Willner (Satellite Collections North).
The transfer of **Mansfeld's World Database of Agricultural and Horticultural Crops** (http://mansfeld.ipk-gatersleben.de) into a database schema compatible with the "Berlin Model" for taxonomic databases was completed, and the web interface was re-developed, retaining the full functionality (R. Narang). The in-house **Database for Checklists of Cultivated Plants** (not online) was extended by a module for exporting checklists and indexes (2008) (K. Herold, H. Knüpffer) and is being updated with information for a planned Inventory of Cultivated Plant Species of Italy (with K. Hammer).

Collaborations (selection)

Within the Institute:

Dept. of Genebank, Research Group Resources Genetics and Reproduction; Dr. A. Börner, Dr. U. Lohwasser;
Dept. of Genebank, Research Group Satellite Collections North; Dr. K.J. Dehmer, E. Willner;
Dept. of Genebank, Research Group Genome Diversity; Dr. B. Kilian.

Outside the Institute:

Julius Kühn Institute (JKI), Federal Research Centre for Cultivated Plants, Quedlinburg; Dr. L. Frese, Dr. C. Germeier;
Federal Agency for Agriculture and Food (BLE), Information Centre for Biological Diversity (IBV), Bonn; Dr. F. Begemann, S. Harrer;
University of Kassel, Faculty of Agriculture, Institute of Crop Science, Department of Agricultural Biodiversity, Witzenhausen; Prof. K. Hammer;
Botanical Garden and Botanical Museum, Berlin-Dahlem; Prof. W. Berendsohn;
Bioversity International, Rome, Italy; Dr. J. Engels, L. Maggioni, M. Mackay, E. Arnaud;
Centre for Genetic Resources The Netherlands (CGN), Wageningen, The Netherlands; Dr. Th. van Hintum;
Nordic Gene Resource Centre (NordGen), Alnarp, Sweden; D.T.F. Endresen.

Publications

Books and Book Chapters

2008

Kell, S.P., H. Knüpffer, S.L. Jury, B.V. Ford-Lloyd & N. Maxted: Crops and wild relatives of the Euro-Mediterranean region: making and using a conservation catalogue. In: Maxted, N., B. Ford-Lloyd, S.P. Kell, J. Iriondo, E. Dulloo & J. Turok (Eds.): Crop wild relative conservation and use. CABI Publishing, Wallingford/UK (2008) 69-109.

2009

Knüpffer, H.: Triticeae genetic resources in *ex situ* genebank collections. In: Feuillet, C. & G. Muehlbauer (Eds.): Genetics and Genomics of the Triticeae. Plant Genetics/Genomics, Vol. 7. Springer Publishers, New York (2009) 31-79.

Research Group: Plant Architecture

Head: Dr. Thorsten Schnurbusch

Scientists

IPK financed
Seidensticker, Tina (Annex, since 01.09.2009)

Grant Positions
Gawroński, Piotr (DFG, since 15.09.2009)

Visiting Scientists/Scholars
Palotta, Margie (self-financed, 02.08.-27.08.2009)

Goals

Elucidating 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 world-wide 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.
We hold a wheat and barley collection with distinct spike phenotypes from various parts of the world; a few wheat mutants of which were previously described in Martinek & Bednář (2001, 4th International Triticeae Symposium, Cordoba, Spain, 10th to 12th Sept., p. 239-244). In collabo-

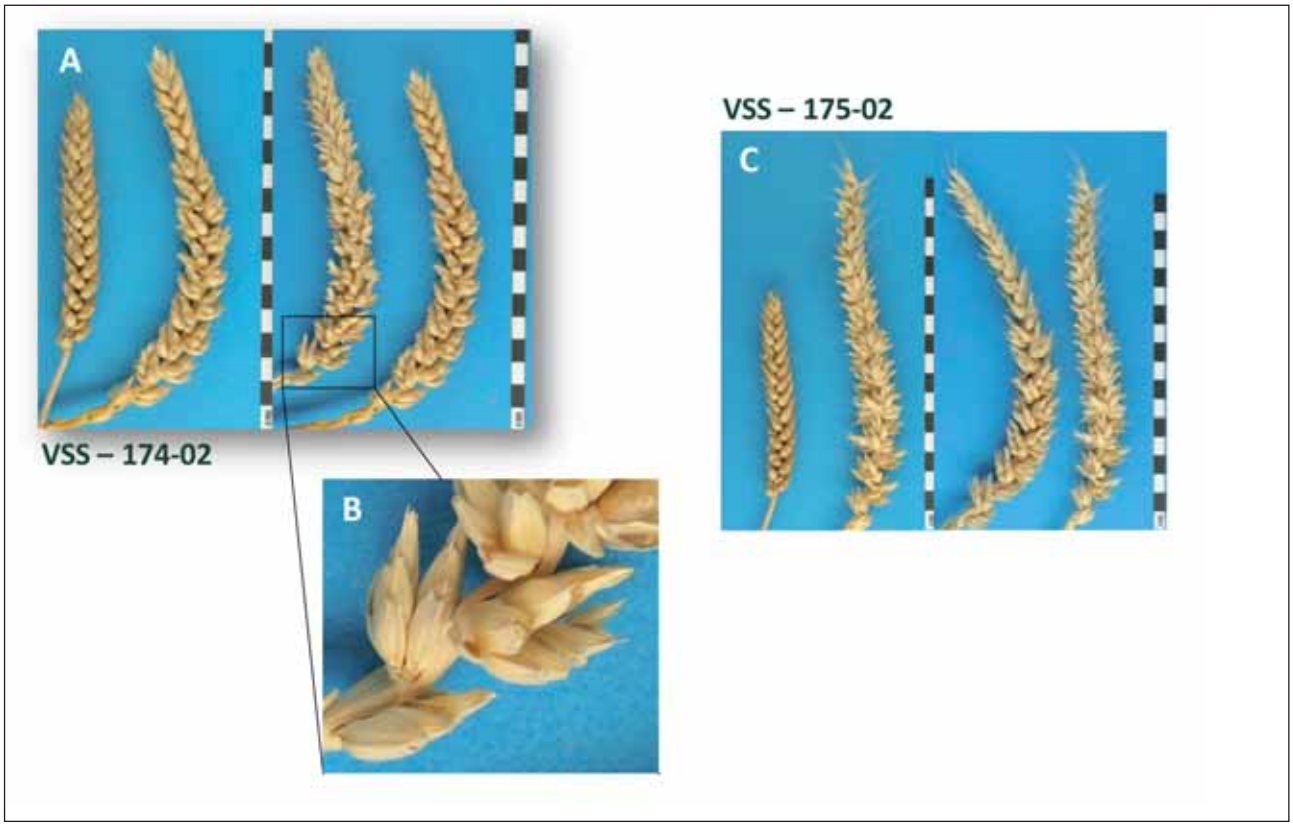

Fig. 13
Non-standard spike phenotypes with double spikelets in hexaploid wheat. (A) and (C) vertical-sessile spikelet or VSS mutant phenotype (right) and standard wheat spike (left). (B) Double spikelets enlarged VSS phenotype (Photos: M. Grau).

ration with Dr. A. Börner's group (Research Group Resources Genetics and Reproduction) we have developed mapping populations (F2) for most distinct spike phenotypes using reciprocal crosses to two wild type parents. Spike phenotypes include mutants e.g. with branched inflorescence, mutants with twisted or screwed rachis and a mutant with two spikelets per rachis node (see Fig. 13 A-C, p. 35, VSS mutants). During this GABI-FUTURE-funded, five-year project (FKZ 0315071, Molecular isolation and analysis of novel genes, regulating spike morphology and development in wheat and related grasses), we will perform detailed phenotypic analyses and molecular mapping of spike mutants in wheat and barley (T. Schnurbusch, T. Seidensticker). Furthermore we aim at identifying and isolate grass- and/or species-specific genes/proteins which regulate spike morphology and development, study their expression pattern, regulation, tissue-specificity and function during spike development in wheat and related grasses.

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. The intrinsic capability of a genotype to flower early is also called *earliness per se*. In the DFG funded project we are interested to investigate an early-heading mutant from diploid einkorn wheat (*Triticum monococcum* L.) which possesses a single major recessive *earliness per se* (*eps*) locus on the very distal end of the long arm of chromosome 3A (P. Gawroński). During this project we will perform detailed phenotypic analyses and high-resolution genetic mapping of the early-heading mutant in diploid einkorn wheat. The early-maturing line is an induced mutant and headed around twenty-four days earlier than the other mapping parent under field conditions. Furthermore, head-related traits in this population co-localised with the *eps* locus and QTLs for spikelet number and head length; both latter traits were significantly reduced in lines carrying the mutant allele at the *eps* locus. Hence, the molecular isolation of genes involved in early spike development may make an important contribution to future fine-tuning of flowering time in small grain cereal crops by providing a better understanding of the developmental genetic processes underlying heading time and spikelet number in wheat and related grasses.

Collaborations (selection)

Within the Institute:
Dept. of Genebank, Research Group Resources Genetics and Reproduction; Dr. A. Börner.

Outside the Institute:
University of Milan, Dept. of Plant Production (Di.Pro. Ve.), Milano, Italy; Dr. L. Rossini.

Publications

Peer Reviewed Papers

(All publications are based on work that has been carried out when Thorsten Schnurbusch was at the University of Adelaide, Australian Centre for Plant Functional Genomics, Australia)

2008

Izanloo, A., A.G. Condon, P. Langridge, M. Tester & T. Schnurbusch: Different mechanisms of adaptation to cyclic water stress in two South Australian bread wheat cultivars. J. Exp. Bot. 59 (2008): 3327-3346.

Schnurbusch, T., P. Langridge & T. Sutton: The *Bo1*-specific PCR marker AWW5L7 is predictive of boron tolerance status in a range of exotic durum and bread wheats. Genome 51 (2008) 963-971.

Programme: Management and Evaluation

Research Group: Resources Genetics and Reproduction

Head: Dr. Andreas Börner

Scientists

IPK financed
Dittbrenner, Anke (0,5 P, till 31.03.2008; 0,25 Annex, 01.04.-31.08.2008)
Lohwasser, Ulrike, Dr. (P)
Nagel, Manuela (0,5 P)
Neumann, Kerstin (0,5/0,25 Annex, 01.10.2008-31.03.2009)
Weidner, Annette, Dr. (0,75 Pakt für Forschung und Innovation, till 31.03.2009)

Grant Positions
Dobrovolskaya, Oxana, Dr. (Overhead, 01.06.-31.08.2008)
Navakode Gangadharan, Sheeba, Dr. (0,5/0,75 BMZ/GTZ, since 01.03.2008)
Neumann, Kerstin (0,5 Saxony-Anhalt, till 30.09.2008)

Visiting Scientists/Scholars
Bálint, Andras, Dr. (self-financed, 01.11.2008-31.01.2009)
Banica, Constantina (DFG, 01.06.-31.08.2008)
Daniel, Isaac, Dr. (Humboldt Foundation, till 15.07.2008)
Dittbrenner, Anke (self-financed, 01.09.-14.09.2008)
Khlestkina, Elena, Dr. (DFG, 01.06.-31.08.2008)
Kobiljski, Borislav, Dr. (self-financed, 21.03.-28.03.2009)
Landjeva, Svetlana, Dr. (DFG, 01.09.-30.11.2008; DFG, 15.09.-14.12.2009)
Mohammadi Mirik, Aliakbar (University Isfahan, 10.05.-10.12.2009)
Navakode Gangadharan, Sheeba (self-financed, till 29.02.2008)
Neumann, Kerstin (self-financed, since 01.04.2009)
Rehman Arif, Mian Abdur (DAAD, since 30.09.2008)
Scalone, Romain (self-financed, 30.11.-05.12.2008)
Shahsevand Hassani, Hossein, Dr. (Iranian government, 02.10.2008-02.11.2009)
Szira, Fruzsina (Hungarian Agrisafe Project, 05.01.-31.03.2009)
Weidner, Annette, Dr. (self-financed, since 01.04.2009)
Zaynali Nezhad, Khalil (Iranian government)

Goals

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

Research Report

The total number of accessions maintained at the Gatersleben site comprises 126,837 samples, of which 122,699 are preserved in the cold store. Safety duplicates are available for 22,350 accessions (ca. 15 % of the whole collection). They are stored at the **Global Seed Vault**, Svalbard, Norway which was opened in February 2008. In the two years period germination tests were performed for 22,891 samples 33,507 accessions (excluding the Satellite Collections North) were distributed to users, two thirds of which were provided to research institutes including IPK (S. Pistrick, A. Börner). During the growing seasons 2007/2008 and 2008/2009 totals of 8,854 and 10,055 accessions were cultivated, respectively, including 1,491 and 1,588 samples grown for evaluation only. A taxonomic classification was performed for 7,058 accessions. Descriptor lists were created or revised for the genera *Allium, Lathyrus, Cicer, Melissa, Nicotiana, Petroselinum* as well as cultivated and wild potatoes (U. Lohwasser).

The main focus of the collection-related research is dedicated to **seed longevity** of crop plants. Comparable studies of long-term stored seeds of different genera/species indicate a high intrageneric/-specific variation (see Fig. 14A, p. 38). Both segregation and association based mapping studies were initiated in barley by exploiting accelerated aging tests following the rules of the International Seed Testing Association. Bi-parental mapping populations saturated with EST-based markers and developed in the Plant Genome Resources Centre of IPK were used for quantitative trait locus (QTL) analyses. Major seed longevity QTLs were identified on chromosomes 2H, 5H and 7H explaining a phenotypic variation of up to 54 % (see Fig. 14B, p. 38). A sequence homology search was performed to derive the putative function of the genes linked to the QTL. For two of the barley QTL co-linearity to loci in rice may be suggested. In co-operation with the Kew Millennium Seed Bank, UK the relationship between the antioxidant glutathione and seed viability was investigated. Germination decreased with the depletion of total glutathione. Correlation coefficients ranged between 0.76** and 0.88** (M. Nagel, H. Vogel, S. Landjeva; collaboration with U. Scholz, research group Bioinformatics and Information Technology).

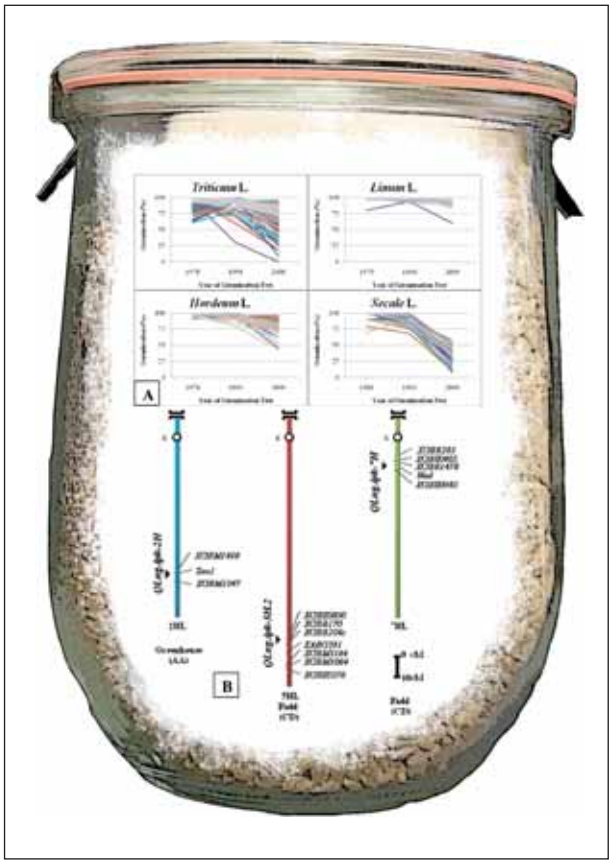

Fig. 14
(A) Mean germination of selected wheat, rye, flax and barley accessions after different periods of storage; (B) Major QTL for seed longevity (*QLng*) detected on barley chromosomes 2HL, 5HL and 7HL. Marker loci within a region of 10 cM (LOD > 3) are given. c = centromere (M. Nagel, S. Pistrick, U. Scholz, A. Börner).

Activities on **characterisation and evaluation** directed to *Papaver* were completed. The taxonomic classification based on morphological characters was checked employing molecular (AFLP) and phytochemical (HPLC) analyses. Molecular studies revealed that the tetraploid *P. somniferum* subsp. *setigerum* form one cluster, while the diploid accessions from subsp. *somniferum* and subsp. *songaricum* were intermixed. The amount and composition of the main alkaloides were highly variable but not reliable for infraspecific classification (A. Dittbrenner, R. Kurch, U. Lohwasser; collaboration with F. Blattner, research group Experimental Taxonomy and H.-P. Mock, research group Applied Biochemistry). Current activities on *Petroselinum, Salvia* and *Coriandrum* are continued as well as the **European project** on conservation and utilisation of leafy vegetables (*Lactuca, Spinacia, Cichorium, Valerianella, Eruca, Diplotaxis*). IPK is sub-coordinating the European-wide activities on regeneration and characterisation (S. Thumm, M.-L. Graichen, U. Lohwasser).

In order to improve the utilisation of the cereal collection, research is focused on agronomic traits including **abiotic stress tolerance** (drought, salt, aluminium) in wheat and barley. Loci determining the traits of interest were detected on different chromosomes via segregation mapping (K. Neumann, K. Zaynali Nezhad, S. G. Navakode; collaboration with M. Röder, research group Gene and Genome Mapping). Parental lines and selected off-springs of barley differing in salt tolerance were used for seed proteome analysis (A. Weidner; collaboration with K. Witzel, H.-P. Mock, research group Applied Biochemistry).

A **genome-wide association** study in wheat was initiated using a core collection of 96 accessions. The germplasm was structured into two sub-populations. Twenty agronomic characters measured in field trials conducted over up to eight growing seasons by external partners were considered. Correlations between traits across seasons were high in almost all cases. Significant marker-trait associations were detected. The intrachromosomal location of many of these coincided with those of known major genes or quantitative trait loci, whereas others were detected in regions where no known genes have been located to date (K. Neumann).

Collaborations (selection)

Within the Institute:
Dept. of Genebank, Research Group Experimental Taxonomy; Dr. F. Blattner;
Dept. of Cytogenetics and Genome Analysis, Research Group Gene and Genome Mapping; Dr. M. Röder;
Dept. of Physiology and Cell Biology, Research Group Applied Biochemistry; Dr. K. Witzel, Dr. H.-P. Mock.

Outside the Institute:
Julius Kühn-Institute (JKI), Federal Centre for Breeding Research on Cultivated Plants, Institute of Plant Analysis, Quedlinburg; Prof. H. Schulz;
Julius Kühn-Institute (JKI), Federal Centre for Breeding Research on Cultivated Plants, Institute of Horticultural Crops, Quedlinburg; Dr. F. Marthe, Dr. H. Budahn;
Martin Luther University Halle-Wittenberg, Institute for Plant Breeding and Plant Protection, Halle/Saale; Prof. W.E. Weber, Prof. K. Pillen;
Martin Luther University Halle-Wittenberg, Institute of Geobotany and Botanical Garden, Halle/Saale; Prof. M. Röser;
University of Veterinary Medicine, Institute for Applied Botany and Pharmacognosy, Vienna, Austria; Prof. J. Novak;
Institute of Cytology and Genetics, Novosibirsk, Russia; Dr. E. Khlestkina, Dr. O. Dobrovolskaya, Dr. T. Pshenischnikova, Dr. I. Leonova;
Agricultural Research Institute of the Hungarian Academy of Sciences, Martonvasar, Hungary; Dr. G. Galiba, Dr. A.F. Bálint;
Institute of Field and Vegetable Crops, University of Novi Sad, Novi Sad, Serbia; Dr. B. Kobiljski.

Publications

Peer Reviewed Papers

2008

Castro, A.M., M.S. Tacaliti, D. Giménez, E. Tocho, O. Dobrovolskaya, A. Vasicek, M. Collado, J.W. Snape & A. Börner: Mapping quantitative trait loci for growth responses to exogenously applied stress induced hormones in wheat. Euphytica 164 (2008) 719-727.

Chesnokov, Y.V., N.V. Pochepnya, A. Börner, U. Lohwasser, E.A. Goncharova & V.A. Dragavtsev: Ecological-genetic organisation of plant quantitative traits and mapping of the loci determining agronomically important traits in soft wheat. Dokl. Biochem. Biophys. 418 (2008) 36-39.

Dittbrenner, A., U. Lohwasser, H.-P. Mock & A. Börner: Molecular and phytochemical studies of *Papaver somniferum* in the context of intraspecific classification. Acta Hortic. 799 (2008) 81-88.

Landjeva, S., V. Korzun, E. Stoimenova, B. Truberg, G. Ganeva & A. Börner: The contribution of the gibberellin-insensitive semi-dwarfing (*Rht*) genes to genetic variation in wheat seedling growth in response to osmotic stress. J. Agr. Sci. 146 (2008) 275-286.

Landjeva, S., K. Neumann, U. Lohwasser & A. Börner: Molecular mapping of genomic regions associated with wheat seedling growth under osmotic stress. Biol. Plant. 52 (2008) 259-266.

Lohwasser, U., A. Börner & H. Krüger: Intraspecific taxonomy of coriander (*Coriandrum sativum* L.) – Comparison of morphological, phytochemical, and molecular data. Acta Hortic. 799 (2008) 111-113.

Pestsova, E.G., V. Korzun & A. Börner: Validation and utilisation of *Rht* dwarfing gene specific markers. Cereal Res. Commun. 36 (2008) 235-246.

Pshenichnikova, T.A., M.F. Ermakova, A.K. Chistyakova, L.V. Shchukina, E.V. Berezovskaya, U. Lohwasser, M.S. Röder & A. Börner: Mapping of the quantitative trait loci (QTL) associated with grain quality characteristics of the bread wheat grown under different environmental conditions. Russ. J. Genet. 44 (2008) 74-84.

Pshenichnikova, T.A., S.V. Osipova, M.D. Permyakova, T.N. Mitrofanova, V.A. Trufanov, U. Lohwasser, M.S. Röder & A. Börner: Mapping of quantitative trait loci (QTL) associated with activity of disulfide reductase and lipoxygenase in grain of bread wheat *Triticum aestivum* L. Russ. J. Genet. 44 (2008) 567-574.

Röder, M.S., X.Q. Huang & A. Börner: Fine mapping of the region on wheat chromosome 7D controlling grain weight. Funct. Integr. Genomics 8 (2008) 79-86.

Szira, F., A.F. Balint, A. Börner & G. Galiba: Evaluation of drought-related traits and screening methods at different developmental stages in spring barley. J. Agron. Crop Sci. 194 (2008) 334-342.

Varshney, R.K., K.F.M. Salem, M. Baum, M.S. Röder, A. Graner & A. Börner: SSR and SNP diversity in a barley germplasm collection. Plant Genet. Res. 6 (2008) 167-174.

2009

Badridze, G., A. Weidner, F. Asch & A. Börner: Variation in salt tolerance within a Georgian wheat germplasm collection. Genet. Resour. Crop Evol. 56 (2009) 1125-1130.

Bálint, A.F., F. Szira, M.S. Röder, G. Gáliba & A. Börner: Mapping of loci affecting copper tolerance in wheat - The possible impact of the vernalisation gene *Vrn-A1*. Environ. Exp. Bot. 65 (2009) 369-375.

Daniel, I.O., K.O. Oyekale, M.O. Ajala, L.O. Sanni & M.O. Okelana: Physiological quality of hybrid maize seeds during containerised-dry storage with silica gel. Afr. J. Biotechnol. 8 (2009) 181-186.

Dittbrenner, A., H.P. Mock, A. Börner & U. Lohwasser: Variability of alkaloid content in *Papaver somniferum* L. J. Appl. Bot. Food Qual. 82 (2009) 103-107.

Dobrovolskaya, O., P. Martinek, A.V. Voylokov, V. Korzun, M.S. Röder & A. Börner: Microsatellite mapping of genes that determine supernumerary spikelets in wheat (*T. aestivum*) and rye (*S. cereale*). Theor. Appl. Genet. 119 (2009) 867-874.

Khlestkina, E.K., A. Giura, M.S. Röder & A. Börner: A new gene controlling the flowering response to photoperiod in wheat. Euphytica 165 (2009) 579-585.

Khlestkina, E.K., T.A. Pshenichnikova, M.S. Röder & A. Börner: Clustering anthocyanin pigmentation genes in wheat group 7 chromosomes. Cereal Res. Commun. 37 (2009) 391-398.

Khlestkina, E.K., E.A. Salina, T.A. Pshenichnikova, M.S. Röder & A. Börner: Glume coloration in wheat: Allelism test, consensus mapping and its association with specific microsatellite allele. Cereal Res. Commun. 37 (2009) 37-43.

Kobiljski, B., S. Dencic, A. Kondic-Spika, U. Lohwasser & A. Börner: Locating stable across environment QTL involved in the determination of agronomic characters in wheat. Cereal Res. Commun. 37 (2009) 327-333.

Nagel, M., H. Vogel, S. Landjeva, G. Buck-Sorlin, U. Lohwasser, U. Scholz & A. Börner: Seed conservation in *ex situ* genebanks - genetic studies on longevity in barley. Euphytica 170 (2009) 5-14.

Navakode, S., A. Weidner, U. Lohwasser, M.S. Röder & A. Börner: Molecular mapping of quantitative trait loci (QTLs) controlling aluminium tolerance in bread wheat. Euphytica 166 (2009) 283-290.

Navakode, S., A. Weidner, R.K. Varshney, U. Lohwasser, U. Scholz & A. Börner: A QTL analysis of aluminium tolerance in barley, using gene-based markers. Cereal Res. Commun. 37 (2009) 531-540.

Sareedenchai, V., M. Ganzera, E.P. Ellmerer, U. Lohwasser & C. Zidorn: Phenolic compounds from *Tragopogon porrifolius* L. Biochem. Syst. Ecol. 37 (2009) 234-236.

Witzel, K., A. Weidner, G.K. Surabhi, A. Börner & H.-P. Mock: Salt stress-induced alterations in the root proteome of barley genotypes with contrasting response towards salinity. J. Exp. Bot. 60 (2009) 3545-3557.

Books and Book Chapters

2008

Börner, A. & J.W. Snape (Eds.): European Wheat Aneuploid Co-operative Newsletter 2008. Proceedings of the 14th International EWAC Conference, Istanbul/Turkey, 06.-10.05.2007. (2008) 180 pp.

Khlestkina, E.K., M.S. Röder, T.A. Pshenichnikova, A.V. Simonov, E.A. Salina & A. Börner: Genes for anthocyanin pigmentation in wheat: review and microsatellite-based mapping. In: Verrity, J.F. & L.E. Abbington (Eds.): Chromosome mapping research developments. NOVA Science Publishers, Inc., New York/USA (2008) 155-175.

2009

Lohwasser, U.: Arznei- und Gewürzpflanzenbestände in der Genbank Gatersleben. In: Verein für Arznei- und Gewürzpflanzen SALUPLANTA e.V. (Eds.): Handbuch der Arznei- und Gewürzpflanzen, Band 1, Grundlagen des Arznei- und Gewürzpflanzenbaus I. Bernburg (2009) 692-712.

Research Group: *In vitro* Storage and Cryopreservation

Head: Dr. Joachim Keller

Scientists

IPK financed
Kaczmarczyk, Anja, Dr. (0,5 P, till 31.01.2008; 0,25/0,75 Annex, 01.02.-30.06.2009; 0,75 P, 01.07.-30.09.2009)

Grant Positions
Kästner, Ute, Dr. (BMBF, till 31.03.2008)
Zanke, Christine, Dr. (EU)

Visiting Scientists/Scholars
Edesi, Jaanika (COST 871, 15.11.-27.11.2009)
Engelmann, Florent, Prof. (self-financed, 15.06.-21.06.2008)
Kotkova, Renata (self-financed, 30.03.-04.04.2008)
Kremer Morales, Carolina (COST 871, 15.11.-27.11.2009)
Nukari, Anna (COST 871, 02.03-20.03.2009, 11.05.-15.05.2009)
Rokka, Veli-Matti, Dr. (self-financed, 02.03.-20.03.2009, 11.05.-15.05.2009)

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.

Research Report

Accessions of the genera ***Allium, Antirrhinum, Artemisia, Brassica, Dioscorea, Mentha, Orthosiphon,*** **and** ***Sechium*** are in *in vitro* maintenance, in total comprising **522 clones of 374 genebank accessions**. Amongst them, **40 clones of garlic and 33 of shallot** are maintained virus-free. For distribution to users, 73 **accessions of potato, mint and yams were provided** (D. Büchner, M. Grübe, A. Senula).
The **potato cryopreservation** research programme was continued and summarised in the frame of a PhD Thesis. In addition to the analysis of soluble sugars, starch, and amino acid concentrations, investigation of gene expression after two different precultures was performed using 2D gel-based **proteomics** studies. Only minor changes were found between explants pre-cultured at constantly 22 °C in comparison with alternating temperatures of 22/8 °C (day/night temperatures), most of the altered proteins were down-regulated. The identified proteins belonged to functional groups of metabolism, signal transduction, defence, transcription, energy and secondary metabolism. **Ultrastructural analyses** revealed major changes after 2 h DMSO treatment. The area of the meristematic dome and parts of the epidermis showed signs of extensive structural damage two days after rewarming. Survival and regeneration of cells were mainly confined to leaf primordial regions and only rarely occurred in the meristematic dome proper. **A comparison** was performed between IPK's standard method **DMSO droplet freezing and droplet vitrification**, the first one being superior to the latter in most of the accessions analysed (A. Kaczmarczyk, M. Grübe, A. Nukari, V.-M. Rokka). The **cryo-collection of potato** was increased to **1,140 clones.** Furthermore, the quality of **6 accessions** was improved by **replacing virus-infected by virus-free** and more vigorous **material. For distribution to users, 7 samples** were provided to the Satellite Collections North (A. Kaczmarczyk, M. Grübe).
The cryo-collection of ***Allium*** was increased to **67 accessions, among those 64 of garlic and 3 of *Allium 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 routinely applied to cold-hardened plants of mint. Presently **40 accessions from 13 species** are cryopreserved with 200 explants each**.** Regeneration rates varied between 30 and 98 %. For cryopreservation single *in vitro* plants were taken out of the long term storage (2 °C), screened for endophytic bacteria, and plants without visible infection were rapidly propagated *in vitro*. **Quality of donor plants was the most important factor** in regeneration processes mainly influenced by the presence of covert bacteria and their outbreaks. The genotype dependence was of lower influence. Fast multiplication of donor material is a precondition for high regeneration after cryopreservation. Antibiotics added to the recovery medium do not change re-growth significantly in visually clean material. However, when infections are visible or explants do not grow they may improve re-growth (A. Senula).
Investigations on **cryopreservation of** ***Orthosiphon*** were continued using droplet vitrification with PVS 2. Differential Scanning Calorimetric (DSC) analyses of *Orthosiphon* shoot tips were performed. They show that incubation in PVS 2 for 20 min caused glass transition. However, ice crystallisation, re-crystallisation and melting occur concomitantly, independent of the loading time. Re-growth was at 82 % in controls without liquid nitrogen contrasting to only 4 % after cryopreservation. Concluding

from thermal analysis, best conditions are loading phases between 20 and 120 min and PVS 2 treatment of 40 or 60 min. Prolongation of PVS 2 treatment to 40 - 60 min avoids ice crystallisation and reduces or avoids re-crystallisation. Re-growth after cryopreservation increased to 12 %, whereas that in the controls decreased to 62 % because of poisoning by PVS 2. Aided by DSC measurements, the non-toxic cryoprotectant PVS 3 was introduced resulting in optimal glass transition and increasing regeneration to 20 - 30 % (A. Senula). **Investigations on shallots** were started using vitrification and droplet vitrification methods with PVS 3. Initially several parameters were tested (donor material, sterilisation time, explant sizes, loading and dehydration times). DSC measurements were used to find optimal times for loading and dehydration in order to achieve the glassy state of cellular solutions (A. Senula).

In the frame of the **EU-funded GEN RES project on garlic and shallot EURALLIVEG** (AGRI GEN RES 050), a training course on techniques of micropropagation and cryopreservation of *in vitro* plants was organised at IPK, and three meetings were performed. The **molecular marker analyses** of the **1,433 accessions of garlic and 460 of shallot** were finished. Project-based **cryopreservation** activities resulted in **24 accessions** with mean re-growth rates of 54 % (bolting) and 36 % (non-bolting genotypes), respectively. Furthermore, **18 bolting and 13 non-bolting accessions** are in the ***in vitro* propagation phase**. Four virus-free accessions are also *in vitro*. A reengineering of the **garlic image database** was carried out (C. Zanke, G. Matzig, J. Keller, F. Blattner, U. Scholz, S. Weise, C. Colmsee).

Data collection on **diversity and biochemical analysis** in selected medicinal plants was finalised and a book was published (H. Schulz, U. Kästner, J. Keller). **Two scientific conferences** were organised at IPK (Society of Low Temperature Biology and COST Action 871 Cryopreservation of crop species in Europe) and of the Association of German In Vitro Growers (ADIVK – whole research group).

Collaborations (selection)

Within the Institute:

Dept. of Genebank, Research Group Resources Genetics and Reproduction; Dr. A. Börner;

Dept. of Genebank, Research Group Satellite Collections North; Dr. K.J. Dehmer;

Dept. of Genebank, Research Group Experimental Taxonomy; Dr. F. Blattner;

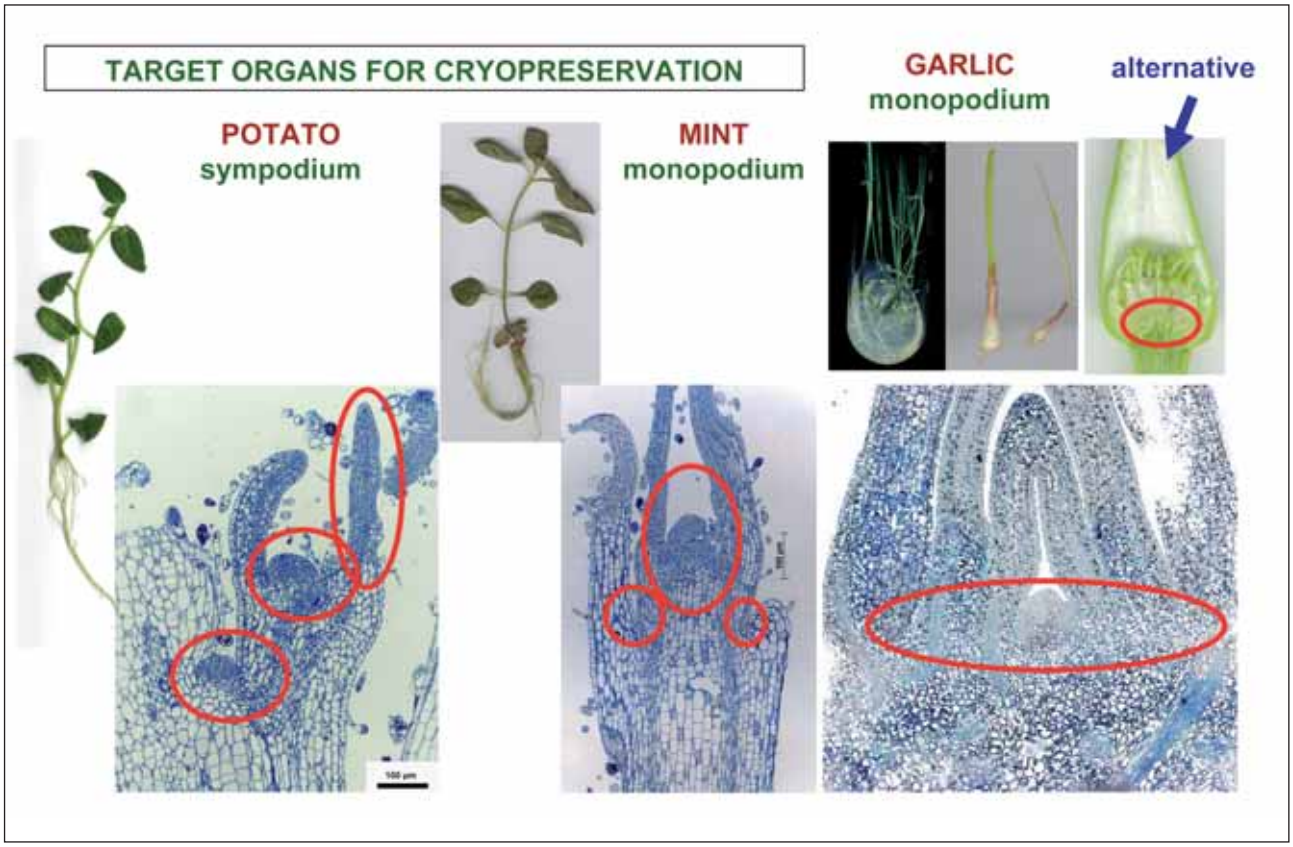

Fig. 15
Target organs of potato, mint and garlic *in vitro* plantlets. In garlic, meristematic parts of unripe inflorescences are used as alternative sources instead of shoot tips. Storage in liquid nitrogen is focussing on maintaining meristematic parts of the organs alive (marked by red circles). Both preparation and assessment of regeneration morphogenesis are only efficient when the characteristics of the target plants are considered. This is especially important in the recovery phase when damages and disturbances are repaired and the topology of the organs is still not completely rearranged (Photos: E.R.J. Keller; semi-thin sections: M. Melzer, T. Rutten, Structural Cell Biology group).

Dept. of Physiology and Cell Biology, Research Group Molecular Plant Nutrition; Dr. M.R. Hajirezaei;
Dept. of Physiology and Cell Biology, Research Group Applied Biochemistry; Dr. H.-P. Mock;
Dept. of Physiology and Cell Biology, Research Group Structural Cell Biology; Dr. M. Melzer, Dr. T. Rutten.

Outside the Institute:
Julius Kühn-Institute (JKI), Federal Centre for Breeding Research on Cultivated Plants, Institute of Plant Analysis, Quedlinburg; Prof. H. Schulz;
Crop Research Institute (CRI), Prague and Olomouc, Czech Republic; Dr. J. Zamečník, Dr. H. Staveliková;
Research Institute of Vegetable Crops (RIVC), Skierniewice, Poland; Dr. T. Kotlinska;
Dipartimento di Scienze dei Sistemi Colturali, Forestali e dell´Ambiente, Università degli Studi della Basilicata (UNIBAS), Potenza, Italy; Prof. V. Miccolis;
Centre for Genetic Resources The Netherlands (CGN), Wageningen, The Netherlands; Dr. C. Kik.

Publications

Peer Reviewed Papers

2008

Islam, M.T., E.R.J. Keller & D.P. Dembele: Effects of growth regulators on *in vitro* propagation and tuberisation of four *Dioscorea* species. Plant Tissue Cult. Biotech. 18 (2008) 25-35.

Kaczmarczyk, A., T. Rutten, M. Melzer & E.R.J. Keller: Ultrastructural changes associated with cryopreservation of potato (*Solanum tuberosum* L.) shoot tips. CryoLetters 29 (2008) 145-156.

Kaczmarczyk, A., N. Shvachko, Y. Lupysheva, M.R. Hajirezaei & E.R.J. Keller: Influence of alternating temperature preculture on cryopreservation results for potato shoot tips. Plant Cell Rep. 27 (2008) 1551-1558.

Keller, E.R.J., A. Kaczmarczyk & A. Senula: Cryopreservation for plant genebanks - A matter between high expectations and cautious reservation. CryoLetters 29 (2008) 53-62.

Books and Book Chapters

2008

Keller, E.R.J., A. Senula & A. Kaczmarczyk: Cryopreservation of herbaceous dicots. In: Reed, B.M. (Ed.): Plant cryopreservation: A practical guide. Springer Science & Business Media, LCC, New York/USA (2008) 281-332.

2009

Kaczmarczyk, A., A. Senula, M. Grübe & E.R.J. Keller: DSC - Anwendung in der Kryokonservierung vegetativer pflanzengenetischer Ressourcen. In: Kunze, W. (Ed.): Anwendungen der Thermischen Analyse, Mikrokalorimetrie & Rheologie im Bereich der Pharmazie, Biotechnologie, Lebensmitteltechnologie & Kosmetik. TA Instruments, Waters GmbH, Eschborn (2009) 15-29.

Schulz, H. & J. Keller: Genetische Variabilität und Analytik von Arznei- und Gewürzpflanzen. Cardamina-Verlag (2009) 511 pp.

Research Group: Satellite Collections North

Head: Dr. Klaus J. Dehmer

Scientists

IPK financed
Willner, Evelin (P)

Grant Positions
Gernand-Kliefoth, Dorota, Dr. (BMELV, since 15.06.2008)
Gerson, Lydia (0,5 Bayerische Landesanstalt für Landwirtschaft/LfL, since 15.04.2009)
Labrenz, Regine, Dr. (0,25 BMELV, 01.01.-31.08.2009)

Visiting Scientists/Scholars
Labrenz, Regine, Dr. (self-financed, 02.06.-31.12.2008)

Goals

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

Research Report

Within three separate collections, the **Groß Lüsewitz Potato Collections** (GLKS; K.J. Dehmer; see Fig. 16) include a total of **6,013 accessions** from **140 tuber bearing *Solanum* species**. They comprise clonally propagated genotypes of Andean or equatorial origin (AKS; 497 entries, mainly seven cultivated species; Fig. 16), 2,666 *Solanum tuberosum* ssp. *tuberosum* cultivars, landraces or breeding lines (KKS, vegetatively propagated) and 2,850 accessions of 139 wild and cultivated species from Southern and Central America (WKS, propagated sexually). **3,352 potato accessions** (2008: 1,705; 2009: 1,647) were distributed in the context of **381 requests** (172; 209), 25 coming from outside Germany (316 accessions shipped).
In 2008 and 2009, a total of 188 AKS (92; 96) and 1,090 KKS accessions (533; 557) were cultivated and characterised for 15 traits in the field with 10 plants each, while 390 WKS accessions (186; 204) were sexually propagated in the greenhouse. Via *in vitro* cultivation, 2,285 KKS and 497 AKS accessions are maintained as microtubers. More than 1,100 KKS accessions are kept as cryopreserved safety duplicates at IPK Gatersleben (research group *In vitro* Storage and Cryo-Preservation).
According to the respective ELISA tests, **2,608 *in vitro* samples** (92%) 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 (490 accs.), quarantine bacteria (771), and PSTVd (1,910).
Evaluations were carried out for resistance to ***Globodera pallida*** (116 WKS accessions/553 genotypes, State Plant Protection Office Rostock) and ***Phytophthora infestans*** on tubers (124 WKS accessions/599 genotypes; JKI/ZL). For both pests, complete resistance was observed in several instances, both on the genotype and even on the accession level. Tubers of 80 KKS entries were cultivated for the **evaluation of** their **taste**, while tuber material of 24 selected accessions was continued to be propagated for a stability research project. In the greenhouse, 80 WKS accessions with up to 10 genotypes each were grown for the production of tubers to be used in **potato wart resistance** tests and as base material for protoplast fusions within the KOSY research project (JKI/A, Phytowelt); in addition, SSR fingerprints of appr. 800 genotypes were generated. For a **project on the evaluation of potato tuber quality**, 80 KKS and 77 AKS accessions, as well as 42 WKS genotypes were cultivated in the field or greenhouse for tuber production. Subsequently, the tubers were evaluated at the University of Rostock and at STZ (R. Labrenz).

Fig. 16
Newly constructed office and laboratory building of IPK's Groß Lüsewitz Potato Collections (left) and glance on tuber variability in the Andean potato collection at the GLKS (right).

The Malchow/Poel **Oil Plants and Fodder Crops Collections** (E. Willner) comprise 2,468 samples of oil plants, 10,260 fodder grasses and 1,341 forage legumes (total **14,069 accessions**) according to GBIS (research group Genebank Documentation).
In 2008 and 2009, a total of 2,037 (989; 1,048) accessions were cultivated, either for multiplication and characterisation (1,422) or evaluation (615).
Germination tests were conducted for 9,013 accessions (2008: 3,564; 2009: 5,449). According to FAO genebank standards, **65** % of the whole Malchow collection is **stored as an active and base collection with safety duplicates** at the Svalbard Global Seed Vault (6,456 accessions, 46 % of total Malchow stocks), while 81 % of the whole collection is available for seed requests. A total of **4,378 samples** (2,319; 2,101) **were provided to 139 users** (62; 77), whereof 61 seed deliveries with 1,740 samples were for foreign countries.
Characterisations for 15 traits were performed on 1,001 grass accessions (536; 465), 258 cruciferous samples (104; 154) and 163 legume entries (23; 140) for an initial description of their morphological and phenological traits as well as for the confirmation of their botanical classification. **Field evaluations** were carried out for *Lolium perenne* (289 accessions); here, 75 entries of European collection material (cooperation with EGB) and 31 of new bred material (LFA) were compared in a two-year trial to standard varieties for trait variability and/or green matter yield.
The **European Central *Poa* Database** (http://poa.ipk-gatersleben.de) was developed further in collaboration with S. Weise (research group Bioinformatics and Information Technology), currently containing passport data of 5,300 accessions from 38 *Poa* species. These entries originate from 56 different countries and are maintained at 21 institutes in 18 European countries. 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.
Genebank and breeding material from the three **grass genera *Dactylis, Lolium* and *Phleum*** was examined in a **project on diversity and introgression studies** (D. Gernand-Kliefoth, joint project with SZS). In cooperation with an external partner (LfL), **analyses of the complex trait 'persistence'** were initiated in ***Lolium perenne*** (L. Gerson).

Collaborations (selection)

Within the Institute:
Dept. of Genebank, Research Group Genebank Documentation; Dr. H. Knüpffer, M. Oppermann, A. Stephanik;
Dept. of Genebank, Research Group *In vitro* Storage and Cryopreservation; Dr. E.R.J. Keller;
Dept. of Cytogenetics and Genome Analysis, Research Group Bioinformatics and Information Technology; Dr. U. Scholz, S. Weise.

Outside the Institute:
Agricultural Research Institute Mecklenburg-Vorpommern (LFA), Institute for Animal Production, Dummerstorf; Dr. H. Jänicke;
Bavarian State Research Center for Agriculture (LfL), Institute of Plant Production and Plant Breeding, Freising-Weihenstephan; Dr. S. Hartmann, Dr. S. Seefelder;
Euro Grass Breeding (EGB), Hof Steimke; Dr. U. Feuerstein;
Julius Kühn-Institute (JKI), Federal Centre for Breeding Research on Cultivated Plants, Institute for Plant Protection in Field Crops and Grassland (JKI/A), Kleinmachnow; Dr. K. Flath;
Julius Kühn-Institute (JKI), Federal Centre for Breeding Research on Cultivated Plants, Institute of Breeding Research on Agricultural Crops (JKI/ZL), Groß Lüsewitz; Dr. T. Hammann;
Phytowelt Green Technologies GmbH, Cologne; Dr. A. Müller, Dr. R. Lührs;
Saatzucht Steinach GmbH (SZS), Steinach and Bornhof; Dr. F. Eickmeyer;
State Plant Protection Office of Mecklenburg-Vorpommern, Rostock; Dr. R. Cernusko, Dr. A. Hofhansel, Dr. J. Kruse;
Steinbeis Transfer Zentrum (STZ) Soil Biotechnology, Rostock; Dr. A. Schlichting;
University of Rostock, Faculty for Agricultural and Environmental Sciences, Chair of Soil Science, Rostock; Prof. P. Leinweber.

Publications

Peer Reviewed Papers

2008

Sretenovic-Rajicic, T., T. van Hintum, A. Lebeda & K.J. Dehmer: Analysis of wild *Lactuca* accessions: conservation and identification of redundancy. Plant Genet. Res. 6 (2008) 153-163.

Books and Book Chapters

2008

Sretenovic-Rajicic, T. & K.J. Dehmer: Analysis of wild *Lactuca* genebank accessions and implication on wild species conservation. In: Maxted, N., B. Ford-Lloyd, S.P. Kell, J. Iriondo, E. Dulloo & J. Turok (Eds.): Crop wild relative conservation and use. CABI Publishing, Wallingford (2008) 429-436.

Programme: Taxonomy and Evolution

Research Group: Experimental Taxonomy

Head: Dr. Frank Blattner

Scientists

IPK financed
Baier, Christina, (0,5 P)
Ekhvaia, Jana (0,5 Annex, 04.03.-03.06.2009)
Jakob, Sabine, Dr. (0,5/1,0 P)
Köhnen, Ines (0,5 P, till 31.03.2008, 0,25 Annex 01.04.-30.04.2008)
Pleines, Thekla (0,25 Annex, 01.05.2008-28.02.2009)

Grant Positions
Harpke, Dörte, Dr. (0,25 DFG, till 14.07.2008; 0,5 DFG, since 16.03.2009)
Nürk, Nicolai Matthias (DFG)
Pleines, Thekla (0,5 DFG, till 30.04.2008)

Visiting Scientists/Scholars
Achigan-Dako, Enoch G., Dr. (DAAD, till 30.11.2008; Vavilov-Frankel-Fellowship, 24.05.-09.06.2009)
Bachmann, Konrad, Prof. (self-financed)
Benor, Solomon (DAAD, since 29.03.2008)
Bordbar, Firouzeh (Iranian Ministry of Technology, 01.05.2008-20.04.2009)
Harpke, Dörte, Dr. (self-financed, 21.07.-31.08.2008; 09.09.-31.12.2008)
Krasovskaya, Lyudmila, Dr. (self-financed, 05.05.-02.06.2008)
Levichev, Igor, Dr. (self-financed, 05.05.-02.06.2008)
Pleines, Thekla (self-financed, 01.03.-30.04.2009)
Puglia, Guiseppe (FIDAF-Studentship, 01.05.-31.05.2008)

Goals

Development and application of molecular marker methods and the identification, characterisation and **phylogenetic classification** of crops and their wild relatives. Experimental studies to link **molecular markers** and **phylogenetic data** with taxonomically and agronomically significant characters, and to analyse **plant–environment interdependency** on and below the species level.

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) influence the ecological niches of organisms and are often also **important agronomic traits**.

In the genus ***Hordeum*** we analyse all aspects related to phylogeny, speciation and ecological adaptation. We generated a chloroplast genealogy of the genus including now data from over 2,000 individuals covering all species, which are used in phylogeographic analyses to reconstruct species histories in different monophyletic groups of diploid species. During the last two years we were able to come up with a first phylogenetic hypothesis for the rapidly evolving diploid New World species of this genus, and started the analyses of specific subgroups within this clade. Population genetic analyses together with modelling of ecological niches resulted in the surprising insight that in southern South America some *Hordeum* species did not migrate towards the equator during cold cycles of the Pleistocene but survived the ice ages *in situ* even in Tierra del Fuego (Fig. 17, p. 47). In a pilot study on polyploidy evolution in wall barley (*H. murinum*) we could show that two extinct diploids together with subsp. *glaucum* were involved in the formation of extant tetra- and hexaploid subspecies of this taxon. This work will be extended to other polyploids in the near future. The work on *Hordeum* during the last years finally resulted in a new infrageneric classification of the genus, now recognising two subgenera and five sections, which are in accord with monophyletic groups of phylogenetic analyses (S. Jakob, T. Pleines).

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. Nuclear microsatellites were developed and used together with chloroplast variation to analyse population genetics and phylogeography of two widespread Bornean *Macaranga* species, one a myrmecophyte (ant-plant), the other without ant mutualists. 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 (C. Baier).

In the DFG-funded project on ***Hypericum*** systematics we finished a cladistic analysis of morphological characters including more than 450 species of the genus plus representatives of other genera of the family Hypericaceae. This analysis provides a framework for in-detail studies of the genus with molecular tools. The project is part of a cooperation with the Natural History Museum London and connected to projects on *Hypericum* in the Apomixis group of T. Sharbel at the IPK and M. Koch's group at the University of Heidelberg (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 fiber plants. These species are so-called neglected crops. We analyse these species phylogenetically, for protein content, secondary compounds, and collect ethnobotanical data, particularly in Ethiopia (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 this taxon we study phylogenetic relationships of the entire genus, and will conduct phylogeographic analyses within a group of species occurring on mountaintops in Anatolia. These species and populations are isolated on sky-islands, as they are not able to migrate through the forest-covered lower landscape separating the mountains. Here we are interested in differentiation processes due to geographical isolation and potential merging of taxa during ice-age cold cycles, when the forests vanished from parts of the Anatolian highlands (D. Harpke).

Cucurbitaceae provide an important group of crop species in Western African countries. They are used as oil seeds, fruits, and vegetables. For this group we are analysing the biodiversity present in West Africa. Morphometric analyses and genome size measurements with flow cytometry, together with phylogenetic and phylogeographic analyses were currently undertaken to identify new species and subspecies and get insights in domestication of native crops of this region (E. Achigan-Dako).

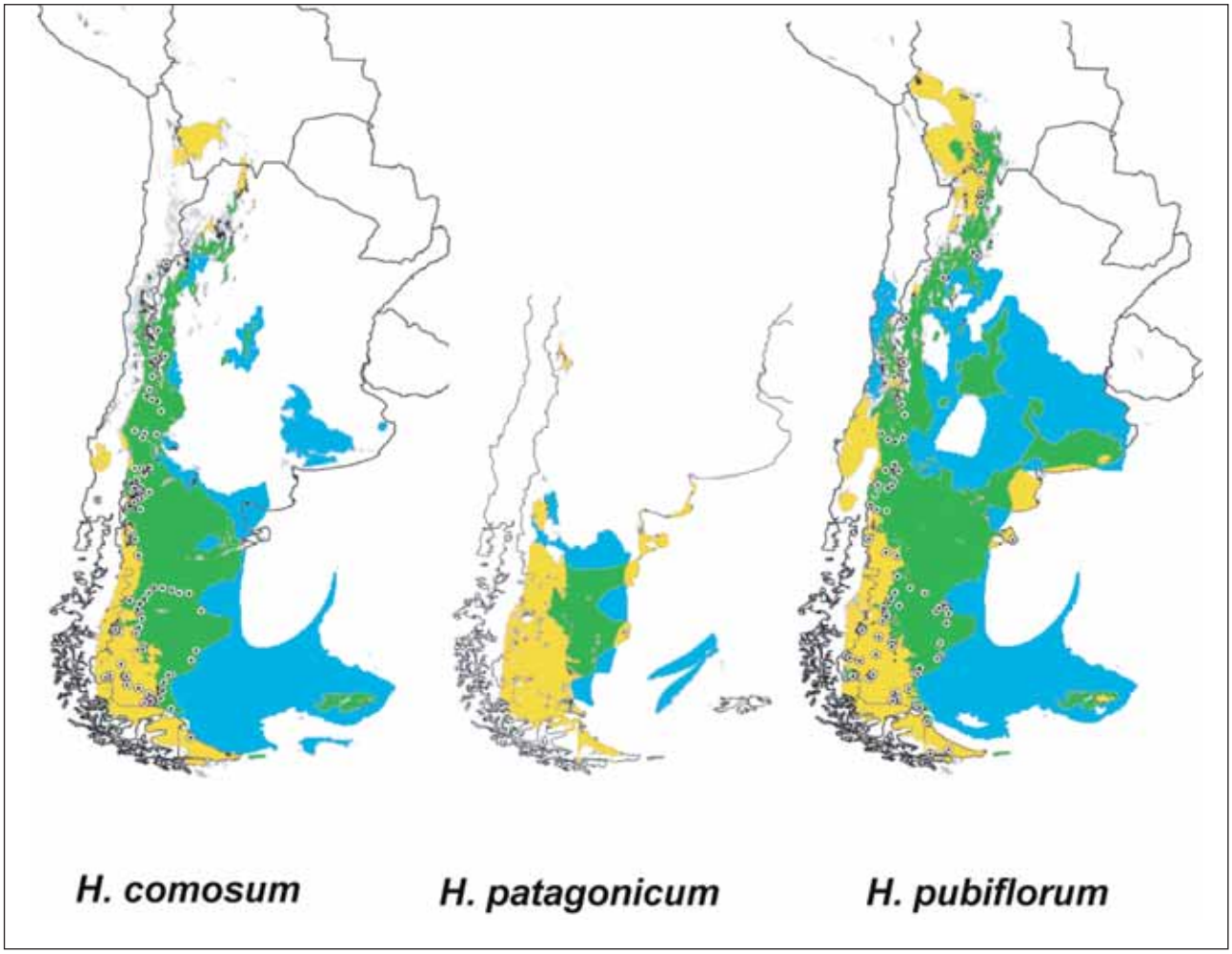

Fig. 17
Distribution models of three *Hordeum* species of southern South America based on 19 "bioclim" parameters. Yellow and green colours indicate the extant distribution areas of the species. Today's climate parameters were used to calculate the distribution of potentially suitable habitats during the last glacial maximum (LGM) about 21,000 years ago. These areas are depicted in green and blue. The models indicate that climate conditions were suitable during the LGM for the species to survive in parts of the areas where they are also distributed today. Figure modified from Jakob et al. (2009).

Collaborations (selection)

Within the Institute:

Dept. of Cytogenetics and Genome Analysis, Research Group Chromosome Structure and Function; Dr. A. Houben;

Dept. of Cytogenetics and Genome Analysis, Research Group Karyotype Evolution, Dr. J. Fuchs;

Dept. of Cytogenetics and Genome Analysis, Research Group Apomixis; Dr. T. Sharbel.

Dept. of Molecular Genetics, Research Group Gene Regulation; Dr. H. Bäumlein,

Dept. of Physiology and Cell Biology, Research Group Structural Cell Biology; Dr. T. Rutten.

Outside the Institute:

Natural History Museum "Bernado Rivadavia", Buenos Aires, Argentina; Dr. M. Arriaga;

Martin Luther University Halle-Wittenberg, Institute of Geobotany and Botanical Garden, Halle/Saale; Prof. I. Hensen, Dr. M.H. Hoffman, Prof. M. Röser, Dr. B. von Hagen;

University of Heidelberg, Institute of Plant Sciences; Prof. M. Koch;

University of Kassel, Systematics and Morphology of Plants, Kassel; Dr. D. Guicking, Prof. K. Weising;

Natural History Museum, London, UK; Dr. J. Vogel, Dr. N. Robson;

University of Osnabrück, Botanical Institute and Botanical Garden, Osnabrück; Dr. N. Friesen.

Publications

Peer Reviewed Papers

2008

Achigan-Dako, E.G., R. Fagbemissi, H.T. Avohou, S.R. Vodouhe, O. Coulibaly & A. Ahanchede: Importance and practices of egusi crops (*Citrullus lanatus* (Thunb.) Matsum. & Nakai, *Cucumeropsis mannii* Naudin and *Lagenaria siceraria (*Molina) Standl. cv. 'Aklamkpa') in socio-linguistic areas in Benin. Biotechnol. Agron. Soc. Environ. 12 (2008) 393-403.

Achigan-Dako, E.G., J. Fuchs, A. Ahanchede & F.R. Blattner: Flow cytometric analysis in *Lagenaria siceraria* (Cucurbitaceae) correlate with usage types (bottle gourds vs. seed consumption) and growing elevation. Plant Syst. Evol. 276 (2008) 9-19.

Achigan-Dako, E.G, S. Ndanikou, A. Ahanchede, J. Ganglo & F.R. Blattner: Phenetic analysis of wild populations of *Momordica charantia* L. (Cucurbitaceae) in West Africa and inference of the definition of the new subspecies *macroloba*. Candollea 63 (2008) 153-167.

Achigan-Dako, E.G., S.R. Vodouhe & A. Sangaré: Morphological characterisation of cultivars of *Lagenaria siceraria* collected in Benin and Togo. (Franz. Titel: Caractérisation morphologique des cultivars locaux de *Lagenaria siceraria* (Cucurbitaceae) collectés au Bénin et au Togo). Belg. J. Bot. 141 (2008) 21-38.

Benor, S., M. Zhang, Z. Wang & H. Zhang: Assessment of genetic variation in tomato (*Solanum lycopersicum* L.) inbred lines using SSR molecular markers. J. Genet. Genomics 35 (2008) 373-379.

Esfeld, K., I. Hensen, K. Wesche, S.S. Jakob, S. Tischew & F.R. Blattner: Molecular data indicate multiple independent colonisations of former lignite mining areas in Eastern Germany by *Epipactis palustris* (Orchidaceae). Biodivers. Conserv. 17 (2008) 2441-2453.

Guicking, D., T. Kröger-Kilian, K. Weising & F.R. Blattner: Single nucleotide sequence analysis: a cost- and time-effective protocol for the analysis of microsatellite- and indel-rich chloroplast DNA regions. Mol. Ecol. Resour. 8 (2008) 62-65.

Gurushidze, M., R.M. Fritsch & F.R. Blattner: Phylogenetic analysis of *Allium* subg. *Melanocrommyum* infers cryptic species and demands a new sectional classification. Mol. Phylogenet. Evol. 49 (2008) 997-1007.

Pleines, T. & F.R. Blattner: Phylogeographic implications of an AFLP phylogeny of the American diploid *Hordeum* species (Poaceae: Triticeae). Taxon 57 (2008) 875-881.

Vodouhe, S.R., E.G. Achigan-Dako, M.E. Dulloo & A. Kouke: Effects of silica gel, sun drying and storage conditions on viability of egusi seeds (Cucurbitaceae*)*. Plant Genet. Res. Newsl. 153 (2008) 36-42.

2009

Baier, C., D. Guicking, K. Prinz, C. Fey-Wagner, T. Wöhrmann, K. Weising, T. Debener, S. Schie & F.R. Blattner: Isolation and characterisation of 11 new microsatellite markers for *Macaranga* (Euphorbiaceae). Mol. Ecol. Resour. 9 (2009) 1049-1052.

Blattner, F.R.: Progress in phylogenetic analysis and a new infrageneric classification of the barley genus *Hordeum* (Poaceae: Triticeae). Breed. Sci. 59 (2009) 471-480.

Jakob, S.S., E. Martinez-Meyer & F.R. Blattner: Phylogeographic analyses and paleodistribution modeling indicate pleistocene *in situ* survival of *Hordeum* species (Poaceae) in southern Patagonia without genetic or spatial restriction. Mol. Biol. Evol. 26 (2009) 907-923.

Pleines, T., S.S. Jakob & F.R. Blattner: Application of non-coding DNA regions in intraspecific analyses. Plant Syst. Evol. 282 (2009) 281-294.

Research Group: Taxonomy of Plant Genetic Resources

Head: Dr. Frank Blattner (provisional)

Scientists

IPK financed
Fritsch, Reinhard, Dr. (0,5 P/ATZ-Freistellungsphase, till 30.09.2009)
Gurushidze, Maia, (0,5 P, till 31.08.2009)
Pistrick, Klaus, Dr. (P)

Visiting Scientists/Scholars
Fritsch, Reinhard, Dr. (self-financed, since 01.10.2009)
Gowayed, Salah (self-financed, 01.07.-31.12.2008)

Goals

Curatorial management of living and archive **taxonomic collections**, investigations of morphological, karyological and anatomical characters resulting in phylogenetic and taxonomic conclusions, and **nomenclatural works**. Research activities target general questions of the **taxonomy of crop plants** jointly with the other research group in the programme "Taxonomy and Evolutionary Biology" of the Genebank department.

Research Report

The **custodial management of the taxonomic reference collections** represents a continuous activity. During the period 2008/2009 about 6,000 herbarium sheets, 2,000 fruit and seed samples, and more than 500 cereal spikes were added to the collection. Apart from members of the Institute, the collections were used by many visitors of the IPK facilities or vouchers were sent abroad in the frame of international herbarium exchange. This part of the work involves also taxonomical determination of genebank materials from a wide variety of plant families (K. Pistrick).

In 2008 and 2009 two collection trips into northern **Georgia** were conducted together with colleagues from the Institute of Botany and Botanical Garden, Tbilisi. While the first collection mission had to be abandoned after three days due to the armed conflict between Georgia and Russia, in 2009 more than 300 accessions of local cereals, legumes, vegetables, herbs, and medicinal plants could be collected (K. Pistrick).

The living ***Allium* reference collection** was used to cultivate new materials from West and Central Asia, which was collected during several research missions within the "PharmAll" project funded by the VolkswagenStiftung. Several new species could be detected (see Fig. 18), particularly during fieldwork in Iran. For a part of these species taxonomic descriptions and determination keys were published. The phylogenetic positions of these newly discovered taxa were all determined by molecular marker analyses (R. Fritsch).

Fig. 18
Pictures of the newly described species *Allium hamedanense* R.M. Fritsch of the drumstick onion group (*Allium* subgenus *Melanocrommyum*). This species was detected on limestone slopes of the Zagros mountain range in northwestern Iran (R. Fritsch).

Large molecular phylogenies of the members of ***Allium* subgenus *Melanocrommyum*** as well as a group of taxa close to **common onion** (*Allium cepa*) based on nuclear rDNA internal transcribed spacer sequences were used to infer the relationships within these groups. This work resulted in clarification of relationships in the section *Cepa* and proposes domestication of common onion from *A. vavilovii* probably involving some geneflow between the crop and wild species or populations after domestication. In subgenus *Melanocrommyum* molecular analyses showed that the traditional taxonomic treatment is not in accord with phylogenetic relationships of species. Moreover, within three species so-called cryptic species were detected. A taxonomic revision of the subgenus with newly circumscribed sections and subsections was published (R. Fritsch, M. Gurushidze).

Collaborations (selection)

Within the Institute:

Dept. of Cytogenetics and Genome Analysis, Research Group Chromosome Structure and Function; Dr. A. Houben;

Dept. of Cytogenetics and Genome Analysis, Research Group Karyotype Evolution, Dr. J. Fuchs;

Dept. of Genebank, Research Group Resources Genetics and Reproduction; Dr. U. Lohwasser;

Dept. of Physiology and Cell Biology, Research Group Structural Cell Biology; Dr. T. Rutten.

Outside the Institute:

Botanical Institute of the Tajik Academy of Sciences, Dushanbe, Tajikistan; Prof. H. Hisoriev, Dr. P. Kurbonova;

Botanika, Centre of the Uzbek Academy of Sciences, Tashkent, Uzbekistan; Dr. F. Khassanov;

Bundessortenamt, Prüfstelle Dachwig; H. Eger;

Iranian Research Institute of Plant Protection, Tehran, Iran; Dr. M. Abbasi;

Martin Luther University Halle-Wittenberg, Institute of Geobotany and Botanical Garden, Halle/Saale; Prof. E.J. Jäger;

Niko Ketskhoveli Institute of Botany, Georgian Academy of Sciences, Tbilisi, Georgia; Prof. G. Nakhutsrishvili, Prof. M. Akhalkatsi;

Philipps University Marburg, Institute of Pharmaceutical Chemistry; Prof. M. Keusgen, Dr. J. Jedelská-Keusgen;

Research Institute of Forests and Rangelands, Tehran, Iran; Prof. A. A. Maassoumi;

University of Kassel, Faculty of Agriculture, Institute of Crop Science, Dept. Agricultural Biodiversity, Witzenhausen; Prof. K. Hammer.

University of Osnabrück, Botanical Institute and Botanical Garden, Osnabrück; Dr. N. Friesen.

University of Tehran, Tehran, Iran; Prof. S. Zarre.

Publications

Peer Reviewed Papers

2008

Fritsch, R.M., M. Gurushidze, J. Jedelská & M. Keusgen: More than a pretty face - ornamental "drumstick onions" of *Allium* subg. *Melanocrommyum* are also potential medicinal plants. Herbertia 60 (2008) 26-59.

Fritsch, R.M. & F.O. Khassanov: New taxa of *Allium* L. subg. *Allium* (Alliaceae) from Tajikistan and Uzbekistan. Feddes Repert. 119 (2008) 625-633.

Gurushidze, M., R.M. Fritsch & F.R. Blattner: Phylogenetic analysis of *Allium* subg. *Melanocrommyum* infers cryptic species and demands a new sectional classification. Mol. Phylogenet. Evol. 49 (2008) 997-1007.

2009

Fritsch, R.M.: New *Allium* L. taxa from Tajikistan, Kyrgyzstan, and Uzbekistan. Bot. Jahrb. Syst. 127 (2009) 459-471.

Fritsch, R.M. & A.R. Abbasi: New taxa and other contributions to the taxonomy of *Allium* L. (Alliaceae) in Iran. Rostaniha 10 Suppl. 1 (2009) 1-72.

Fritsch, R.M. & N. Friesen: *Allium oreotadzhikorum* and *A. vallivanchense*, two new species of *Allium* subg. *Polyprason* (Alliaceae) from the Central Asian Republic Tajikistan. Feddes Repert. 120 (2009) 221-231.

Namin, H.H., S.S. Mehrvarz, S. Zarre & R. Fritsch: Pollen morphology of selected species of *Allium* (Alliaceae) distributed in Iran. Nord. J. Bot. 27 (2009) 54-60.

Neshati, F. & R.M. Fritsch: Seed characters and testa sculptures of some Iranian *Allium* L. species (Alliaceae). Feddes Repert. 120 (2009) 322-332.

Neshati, F., R.M. Fritsch & S. Zarre: Pollen morphology of some *Allium* L. species (Alliaceae) from Iran. Bot. Jahrb. Syst. 127 (2009) 433-451.

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Abteilung Cytogenetik und Genomanalyse/ Department of Cytogenetics and Genome Analysis

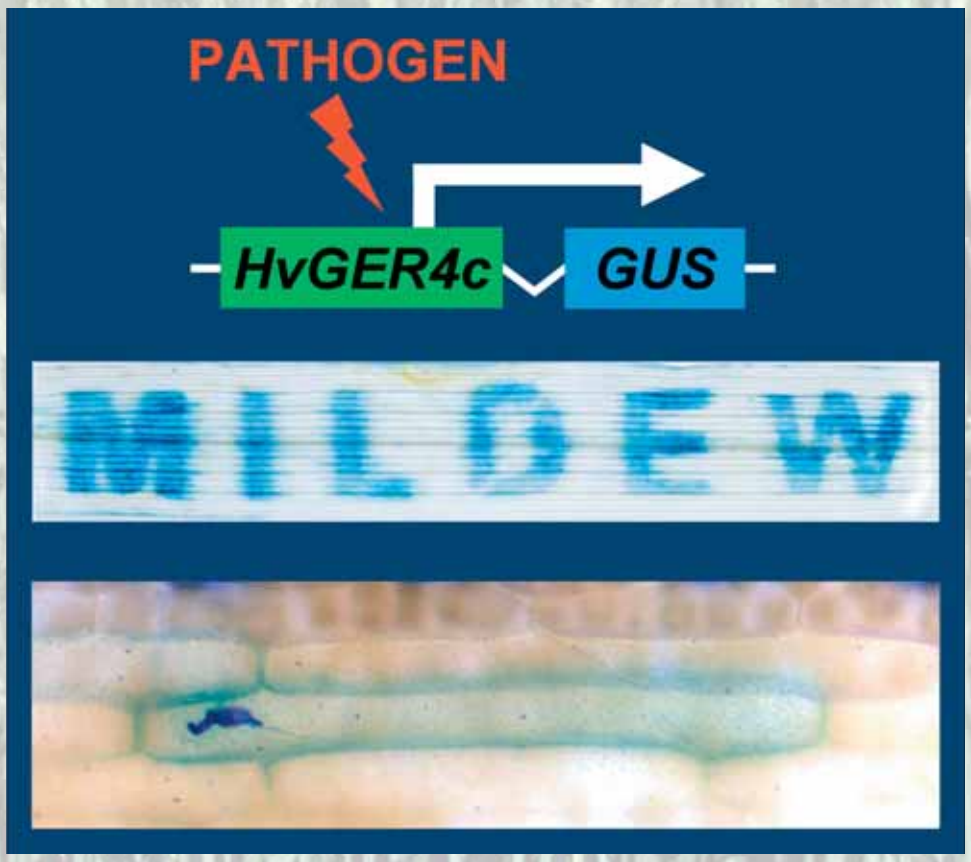

Fig. 19
Der *HvGER4c*-Promotor der Gerste reguliert pathogen-induzierbare Expression eines germinähnlichen Proteins, welches in der Blattepidermis von pathogenbefallenen Pflanzen akkumuliert wird. Nach Inokulation von Blättern einer transgenen Pflanze (HvGER4c:GUS) mit Mehltausporen in einem Muster, das dem Schriftzug „MILDEW" entspricht, konnte strikt lokale Expression des GUS-Reportergens gezeigt werden. Das untere Bild zeigt spezifische Induktion des Promotors nur in derjenigen Epidermiszelle, die in direktem Kontakt mit einer Mehltauspore war (dunkelblau) (A. Himmelbach, G. Hensel).

The *HvGER4c* promoter of barley drives the pathogen-inducible expression of a germin-like protein that accumulates in the epidermis of attacked plants. Here the highly localised induction of GUS-expression is shown in a leaf by an inoculation pattern with *Blumeria graminis* spores that formed the letters "MILDEW". The bottom panel of the image shows GUS-induction only in the epidermal cell that was in direct contact with a fungal spore (dark blue) (A. Himmelbach, G. Hensel).

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).
Eine Arbeitsgruppe (*In vitro*-Differenzierung) arbeitet mit embryonalen und adulten Stammzellen vornehmlich der Maus.

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 - Abteilung 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);
- Erzeugung von Minichromosomen u. a. Ansätze zum gezielten Gentransfer in Gerste (Arbeitsgruppen Chromosomenstruktur und -funktion, Karyotypevolution und Epigenetik, sowie Pflanzliche Reproduktionsbiologie - Abteilung Physiologie und Zellbiologie);
- Aufklärung des Differenzierungspotenzials und der genetischen und epigenetischen Regulation von Differenzierungsprozessen pluripotenter embryonaler und adulter Säugerstammzellen *in vitro* für künftige Entwicklungsstrategien zur Zell- und Geweberegeneration (Arbeitsgruppe *In vitro*-Differenzierung).

Department of Cytogenetics and Genome Analysis

Head: Prof. Ingo Schubert

Research Goals

The research topics of the Department are focussed 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).
One research group (*In vitro* Differentiation) is working with embryonic and adult murine stem cells.

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 Plant Reproductive Biology; Dept. of Physiology and Cell 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 Data Inspection; Dept. of Molecular Genetics).
- Developmental and experimentally induced (mutants; DNA damage) genome dynamics and its biological consequences (altered interphase chromatin arrangement; chromosome rearrangements) (research group Karyotype Evolution).
- Generation of minichromosomes as gene transfer vehicles and approaches for gene targeting in barley (research groups Chromosome Structure and Function, Karyotype Evolution, Epigenetics, and Plant Reproductive Biology; Dept. of Physiology and Cell Biology).
- Elucidation of potential and regulation of differentiation of pluripotent embryonic and adult mammalian stem cells in culture for future tissue regeneration (research group *In vitro* Differentiation).

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 genregulatorische Muster in Getreidepflanzen, die unter (a) biotischem Stress leiden oder Resistenzen aufweisen (Arbeitsgruppen Transkriptomanalyse, Gen- und Genomkartierung, Bioinformatik und Informationstechnologie);
- Etablierung von Ontologien bzw. kontrollierten Vokabularien zur Strukturierung, Integration und Vernetzung diverser Datenbanken (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. In PGRC-Dienstleistungsmodulen, die in den Arbeitsgruppen Transkriptomanalyse sowie Bioinformatik und Informationstechnologie verankert sind, werden 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

Zur Verstärkung der Abteilung Molekulare Genetik wurde 2008 die Gruppe Expressionskartierung in diese Abteilung überführt. Die Gruppe Mustererkennung wurde mit dem Weggang ihres Leiters Dr. U. Seiffert aufgelöst und das entsprechende Know-how soweit als möglich in andere Gruppen eingegliedert.

In den Jahren 2008/2009 wurden eine Habilitation, fünf Dissertationen, zwölf Diplomarbeiten und eine Bachelorarbeit erfolgreich abgeschlossen.

Für die abteilungsinterne, die institutsweite und die institutsübergreifende Zusammenarbeit spielten auch 2008/2009 molekulare Markersysteme, lasergestützte Durchflusszytometrie, Fluoreszenzmikroskopie und Bioinformatik eine wesentliche Rolle. Alle Gruppen der Ab-

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 allele-phenotype relationships and of gene regulation patterns in cereals under (a)biotic stress (research groups Transcriptome Analysis, Gene and Genome Mapping, Bioinformatics and Information Technology).
- Establishing of ontologies and controlled vocabularies for structuring, integration and linking of diverse databases (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 the Reporting Period

To support the Department of Molecular Genetics, the research group Expression Mapping has been transferred into this department in 2008. The group Pattern Recognition has been closed after the head Dr. U. Seiffert had left IPK. As far as possible, the know-how of this group has been integrated into other bioinformatics groups.

In 2008 and 2009 one habilitation, five dissertations (PhD), twelve Diploma theses and one bachelor thesis have been finished successfully.

Besides PGRC services, molecular marker systems and flow-cytometry were important issues for collaboration within the Department and with other groups inside and outside the IPK last year. All groups of the Department collaborate with internal and external partners within the frame of large national and international research networks such as GABI (BMBF), "Pakt für Forschung und Innovation" (Leibniz Association) and Excellence Network (Saxony-Anhalt) projects. For the multiple cooperative links of the individual groups see their detailed reports and publication records.

teilung kooperieren innerhalb und außerhalb des IPK, z. B. im Rahmen von GABI, des „Paktes für Forschung" der *WGL* und des Exzellenz-Netzwerks des Landes Sachsen-Anhalt. 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 2008/2009 erbrachten Forschungsleistungen seien die Folgenden besonders hervorgehoben:

Schwesterchromatidenkohäsion ist durch DNA-Brüche induzierbar und erforderlich für die Genomstabilität
Die Kohäsion der Schwesterchromatiden von der Replikation bis zur Segregation der nuklearen Erbanlagen wird durch den sog. Kohäsinkomplex bewirkt und ist essentiell für die postreplikative homologe Rekombinationsreparatur sowie für die korrekte Aufteilung der Chromosomen während der Kernteilung. Erstmalig für einen pflanzlichen Organismus (*Arabidopsis thaliana*) wurden für sämtliche Kohäsinkomponenten und weitere kohäsionsrelevante Proteine (insgesamt 9 Gene) DNA-Insertionsmutanten hinsichtlich Lebensfähigkeit, Expression und Phänotyp untersucht: i) homozygote Null-Mutanten sind nur lebensfähig, wenn es sich um eine Genfamilie handelt; ii) homozygote Mutationen, die unvollständige Produkte kodieren, oder heterozygote Mutanten (selbst bei im Vergleich zum Wildtyp nur leicht verringertem Transkriptionslevel) führen zu verminderter Kohäsionsfrequenz entlang der Chromosomenarme und z. T. auch der Zentromere; iii) die meisten Mutanten vermindern die Genomstabilität deutlich (signifikanter Anstieg an Anaphasen mit Brücken) (s. Fig. 22, S. 59, V. Schubert, A. Weißleder, H. Ali, J. Fuchs, I. Lermontova, A. Meister, I. Schubert; Chromosoma 2009).
In Zusammenarbeit der Gruppe Karyotypevolution mit der Gruppe von Prof. H. Puchta (Universität Karlsruhe) konnte darüber hinaus gezeigt werden, dass pflanzliche Genome auf DNA-Schädigung mit einer transient verstärkten Annäherung der Schwesterchromatiden reagieren. Für diesen Prozess müssen die Gene des SMC5/6-Komplexes sowie die replikationskorrelierte Schwesterchromatidenkohäsion intakt sein. Diese schadensbedingte Genomdynamik dient der homologen Rekombinationsreparatur zwischen Schwesterchromatiden (K. Watanabe, M. Pacher, S. Dukovic, V. Schubert, H. Puchta, I. Schubert; Plant Cell 2009).

Evolution eines Wildgrases aufgeklärt
Der evolutionäre Ursprung der Wildgrasart ***Zingeria kochii* (2n = 12)** wurde gemeinsam mit einer russischen, einer japanischen und mehreren IPK-Arbeitsgruppen aufgeklärt. Mit Hilfe der genomischen *in situ*-Hybridisierung konnte nachgewiesen werden, dass *Z. kochii* hexaploid ist und aus interspezifischen Hybridisierungen hervorging, an denen *Z. biebersteiniana* (2n = 4), *Colpodium versicolor* (2n = 4) und eine unbekannte Art beteiligt waren. Im Anschluss an die Allopolyploidisierung kam

The following scientific achievements are considered as highlights of the Department in 2008/2009:

Sister chromatid cohesion is enforced by DNA breaks and is required for genome stability
The cohesion of sister chromatids from replication phase until segregation of chromosomes is mediated by the cohesin complex and is required for postreplicative homologous recombination repair as well as for correct chromosome segregation during nuclear divisions. For all cohesin components and some cohesion-related proteins of *Arabidopsis thaliana* (in total 9 genes), T-DNA insertion mutants were studied as to their viability, phenotype and expression and yielded the following main results: i) homozygous null mutants survive only when (partially) compensated by other members of the gene family; ii) homozygous mutations yielding a truncated gene product, or heterozygous mutants (with a reduced transcript level in comparison to wild-type) lower the cohesion frequency along chromosome arms and (in some cases) at centromeres; iii) most mutants display genome instability (significant increase in anaphases with chromatin bridges) (see Fig. 22; p. 59, V. Schubert, A. Weißleder, H. Ali, J. Fuchs, I. Lermontova, A. Meister, I. Schubert; Chromosoma 2009).
In collaboration with the group of Prof. H. Puchta, University Karlsruhe, the research group Karyotype Evolution could show that DNA breaks cause a transient increase of sister chromatid cohesion frequency. This process requires functional SMC5/6 complex components as well as replication-dependent sister chromatid cohesion and facilitates homologous recombination repair between sister chromatids (K. Watanabe, M. Pacher, S. Dukovic, V. Schubert, H. Puchta, I. Schubert; Plant Cell 2009).

Evolution of a grass species elucidated
The evolutionary origin of the wild grass ***Zingeria kochii*** (2n = 12) has been elucidated in collaboration with a Russian, a Japanese and several IPK research groups. Genomic *in situ* hybridisation revealed that *Z. kochii* evolved from a hexaploid interspecific hybrid involving species closely related to contemporary *Z. biebersteiniana, Colpodium versicolor* and a third unknown species. Subsequent to this allopolyploidisation, the *biebersteiniana*-like parental chromosomes underwent loss of ribosomal DNA. Homogenisation of 45S rDNA of the other two species did not take place in *Z. kochii*. Phylogenetic analysis showed that *C. versicolor* contributed its genome to *Z. kochii* relatively recently (see Fig. 20, p. 56, V. Kotseruba, K. Pistrick, F.R. Blattner, K. Kumke, O. Weiss, T. Rutten, J. Fuchs, T. Endo, S. Nasuda, A. Ghukasyan, A. Houben; Mol. Phyl. Evol., in press).

A novel approach to study the origin of apomictic seed formation
Deregulation of reproductive pathways, as induced by interspecific hybridisation between sexual species, has been

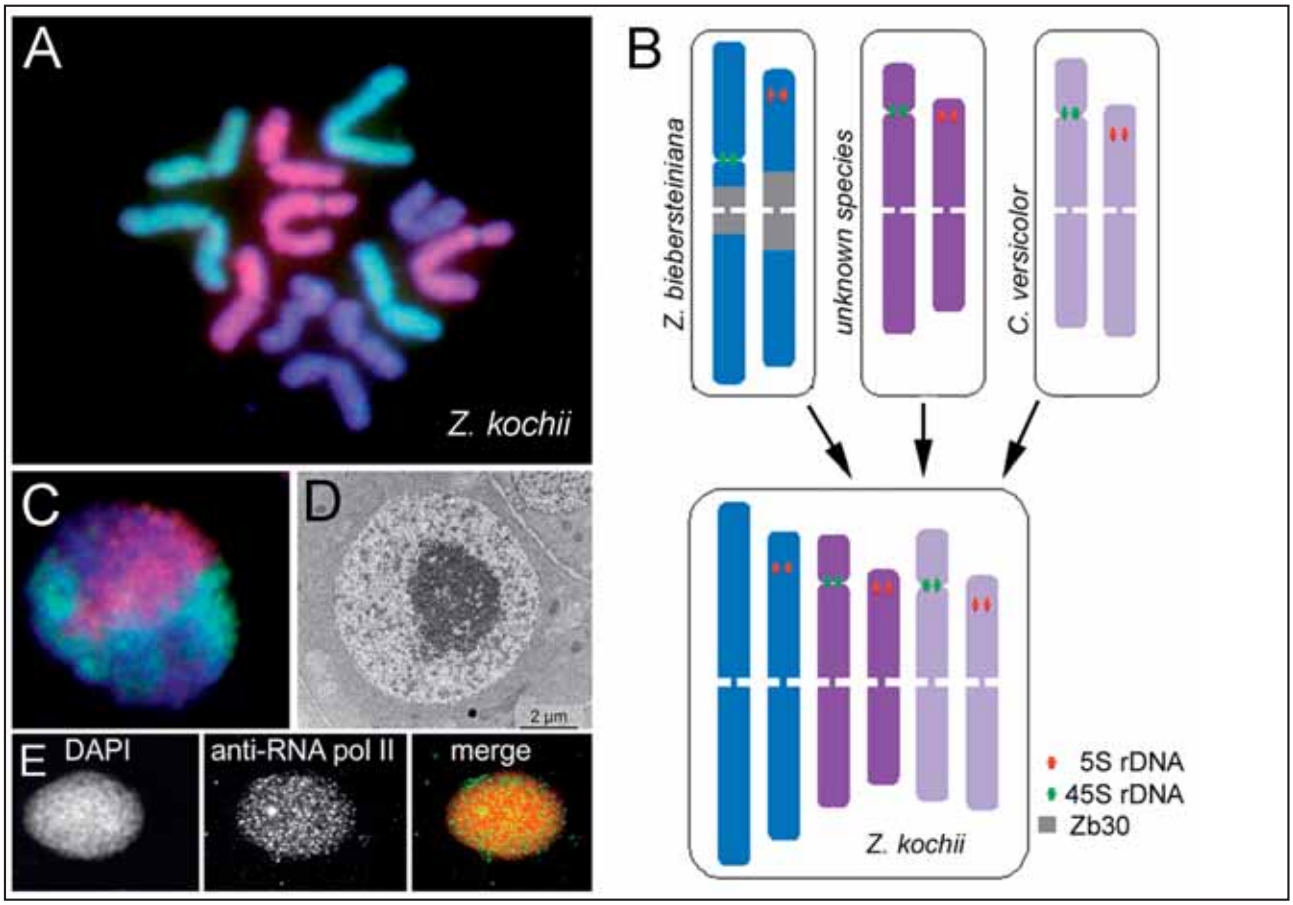

Fig. 20
Genomic *in situ* hybridisation on (A) mitotic and (C) interphase chromosomes of *Zingeria kochii* with labelled genomic DNA of *Z. biebersteiniana* (in green) and of *Colpodium versicolor* (in red) demonstrates its allopolyploid origin. (B) Scheme of the evolutionary steps involved in formation of *Z. kochii*. (D) No subgenome-like domains are detectable in the nucleus of *Z. kochii* by electron microscopy. (E) Distribution of RNA polymerase II in the nucleus of *Z. kochii* indicates that all subgenomes are transcription active (K. Kumke, O. Weiss, T. Rutten, A. Houben).

es zum Verlust der *Z. biebersteiniana*-ähnlichen ribosomalen DNA. Phylogenetische Analysen ergaben, dass die Chromosomen von *C. versicolor* zuletzt in das Genom von *Z. kochii* gelangten und keine Homogenisierung der 45S rDNA von *C. versicolor* und der noch unbekannten dritten Ausgangsart erfolgte (s. Abb. 20, V. Kotseruba, K. Pistrick, F.R. Blattner, K. Kumke, O. Weiss, T. Rutten, J. Fuchs, T. Endo, S. Nasuda, A. Ghukasyan, A. Houben; Mol. Phyl. Evol., im Druck).

Ein neuer Ansatz zur Aufklärung der apomiktischen Samenbildung

Fehlregulation von Reproduktionswegen in interspezifischen Hybriden zwischen sexuellen Arten könnte die Ursache für das Vorkommen natürlicher Apomikten sein, als auch der Induktion apomiktischer Samenbildung dienen. Zur Überprüfung dieser Hypothese wurden die Transkriptionsprofile aus lebenden mikrodissektierten Ovulen von sexuellen und apomiktischen *Boechera*-Pflanzen in vier verschiedenen Entwicklungsstadien verglichen (s. Fig. 24, S. 66). Apomiktische Megasporenmutterzellen zeigten eine globale Abregulation v. a. von an der Reproduktion beteiligten Genen. Transkriptionsfaktoren sind proposed to explain the origin of naturally occurring apomicts and to induce apomictic seed production. To test this hypothesis, the transcript profiles of microdissected live ovules at four developmental stages between a diploid sexual and a diploid apomictic *Boechera*, were compared (see Fig. 24, p. 66). Apomictic megaspore mother cells were characterised by global down-regulation of genes, many (n=110) of which were associated with reproduction. Transcription factors were over-represented among genes which were differentially expressed between sexual and apomictic ovules. These data suggest that apomixis arises through heterochronic expression of reproduction genes, with regulatory (e.g. transcription) factors responsible for heterochrony. Since apomictic *Boechera* plants are hybrids, the relative titer of *trans*-acting regulatory factors might be lowered in the hybrid genome due to divergence in transcriptional regulator and promoter sequences within the genomes of their sexual parents. These data are the basis for subsequent microarray experiments to distinguish genotypic variation from genes showing consistently differential expression between sexual and apomictic ovules. Additionally, sequencing of small RNAs is being used to identify regulatory factors which control candidate gene expression (research group Apomixis).

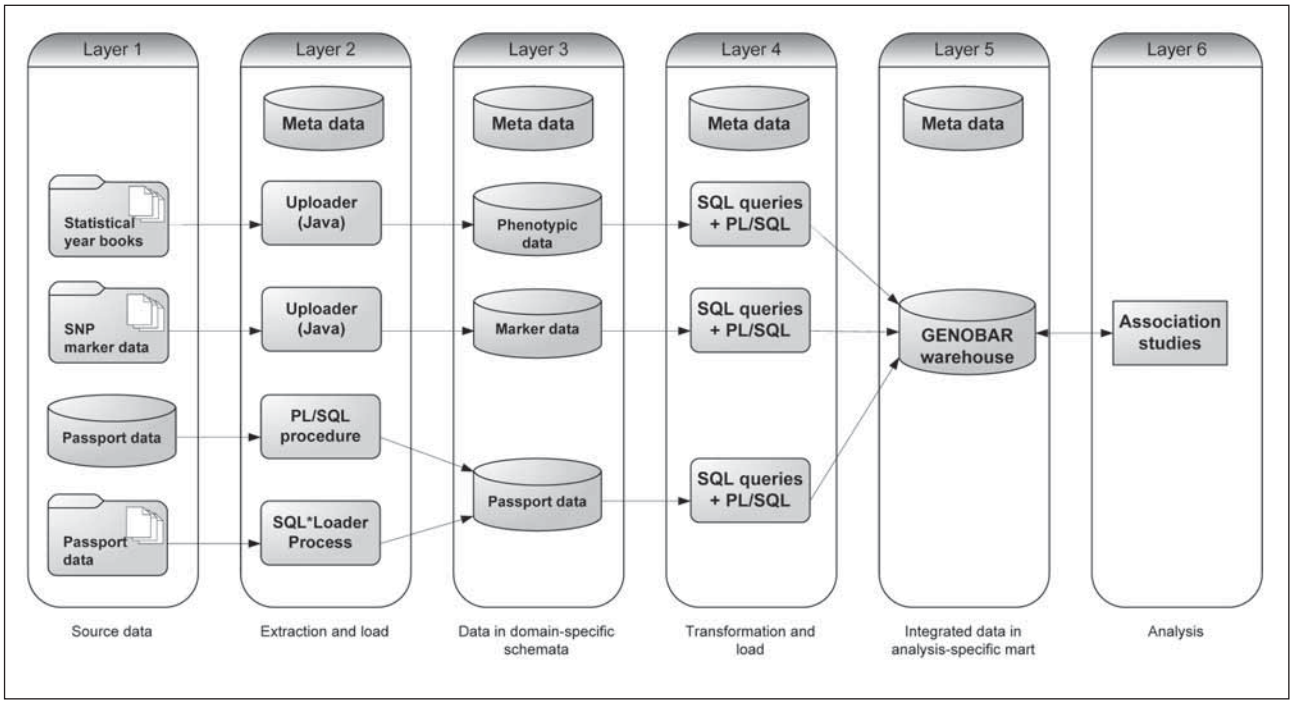

Fig. 21
Association pipeline according to C. Kuenne, I. Grosse, I. Matthies, U. Scholz, T. Sretenovic-Rajicic, N. Stein, A. Stephanik, B. Steuernagel, S. Weise, J. Integrat. Bioinf. 2007.

überproportional unter den Genen zu finden, die zwischen sexuellen und apomiktischen Ovulen differenziell exprimiert werden. Diese Ergebnisse legen nahe, dass Apomixis durch heterochrone Expression von ‚Reproduktionsgenen' bedingt ist, und ‚regulatorische Elemente' (z. B. Transkriptionsfaktoren) für die Heterochronie verantwortlich sind. Da Apomikten der Gattung *Boechera* Arthybriden representieren, könnte der relative Titer transaktivierender Faktoren auf Grund der Divergenz von Transkriptionsregulator- und Promoter-Sequenzen zwischen den Genomen der sexuellen Eltern deutlich verringert sein. Diese Ergebnisse bilden die Basis für Micro-Array-Experimente, um genotypspezifische Expressionsmuster von differenziell exprimierten Genen zwischen apomiktischen und sexuellen Ovulen zu unterscheiden. Darüber hinaus wird über die Sequenzierung kleiner RNAs die Identifikation von Regulationsfaktoren, die die Expression von Apomixis-Kandidatengenen kontrollieren, vorangetrieben (Arbeitsgruppe Apomixis).

Die RNA-abhängige RNA-Polymerase RDR5 ist für die Transkriptmengen-abhängige post-transkriptionelle Geninaktivierung essentiell

Die Bildung doppelsträngiger RNA durch RNA-abhängige RNA-Polymerasen (RDRs) ist ein zentraler Schritt der post-transkriptionellen Geninaktivierung in Pflanzen. Das Genom von *Arabidopsis thaliana* kodiert für sechs Mitglieder der RDR-Genfamilie. *RDR1* ist an der Abwehr von Viren beteiligt, *RDR2* ist für die RNA-vermittelte DNA-Methylierung bestimmter Sequenzen notwendig und *RDR6* spielt eine Schlüsselrolle bei der post-transkriptionellen Inaktivierung von Transgenen und bei der Bildung von

RNA-directed RNA Polymerase RDR5 is essential for transcript level-dependent post-transcriptional gene silencing

Formation of double stranded RNA by RNA-directed RNA polymerases (RDRs) is a pivotal step of post-transcriptional gene silencing (PTGS) pathways in plants. Of six gene family members present in the *Arabidopsis thaliana* genome, *RDR1* has a role in the defence against viruses, *RDR2* is essential for RNA-directed DNA methylation (RdDM) of particular sequences and *RDR6* is a key factor in PTGS of transgenes and in the formation of endogenous tasiRNAs. No function had so far been assigned to *RDR3*, *RDR4* and *RDR5*. We could show that introgression of mutant *rdr5* into a line containing multiple copies of a *GUS* reporter construct releases *GUS* silencing and reduces *GUS* 21nt siRNA formation and RNA-directed DNA methylation of the *GUS* coding region. Thus, RDR5 is pivotal to transcript-level dependent PTGS (see Fig. 26, p. 70, research groups Epigenetics and Genome Plasticity).

Automated genome-wide association studies

Already within the frame of the projects GABI-MALT and Bioinformatics Centre Gatersleben-Halle, the research groups Gene and Genome Mapping and Bioinformatics and Information Technology started a collaboration which was intensified during the joint GABI-GENOBAR project and led to *automated genome-wide association studies* in barley (see Fig. 21). This tool facilitates the directed exploitation of the genetic diversity of the primary barley gene pool. Such genome-wide association data can be applied for allele-based improvement of this (and other) crop(s) using the in-house established integration

endogenen tasiRNAs. Bisher waren keine Funktionen von *RDR3*, *RDR4* und *RDR5* bekannt. Die Einkreuzung eines mutierten *rdr5* Allels in eine Linie mit mehreren Kopien eines *GUS*-Reporterkonstrukts verhinderte die Inaktivierung der *GUS*-Expression und reduzierte die Bildung von *GUS* 21nt siRNAs und die RNA-vermittelte DNA-Methylierung der *GUS*-kodierenden Region. Somit ist RDR5 essenziell für die Transkriptmengen-abhängige post-transkriptionelle Geninaktivierung (s. Fig. 26, S. 70, Arbeitsgruppen Epigenetik und Genomplastizität).

Automatisierung genomweiter Assoziationsstudien

Bereits im Rahmen von GABI-MALT und dem Bioinformatik-Centrum Gatersleben-Halle etablierten die Arbeitsgruppen Gen- und Genomkartierung sowie Bioinformatik und Informationstechnologie eine enge Zusammenarbeit, die im Verlauf des GABI-GENOBAR-Projektes weiter vertieft wurde und zu einer *Automatisierung genomweiter Assoziationsstudien* bei Gerste führte. Auf diese Weise wird unter Anwendung der am IPK etablierten Plattform ‚CropHouse' eine direkte Nutzung der genetischen Diversität des primären Genpools der Gerste zur züchterischen Verbesserung dieser Kulturart ermöglicht. Bei Eingabe entsprechender Daten in CropHouse ist das System auch für andere Kulturarten anwendbar (s. Fig. 21, S. 57), I. Matthies, S. Weise, J. Förster, M. Röder; Euphytica 2009 und I. Matthies, S. Weise, M. Röder; Mol. Breed. 2009).

Ingo Schubert, Januar 2010

platform CropHouse (I. Matthies, S. Weise, J. Förster, M. Röder; Euphytica 2009 and I. Matthies, S. Weise, M. Röder, Mol. Breed. 2009).

Ingo Schubert, January 2010

Programme: Cytogenetics

Research Group: Karyotype Evolution

Head: Prof. Ingo Schubert

Scientists

IPK financed
Fuchs, Jörg, Dr. (P)
Ma, Lu, Dr. (0,5 Pakt für Forschung und Innovation, since 01.02.2009)
Moraes, Izabel (0,5 P, since 01.02.2008)
Schubert, Veit, Dr. (P)
Weißleder, Andrea (0,5 P, till 30.06.2009)

Grant Positions
Borisova-Todorova, Branimira, Dr. (0,5 Saxony-Anhalt, since 11.02.2008)
Jovtchev, Gabriele, Dr. (Saxony-Anhalt, 01.04.-30.06.2008)
Lermontova, Inna, Dr. (DFG)
Watanabe, Koichi, Dr. (BMBF)

Visiting Scientists/Scholars
Dvorackova, Martina (Czech Acad. of Science, 23.11.-11.12.2009)
Endo, Takashi R., Prof. (University Kyoto, 21.01.-02.02.2008)
Farre, Alba, Dr. (self-financed, 28.01.-30.04.2009)
Lysak, Martin Adam, Dr. (Humboldt fellow, 01.03.-31.12.2009)
Peska, Vratislav (Czech Acad. of Science, 23.11.-11.12.2009)
Weißleder, Andrea (self-financed, 01.07.-31.12.2009)
Yokota, Etsuko, Dr. (IPK, 01.10.-30.11.2009)

Goals

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

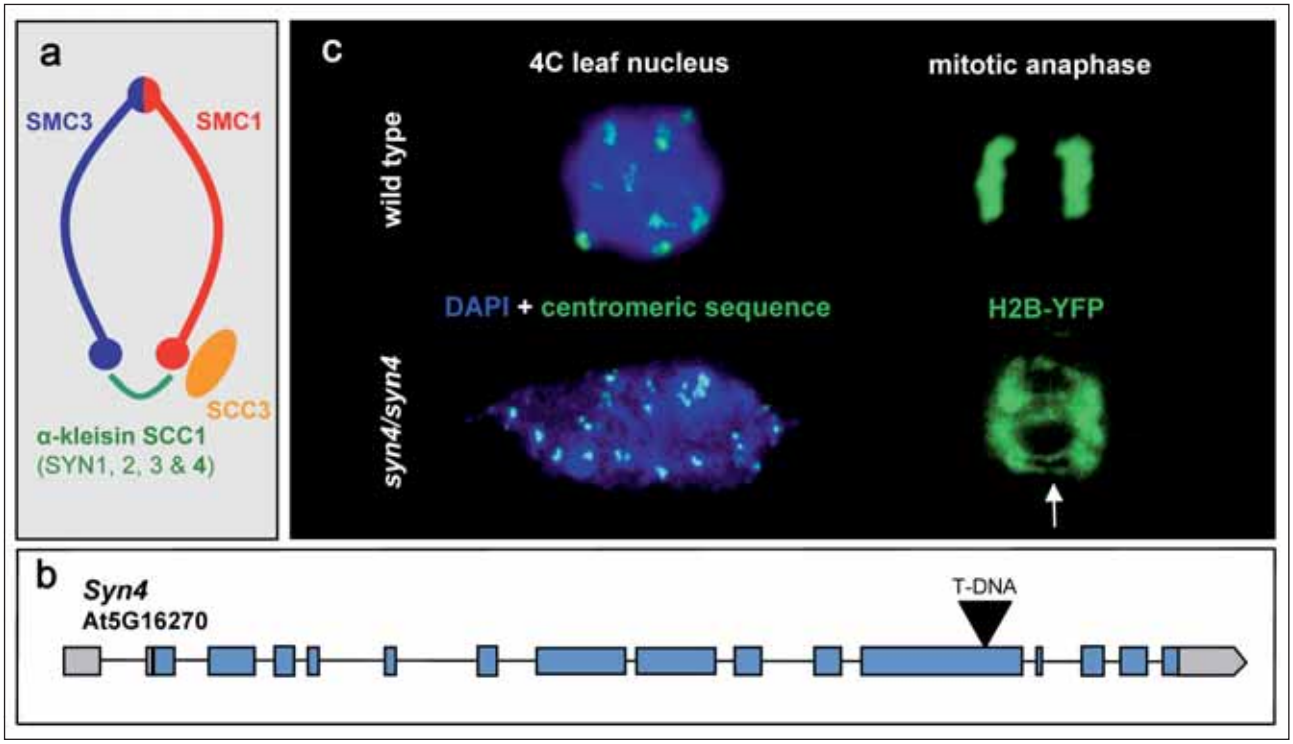

Fig. 22
Cohesin is essential for sister chromatid cohesion and genome stability in *Arabidopsis thaliana*.
(a) Model of the cohesin complex of yeast (Nasmyth and Haering, 2005) consisting of SMC1, SMC3, SCC3, and the -kleisin SCC1. The latter is represented by four homologues (SYN1-4) in *A. thaliana*.
(b) Gene structure of Syn4; exons = blue; UTRs = grey. The T-DNA insertion causes a truncated SYN4 protein, which is only partially functional. (c) Sister centromere separation in a 4C interphase nucleus of a syn4/syn4 mutant compared to wild-type (left). Anaphase bridges (arrow) in a syn4/syn4 mutant indicating chromosomal rearrangements (right) (V. Schubert, A. Weißleder).

Research Report

Centromere research. Fluorescence recovery after photobleaching of recombinant EYFP-CENH3 in *Arabidopsis thaliana* confirmed our previous finding that the centromeric histone H3 variant is incorporated (and not only accumulated) in late G2-phase, i.e., before mitotic separation of sister chromatids (and not thereafter as in metazoans). *In planta* expression of split CENH3 protein revealed that the C-terminal part of CENH3 is sufficient for targeting centromeres, while its N-terminal part is required for centromere function, presumably to recruit essential kinetochore proteins - a hypothesis to be tested in future (DFG; I. Lermontova). The *Arabidopsis* spindle checkpoint protein Bub3.1 was shown to be expressed during mitosis and to be essential for male and female gametophyte development (I. Lermontova, J. Fuchs & I. Schubert, Front Biosci. 2008). A second CENH3 variant was found for the holocentric plant *Luzula nivea*. Newly arisen antibodies indicate that both variants are expressed and incorporated along mitotic chromosomes (I. Moraes).

Chromatin modifications. After comparing evolutionary conservation and subchromosomal distribution of histone modifications (in particular, mono-, di- and tri-methylation of lysine residues) between angiosperms and gymnosperms (J. Fuchs, G. Jovtchev, I. Schubert; Chromosome Res. 2008), the mosses *Barbula crocea* (240 Mbp/1C) and *Ceratodon purpureus* (380 Mbp/1C) were studied. Similar as in seed plants, H3K4me1,2,3 were exclusively found in the euchromatin. H3K9me2 and H3K27me1,2 are associated with heterochromatin in both species. H3K9me1 displays euchromatin-specific distribution in *B. crocea* but is enriched at heterochromatin in *C. purpureus.* H3K9me3 was at euchromatin in *C. purpureus* but yielded only weak signals in *B. crocea*. Thus, the heterochromatin-specific marks in *C. purpureus* resemble that typically for angiosperms (H3K9me1,2 and H3K27me1,2), whereas the preferential association of H3K9me1 with euchromatin in *B. crocea* resembles its distribution in gymnosperms, strengthening our conclusion that histone methylation marks are conserved in plants but their distribution (and possibly the functional meaning) may diverge during evolution. Now the focus is on sex-chromosome-specific marks of *Silene* and *Rumex* species (Saxony-Anhalt Excellence Cluster, J. Fuchs, G. Jovtchev, B. Borisova-Todorova).

Interphase chromatin arrangement. T-DNA insertion mutants of nine *A. thaliana* genes involved in sister chromatid cohesion were characterised for viability, expression and phenotype (see Fig. 22, p. 59). Homozygous mutants were viable only when gene families are concerned. Even heterozygous mutants with a slight reduction of transcript level revealed reduced sister chromatid cohesion along chromosome arms and in some cases also at centromeres. Strikingly, six of these mutants displayed significantly increased genome instability (5.7 to 43.8 % of anaphase bridges) indicating that disturbed sister chromatid cohesion leads to a switch from correct homologous recombination repair toward error-prone non-homologous end-joining of DNA double-strand breaks (V. Schubert, A. Weißleder, H. Ali, J. Fuchs, I. Lermontova, A. Meister, I. Schubert, Chromosoma 2009; for review V. Schubert, Cytogenet. Genome Res. 2009).
Furthermore, in collaboration with Prof. H. Puchta's group, University of Karlsruhe, we could show that in *A. thaliana* the SMC (structural maintenance of chromosomes) 5/6 complex, together with cohesins, (transiently) enhances sister chromatid alignment required for homologous recombination repair in replicated (4C) nuclei after DNA breakage (K. Watanabe, M. Pacher, S. Dukowic, V. Schubert, H. Puchta, I. Schubert, Plant Cell 2009).
For the impact of tandem repeats on interphase chromosome architecture see report of the Epigenetics group (M.F. Mette).

Biological consequences of targeted DNA DSBs in barley. All necessary constructs to estimate the frequency of double-strand breaks and of gene conversion, single strand annealing repair, sister chromatid exchange, chromatid aberrations and gene targeting events at transgenic recombination substrate after endonuclease cleavage are generated and transformed into barley 'Golden Promise' (collaboration with J. Kumlehns group). All transgenic lines were confirmed by PCR. For most constructs, lines with single (copy) loci were selected by Southern hybridisation and mapped to distinct chromosomes by FISH (K. Watanabe, GABI PRECISE, since 01.01.2008).
A joint 'Pakt für Forschung und Innovation' project (Houben, Mette, Kumlehn, Schubert) is aimed to generate **barley minichromosomes** as potential vehicles for gene transfer by telomere-mediated chromosome arm truncation. As a prerequisite, homologous and heterologous short single copy sequences were applied to chromosomal mapping by FISH: A contig of four *Brachypodium sylvaticum* BACs could be localised on chromosome 1p of *B. distachyon* (2n=10). Unique sequences (~10 kb) from BACs of the homeologous barley region (harbouring the dwarfing gene sdw3) could be mapped in the middle of 2HS (L. Ma, in collaboration with G. Vu, University of Aberystwyth, and N. Stein, Genebank).

Collaborations (selection)

Within the Institute:
Dept. of Genebank, Research Group Genome Diversity; Dr. N. Stein;
Dept. of Genebank, Research Group Taxonomy of Plant Genetic Resources; Dr. F. Blattner, Dr. M. Gurushidze;
Dept. of Cytogenetics and Genome Analysis, Research Group Chromosome Structure and Function; Dr. A. Houben, Dr. D. Demidov;
Dept. of Cytogenetics and Genome Analysis, Research Group Epigenetics; Dr. M.F. Mette;

Dept. of Cytogenetics and Genome Analysis, Research Group *In vitro* Differentiation; Prof. A.M. Wobus, Dr. S. Sulzbacher, Dr. I. Schröder;
Dept. of Molecular Genetics, Research Group Seed Development; Dr. W. Weschke;
Dept. of Physiology and Cell Biology, Research Group Structural Cell Biology; Dr. T. Rutten;
Dept. of Physiology and Cell Biology, Research Group Plant Reproductive Biology; Dr. J. Kumlehn.

Outside the Institute:
Martin Luther University Halle-Wittenberg, Institute of Genetics, Halle/Saale; Prof. G. Reuter;
Institute of Vegetable and Ornamental Crops, Erfurt; Dr. A. Hohe, Dr. T. Borchert;
Humboldt University, Department of Biology, Berlin; Prof. T. Börner, E. Cincu;
University of Karlsruhe, Institute of Botany II, Karlsruhe; Prof. H. Puchta, Dr. F. Hartung;
Max Planck Institute for Plant Breeding Research, Cologne; Dr. B. Reiss;
Masaryk University, Brnó, Czech Republic; Dr. M. Lysak, Dr. E. Sykorova;
Flanders Institute of Biotechnology (VIB), Ghent, Belgium; Dr. L. deVeylder;
University of Zurich, Institute of Systematic Biology, Zurich, Switzerland; Dr. A. Schmidt-Lebuhn;
Université de Strasbourg, Institut de Biologie Moléculaire des Plantes, Strasbourg, France; Dr. A. Berr;
University of Kyoto, Kyoto, Japan; Prof. T.R. Endo.

Publications

Peer Reviewed Papers

2008

Achigan-Dako, E.G., J. Fuchs, A. Ahanchede & F.R. Blattner: Flow cytometric analysis in *Lagenaria siceraria* (Cucurbitaceae) correlate with usage types (bottle gourds vs. seed consumption) and growing elevation. Plant Syst. Evol. 276 (2008) 9-19.

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Houben, A., R.K. Dawe, J. Jiang & I. Schubert: Engineered plant minichromosomes: a bottom-up success? Plant Cell 20 (2008) 8-10.

Jovtchev, G., K. Watanabe, A. Pecinka, F.M. Rosin, M.F. Mette, E. Lam & I. Schubert: Size and number of tandem repeat arrays can determine somatic homologous pairing of transgene loci mediated by epigenetic modifications in *Arabidopsis thaliana* nuclei. Chromosoma 117 (2008) 267-276.

Lermontova, I., J. Fuchs & I. Schubert: The *Arabidopsis* checkpoint protein Bub3.1 is essential for gametophyte development. Front. Biosci. 13 (2008) 5202-5211.

Schmidt-Lebuhn, A.N., J. Fuchs & M. Kessler: Flow cytometric measurements do not reveal different ploidy levels in *Minthostachys* (Lamiaceae). Plant Syst. Evol. 271 (2008) 123-128.

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Schubert, V., Y.M. Kim & I. Schubert: *Arabidopsis* sister chromatids often show complete alignment or separation along a 1.2-Mb euchromatic region but no cohesion "hot spots". Chromosoma 117 (2008) 261-266.

Vaillant, I., S. Tutois, Z. Jasencakova, J. Douet, I. Schubert & S. Tourmente: Hypomethylation and hypermethylation of the tandem repetitive 5S rRNA genes in *Arabidopsis*. Plant J. 54 (2008) 299-309.

2009

Borchert, T., K. Eckardt, J. Fuchs, K. Krueger & A. Hohe: Who's who! in two different flower types of *Calluna vulgaris* (Ericaceae): morphological and molecular analyses of flower identity. BMC Plant Biol. 9 (2009) 148.

Demidov, D., S. Hesse, A. Tewes, T. Rutten, J. Fuchs, R.K. Ashtiyani, S. Lein, A. Fischer, G. Reuter & A. Houben: Aurora1 phosphorylation activity on histone H3 and its crosstalk with other post-translational histone modifications in *Arabidopsis*. Plant J. 59 (2009) 221-230.

Dhar, M.K., J. Fuchs & A. Houben: Distribution of eu- and heterochromatin of *Plantago ovata*. Cytogenet. Genome Res. 125 (2009) 235-240.

Lysak, M.A., M.A. Koch, J.M. Beaulieu, A. Meister & I.J. Leitch: The dynamic ups and downs of genome size evolution in *Brassicaceae*. Mol. Biol. Evol. 26 (2009) 85-98.

Schubert, V.: SMC proteins and their multiple functions in higher plants. Cytogenet. Genome Res. 124 (2009) 202-214.

Schubert, V., A. Weissleder, H. Ali, J. Fuchs, I. Lermontova, A. Meister & I. Schubert: Cohesin gene defects may impair sister chromatid alignment and genome stability in *Arabidopsis thaliana*. Chromosoma 118 (2009) 591-605.

Watanabe, K., M. Pacher, S. Dukowic, V. Schubert, H. Puchta & I. Schubert: The structural maintenance of chromosomes 5/6 complex promotes sister chromatid alignment and homologous recombination after DNA damage in *Arabidopsis thaliana*. Plant Cell 21 (2009) 2689-2699.

Xu, L., R. Menard, A. Berr, J. Fuchs, V. Cognat, D. Meyer & W.H. Shen: The E2 ubiquitin-conjugating enzymes, AtUBC1 and AtUBC2, play redundant roles and are involved in activation of FLC expression and repression of flowering in *Arabidopsis thaliana*. Plant J. 57 (2009) 279-288.

Research Group: Chromosome Structure and Function

Head: Dr. Andreas Houben

Scientists

IPK financed
Agueci, Francesco (0,5/0,25 Annex, 01.10.2008-30.06.2009)
Heckmann, Stefan (0,25 Annex, 01.04.-30.06.2009; 0,5 P, since 01.07.2009)
Ma, Lu, Dr. (0,5 Pakt für Forschung und Innovation, since 01.02.2009)

Grant Positions
Agueci, Francesco (0,5 Saxony-Anhalt, till 30.09.2008)
Banaei Moghadam, Ali Mohammad (0,5/1,0 DFG)
Carchilan, Mariana (DFG, 15.03.-31.07.2008)
Demidov, Dmitri, Dr. (DFG)
Karimi Ashtiyani, Raheleh (0,5/1,0 Saxony-Anhalt)
Pickering, Richard, Dr. (EU, 07.09.2008-06.09.2009)
Sanei, Maryam (0,5 DFG, since 01.10.2008)
Vlasenko, Liudmila (0,5 DFG, till 15.01.2009)

Visiting Scientists/Scholars
Agueci, Francesco (self-financed, since 01.07.2009)
Carchilan, Mariana (self-financed, 01.01.-14.03.2008)
Dhar, Manoj, Prof. (DFG, 29.05.-28.07.2008)
Nasuda, Shuhai, Dr. (University Kyoto, 19.02.-06.03.2008; 25.11.-22.12.2008)
Pickering, Richard, Dr. (DFG, 07.05.-06.09.2008)

Goals

Analysis and manipulation of structure and regulation of plant chromosomes.

Research Report

Hordeum vulgare × *H. bulbosum* crosses were used to study the **process of uniparental chromosome elimination** which occurs in some plant interspecific hybrids. Lagging *H. bulbosum* chromosomes of hybrid embryos are CENH3-negative indicating an important role of the centromeric histone H3 in chromosome elimination (Fig. 23). Cloning and mapping of the CENH3 gene of *H. vulgare* and *H. bulbosum* revealed two variants in each species located on chromosomes 1H (αCenH3) and 6H (βCenH3). The

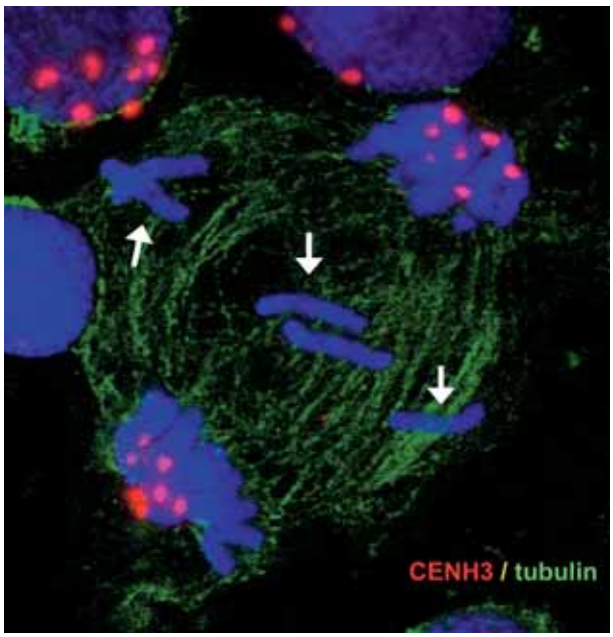

Fig. 23
Immunostaining of unstable *Hordeum vulgare* × *Hordeum bulbosum* hybrid embryos revealed no CENH3-signal (in red) of lagging anaphase chromosomes (arrowed). Absence of CENH3 suggests centromere inactivity. Missegregation and elimination of chromosomes via micronuclei formation is the consequence of CENH3 inactivity (M. Sanei, R. Pickering, A. Houben).

CenH3 variants of both parental genomes are transcribed in stable and unstable hybrid embryos. Hence, either mRNA of *H. bulbosum* CenH3s is not translated into an active protein, or no CENH3 protein is loaded to centromeres of *H. bulbosum* (M. Sanei, R. Pickering, A. Houben).

The **enzymological properties of AtAurora1**, a kinase responsible for the cell cycle-dependent phosphorylation of histone H3 at S10, and its **cross-talk with other post-translational histone modifications**, were determined (Demidov et al. 2009). Two putative AtAurora1 interactor proteins (a transcription regulator and a chromosome segregation ATPase), which act as *in vitro* kinase assay substrate of AtAurora1, were characterised. C/N-GFP reporter constructs of both interactor proteins co-localised with heterochromatic interphase regions of stably transformed *A. thaliana* plants. A similar distribution was found in transiently transformed *Nicotiana benthamiana* mesophyll cells. The distribution of the GFP-tagged chromosome segregation ATPase was dynamic during the cell cycle in tobacco BY2 suspension cells (D. Demidov in collaboration with T. Rutten, research group Structural Cell Biology).

An orthologue of the **histone H3-specific Haspin kinase** of mammals has been analysed in *A. thaliana*. *In vitro* it phosphorylates histone H3T3 and is highly expressed in proliferating and differentiating tissues. Altered expression of AtHaspin (via RNAi and overexpression) results in pleiotropic phenotypes with defects in floral organs and vascular tissue, reduced fertility, loss of apical dominance and multiple shoots and rosettes formation. Complete

inactivation of haspin was lethal for plants. To generate sublethal AtHaspin alleles the TILLING strategy is currently applied. The AtHaspin might be directly or indirectly involved in hormone signal transduction pathways to regulate cell proliferation and differentiation (R. Karimi).

The **function of** members of the conserved **NIMA kinase family** was studied in *Arabidopsis.* One functional gene copy of AtNIMA 2 is required for plant survival. Down-regulation of AtNIMA 2 slows down plant development and vascularisation. Signals obtained from expression of a 35S::YFP::AtNIMA2 construct in *Nicotiana benthamiana* colocalise with microtubule-like structures, which disappear when depolymerising drugs are applied. AtNIMA 2 promoter-GUS signals colocalise with the vascular bundles of leaves, stem, roots and floral organs. An interaction of AtNIMA 2 and tubuline might contribute to the regulation of plant development (F. Agueci in collaboration with T. Rutten, research group Structural Cell Biology).

Arabidopsis cv. Col-0, C24, Cvi, and their reciprocal hybrids were employed to investigate the **potential relationship between changes in DNA methylation, histone modifications, endopolyploidisation and expression of heterosis after intraspecific hybridisation**. Nucleolus size, endopolyploidisation level and distribution of DNA and histone H3 methylation at the microscopic level do not differ between Col-0, C24, and their hybrids. Methylation sensitive amplified polymorphism revealed a largely constant pattern of DNA methylation in Col-0/C24 crosses. No correlation was found between the expression pattern of a set of preselected genes and DNA methylation levels at restriction sites within their 5′ regulatory regions (Banaei et al. 2009). Genome-wide ChIP-on-chip analysis revealed few variations of histone H3K4 and H3K27 methylation among the tested accessions Col-0, C24 and Cvi. Parental H3 methylation patterns were mostly additively inherited in the offspring of Col-0/C24 and Col-0/Cvi crosses (A. Banaei in collaboration with Dr. M.F. Mette, research group Epigenetics; Dr. M. Strickert, M. Seifert, research group Research Group Data Inspection; V. Colot, F. Rodier, Epigenomics and Epigenetics of *Arabidopsis* group, France).

For the joint 'Pakt für Forschung und Innovation' project (A. Houben, M.F. Mette, I. Schubert, J. Kumlehn) to generate **barley mini-chromosomes** as potential vehicles for gene transfer by telomere-mediated chromosome arm truncation, see reports of the research groups Karyotype evolution and Epigenetics.

Collaborations (selection)

Within the Institute:

Dept. of Cytogenetics and Genome Analysis, Research Group Karyotype Evolution; Dr. I. Lermontova, Dr. J. Fuchs, Prof. I. Schubert;

Dept. of Cytogenetics and Genome Analysis, Research Group Epigenetics; Dr. F.M. Mette;

Dept. of Molecular Genetics, Research Group Data Inspection; Dr. M. Strickert, M. Seifert;

Dept. of Physiology and Cell Biology, Research Group Structural Cell Biology; Dr. T. Rutten.

Outside the Institute:

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Ludwig Maximilians University, Munich; Prof. G. Wanner, Dr. E. Schroeder-Reiter;

Universidad Complutense, Madrid, Spain; Prof. M. Puertas;

University of Wales, Aberystwyth, UK; Prof. J.N. Jones;

Okayama University, Okayama, Japan; Prof. M. Murata, Dr. K. Nagaki;

Kyoto University, Kyoto, Japan; Prof. T.R. Endo, Dr. S. Nasuda;

University Aalborg, Aalborg, Denmark; Prof. K.D. Grasser;

Institute for Crop and Food Research, Christchurch, New Zealand; Dr. R. Pickering;

Ecole Normale Supérieure, Paris, France; Prof. V. Colot; Institute of Experimental Botany, Olomouc, Czech Republic; Dr. J. Doležel.

Publications

Peer Reviewed Papers

2008

Caperta, A.D., M. Rosa, M. Delgado, R. Karimi, D. Demidov, W. Viegas & A. Houben: Distribution patterns of phosphorylated Thr 3 and Thr 32 of histone H3 in plant mitosis and meiosis. Cytogenet. Genome Res. 122 (2008) 73-79.

Cohen, S., A. Houben & D. Segal: Extrachromosomal circular DNA derived from tandemly repeated genomic sequences in plants. Plant J. 53 (2008) 1027-1034.

Houben, A., R.K. Dawe, J. Jiang & I. Schubert: Engineered plant minichromosomes: a bottom-up success? Plant Cell 20 (2008) 8-10.

Jones, R.N., W. Viegas & A. Houben: A century of B chromosomes in plants: So what? Ann. Bot. 101 (2008) 767-775.

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Lildballe, D.L., D.S. Pedersen, R. Kalamajka, J. Emmersen, A. Houben & K.D. Grasser: The expression level of the chromatin-associated HMGB1 protein influences growth, stress tolerance, and transcriptome in *Arabidopsis*. J. Mol. Biol. 384 (2008) 9-21.

Tikhenko, N., T. Rutten, A. Voylokov & A. Houben: Analysis of hybrid lethality in F-1 wheat-rye hybrid embryos. Euphytica 159 (2008) 367-375.

2009

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Demidov, D., S. Hesse, A. Tewes, T. Rutten, J. Fuchs, R.K. Ashtiyani, S. Lein, A. Fischer, G. Reuter & A. Houben: Aurora1 phosphorylation activity on histone H3 and its crosstalk with other post-translational histone modifications in *Arabidopsis*. Plant J. 59 (2009) 221-230.

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Johnston, P.A., G.M. Timmerman-Vaughan, K.J. Farnden & R. Pickering: Marker development and characterisation of *Hordeum bulbosum* introgression lines: a resource for barley improvement. Theor. Appl. Genet. 118 (2009) 1429-1437.

Wicker, T., S. Taudien, A. Houben, B. Keller, A. Graner, M. Platzer & N. Stein: A whole-genome snapshot of 454 sequences exposes the composition of the barley genome and provides evidence for parallel evolution of genome size in wheat and barley. Plant J. 59 (2009) 712-722.

Books and Book Chapters

2009

Houben, A. (Ed.): Chromosome Structure and Function. Reprint of: Cytogenetic and Genome Research 2009, Vol. 124, No. 3-4. Karger (2009) 180 pp.

Houben, A. & R. Pickering: Applying cytogenetics and genomics to wide hybridisations in the genus *Hordeum*. In: Feuillet, C. & G. Muehlbauer (Eds.): Genetics and Genomics of the Triticeae. Plant Genetics/Genomics, Vol 7. Springer Publishers, New York (2009) 137-162.

Research Group: Apomixis

Head: Dr. Timothy F. Sharbel

Scientists

IPK financed
Aliyu, Olawale Mashood, Dr. (1,0/0,75 Annex, till 30.09.2008)
Corall García, José María, Dr. (Pakt für Forschung und Innovation)
Mau, Martin (0,5 Annex, 01.09.2008-31.12.2008 ; 0,5 P, since 01.01.2009)
Voigt, Marie-Luise (0,5 P, till 31.12.2008 ; 0,25 Annex, 01.01.-31.03.2009)

Grant Positions
Aliyu, Olawale Mashood, Dr. (DFG, since 01.10.2008)
Galla, Giulio (DFG, 06.07.-30.11.2009)
Puente Molins, Marta, Dr. (DFG)

Visiting Scientists/Scholars
Abdelaziz, Mohamed (self-financed, 08.03.-15.05.2008)
Amiteye, Samuel (International Max Planck Research School grant, since 23.02.2009)
Bringezu, Thomas, Dr. (Innoplanta e.V., 01.01.-30.11.2008)
Dobes, Christoph, Dr. (DFG, 18.02.-24.02.2008)
Duszynska, Dorota (Irish Research Council for Science, Engineering and Technology (IRCSET), 15.01.-30.06.2009)
Fortunato, Valeria (Leonardo da Vinci Programme, 03.07.-24.10.2009)
Galdeano, Florencia (Universidad Nacional del Nordeste, Argentina, 28.02.-07.03.2008)
Galla, Giulio (University Padua, 01.01.-26.01.2008; 17.07.-24.08.2008; self-financed, 03.11.-09.11.2008)
Otto, Lars-Gernot, Dr. (self-financed, 15.04.-31.12.2008; since 01.04.2009)
Paule, Juraj (DFG, 18.02.-24.02.2008)
Thiel, Thomas (International Max Planck Research School grant)
Voigt, Marie-Luise (self-financed, 01.04.-31.05.2009)

Goals

Genomic and transcriptomic analyses to identify candidate apomixis factors in wild accessions of *Hypericum perforatum* and in the *Boechera holboellii* complex.

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 collected and are undergoing statistical analysis. The results demonstrate very high levels of polymorphism and heterozygosity, which support hypotheses of the allopolyploid origin of *H. perforatum*. A flow cytometric analysis of 48 seeds per one individual of each of the 650 accessions has been performed, and demonstrates genotype-specific quantitative variation for sexual and apomictic seed production. These data have been used to choose genotypes for crosses in 2008-2009, in order to test whether genetic distance between parents used in a cross has a quantitative effect on sexual versus different modes of apomictic seed production in their offspring. Embryological analyses of different sexual and apomictic accessions have also been completed in order to compare the origin of aposporous initial cells in different genetic lineages (J.M. Corral, M. Molins, O.M. Aliyu in collaboration with H. Bäumlein, research group Gene Regulation; G. Galla, G. Barcaccia, Padua; J. Maron, Montana). Finally, we have **sequenced the complete flower transcriptomes (normalised cDNA) of two sexual and two apomictic accessions using 454 FLX technology** (in house), for a total of over 700 000 high quality reads (median read length = 400 bps). These data will be used to design and spot microarrays (Agilent technology) for which comparative transcriptomic analyses of microdissected ovules from sexual and apomictic accessions will be made in 2010.

The *Boechera holboellii* complex: We have chosen one diploid sexual and one unrelated diploid apomictic accession, from each of which ten live ovules of four developmental stages were isolated. Using a SuperSAGE (serial analysis of gene expression) approach, **over 2.2 million mRNA tags were DNA sequenced from the eight microdissected ovule samples**. A comparison of the eight gene expression profiles identified: (1) heterochronic tags (N=595) which demonstrated significantly different patterns of expression between sexual and apomictic ovules across all developmental stages, (2) stage-specific tags (N=577) which were found in a single developmental stage and differentially-expressed between the sexual and apomictic ovules, and (3) sex-specific (N=237) and apomixis-specific (N=1106) tags which were found in all four developmental stages but only in one reproductive mode. Corresponding gene sequences were mined from sexual and apomictic flower-derived cDNA libraries generated using 454 technology. **Most heterochronic and stage-specific tags were significantly downregulated during early apomictic ovule development, and 110 were associated with reproduction** (see Fig. 24, p. 66). In contrast, most late stage-specific tags were upregulated in the apomictic ovules, likely the result of increased gene copy number in apomictic (hexaploid) versus sexual (triploid) endosperm. Finally, we show that apomixis-specific gene expression is characterised by a significant over-representation of transcription factor activity. We hypothesise that apomeiosis is associated with global down-regulation at the megaspore mother cell stage, as influenced by

the relative titer of *trans*-acting regulatory factors, which is effectively halved in the hybrid (apomictic) genome due to divergent transcriptional regulator and promoter sequence evolution in the parental genomes.

Using our newly-developed *Boechera* gene expression microarray (see below), global gene expression in microdissected live ovules from eight sexual, eight diploid apomictic and eight triploid apomictic accessions have been compared (J.M. Corral). The goal of this project is to narrow the list of differentially expressed genes by identifying consistent patterns of expression between sexual and apomictic MMCs in multiple genotypes (i.e. identifying transcriptomal noise associated with genotype and/or ploidy). J.M. Corral has microdissected three replicates (ten ovules per replicate) from each of the 24 accessions, and has isolated enough RNA for two microarray hybridisations per replicate. Besides the production of unreduced egg cells (apomeiosis), *Boechera* also produces high frequencies of unreduced pollen, thus opening the possibility that a similar mechanism controls both processes. We have thus initiated a pollen development project (M. Mau) in order to compare the transcriptomic profiles of unreduced egg and pollen formation. Three sexual and three highly expressive (> 98 % unreduced pollen formation) apomictic accessions are presently undergoing cytohistological analyses in order to identify the mechanism of unreduced pollen formation (e.g. first division restitution), and the cells involved (M. Mau).

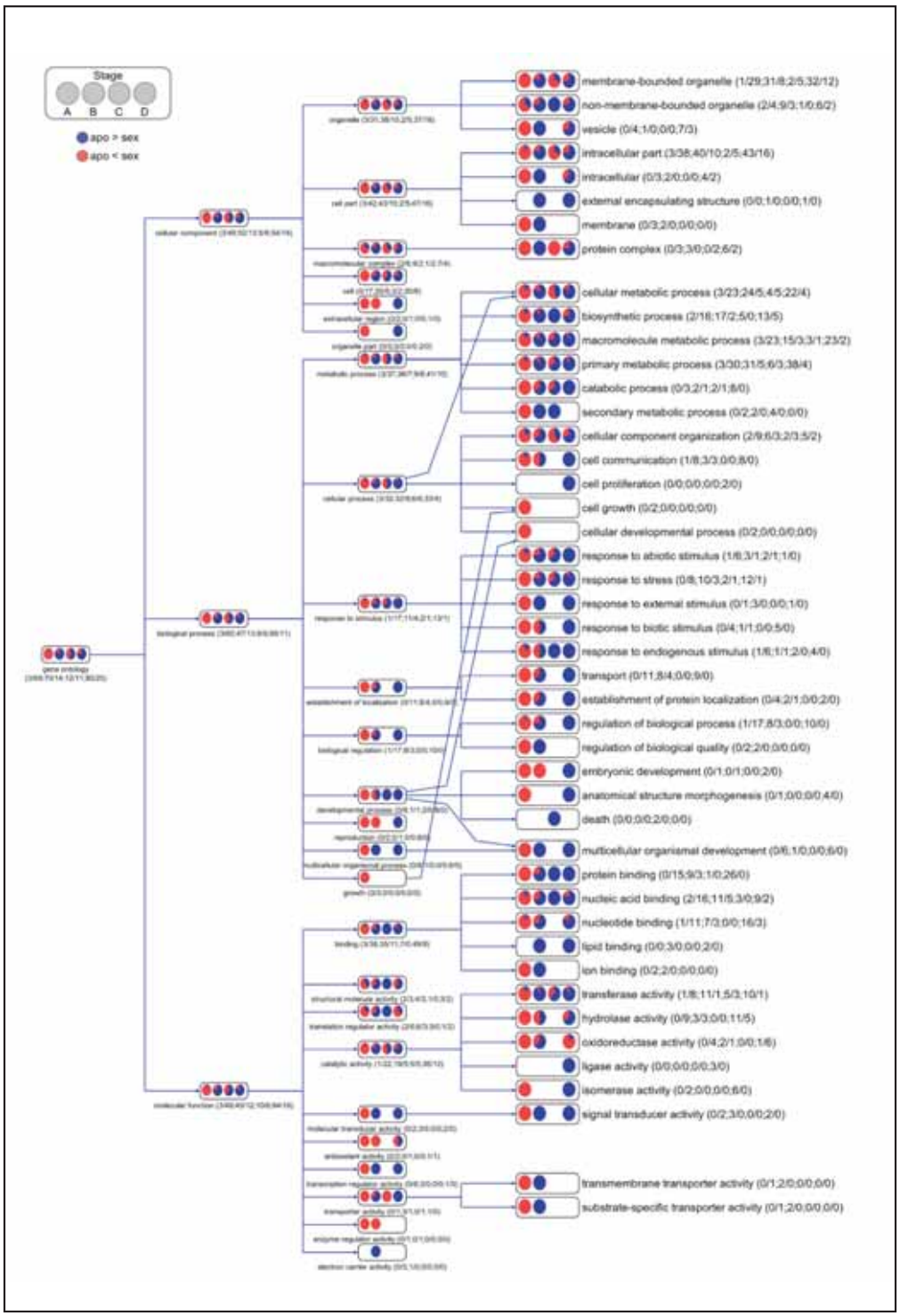

Fig. 24
Piecharts showing relative proportions of stage-specific differentially-expressed cDNAs (ordered according to gene ontology) between sexual and apomictic *Boechera* ovules across four developmental stages (A to D) ranging from pre-megaspore mother cell (A) to early endosperm formation (D). Numbers of up-regulated genes in the apomictic (blue) and sexual libraries (red) for each developmental stage are shown in parentheses (T.F. Sharbel, M.-L. Voigt, J.M. Corral, J. Kumlehn, C. Klukas, F. Schreiber, H. Vogel, B. Rotter).

We have recently completed a miRNA isolation and sequencing (Solexa) project using pooled flower stages in a sexual and an apomictic *Boechera* accession. Initial bioinformatics analyses of the sequences have identified 600 known or predicted *A. thaliana* miRNAs, and structural analyses have revealed many more

Boechera-specific candidate miRNAs (S. Amiteye). We have furthermore completed a 3'-UTR anchored cDNA sequencing project (454 FLX) from pooled sexual and apomictic flowers to complement the miRNA analyses. In addition, the 454 sequences were used to design a *Boechera*-specific expression microarray (Agilent technology) with imaGenes GmbH (Berlin). In short, fourteen 60-mer oligonucleotides (sense and antisense) per gene were spotted on a test array (2 million features in total) and this was hybridised with both genomic DNA and a complex RNA mixture. Based upon the hybridisation results, a final 105K array was designed for comparative transcriptomic analyses of microdissected ovules (J.M. Corral) and pollen cells (M. Mau).

Collaborations (selection)

Within the Institute:

Dept. of Molecular Genetics, Research Group Gene Regulation; Dr. H. Bäumlein;
Dept. of Molecular Genetics, Research Group Plant Bioinformatics; Prof. F. Schreiber;
Dept. of Physiology and Cell Biology, Research Group Structural Cell Biology; Dr. M. Melzer;
Dept. of Physiology and Cell Biology, Research Group Plant Reproductive Biology; Dr. J. Kumlehn.

Outside the Institute:

Max Planck Institute for Chemical Ecology, Jena; Dr. H. Vogel;
University of Heidelberg, Institute of Plant Sciences, Department of Biodiversity and Plant Systematics, Heidelberg; Prof. M. Koch;
GeneXPro GmbH, Frankfurt am Main; Dr. B. Rotter;
University of Perugia, Department of Plant Biology and Agroenvironmental and Animal Biotechnology, Perugia, Italy; Dr. E. Albertini;
University of Padova, Department of Environmental Agronomy and Crop Science, Padova, Italy; Dr. G. Barcaccia;
University of Montana, Missoula, Montana, USA; Prof. J. Maron.

Publications

Peer Reviewed Papers

2008

Aliyu, O.M.: Compatibility and fruit-set in cashew (*Anacardium occidentale* L.). Euphytica 160 (2008) 25-33.

Prodanovic, S., F. Matzk & D. Zoric: Effect of dicamba on wheat haploid embryo development. Cereal Res. Commun. 36 (2008) 43-51.

2009

Anssour, S., T. Krugel, T.F. Sharbel, H.P. Saluz, G. Bonaventure & I.T. Baldwin: Phenotypic, genetic and genomic consequences of natural and synthetic polyploidisation of *Nicotiana attenuata* and *Nicotiana obtusifolia*. Ann. Bot. 103 (2009) 1207-1217.

Kiefer, C., C. Dobe , T.F. Sharbel & M.A. Koch: Phylogeographic structure of the chloroplast DNA gene pool in North American *Boechera* - A genus and continental-wide perspective. Mol. Phylogenet. Evol. 52 (2009) 303-311.

Nyabuga, F.N., H.D. Loxdale, T.F. Sharbel, M. Todd & W.W. Weisser: Microsatellites from *Lysiphlebus hirticornis* Mackauer (Hymenoptera: Braconidae), a specialist primary parasitoid attacking the specialist tansy aphid, *Metopeurum fuscoviride* Stroyan (Hemiptera: Aphididae). Mol. Ecol. Resour. 9 (2009) 931-934.

Sharbel, T.F., M.L. Voigt, J.M. Corral, T. Thiel, A. Varshney, J. Kumlehn, H. Vogel & B. Rotter: Molecular signatures of apomictic and sexual ovules in the *Boechera holboellii* complex. Plant J. 58 (2009) 870-882.

Books and Book Chapters

2009

Corral, J.M., M. Piwgzynski & T.F. Sharbel: Allelic sequence divergence in the apomictic *Boechera holboellii* complex. In: Schön, I., K. Martens & P. van Dijk (Eds.): Lost sex. The evolutionary biology of parthenogenesis. Springer-Verlag, Dordrecht-Heidelberg-London-New York (2009) 495-516.

Patents

2008

Sharbel, T. & U. Blumenthal: Multi-hole test device. WO 2008/129072, Anmeldetag: 24.04.2007, Anmelder: IPK, Offenlegung: 30.10.2008, IPK Nr. 2006/08.

Research Group: Genome Plasticity

Head: Dr. Renate Schmidt

Scientists

IPK financed
Bach, Katrin, Dr. (Annex, till 31.10.2008)

Grant positions
Bach, Katrin, Dr. (BMBF, 01.11.2008-14.12.2008)
Boudichevskaia, Anastassia, Dr. (BMBF, since 01.10.2008)
Voigtländer, Susan (0,5 Saxony-Anhalt, since 01.09.2009)

Goals

A **comparative genomics approach** to reveal patterns of **genome evolution** in members of the Brassicaceae.

Research Report

Arabidopsis thaliana genes that play a major role in oil biosynthesis, seed development and/or storage compound allocation in seed were chosen as candidate genes to identify the corresponding *Brassica napus* genes. Between two and 25 copies per candidate gene were found in the rapeseed genome, in total 103 *B. napus* genes corresponded to eighteen different *Arabidopsis* candidate genes. **Sequence comparisons of homeologous *B. napus* genes revealed the presence of gene pairs**. Genes constituting such pairs are more similar to each other than to the other homeologues. Moreover, one copy each was derived from the *B. olearacea* and *B. rapa* progenitor genomes, respectively. The presence of the gene pairs reflects the allopolyploidisation event in which the *B. rapa* and *B. olearacea* genomes that diverged ca. 4 million years ago were combined to form the *B. napus* genome. Gene expression studies were carried out for a selected number of gene pairs. The two copies constituting a particular gene pair generally showed very similar expression patterns and in the majority of cases the expression level of both copies was comparable (K. Bach, A. Boudichevskaia, R. Schmidt).

The sequence information of the homeologous *B. napus* genes was a prerequisite for a **detailed analysis of allelic diversity in rapeseed**. So far, almost 150 amplicons were developed that correspond to approximately 50 *B. napus* genes. **Nearly half of the amplicons turned out to be monomorphic in a set of eleven diverse rapeseed genotypes**. Thus, despite the development of multiple amplicons for most genes, polymorphisms could only be detected in approximately two-thirds of the *B. napus* genes analysed. The most polymorphic amplicon for each of the rapeseed genes was chosen to assess the polymorphism level in a broader set of rapeseed accessions. Nineteen of these accessions represent modern European breeding lines of winter oilseed rape. Approximately two haplotypes per amplicon were found on average in these accessions. In

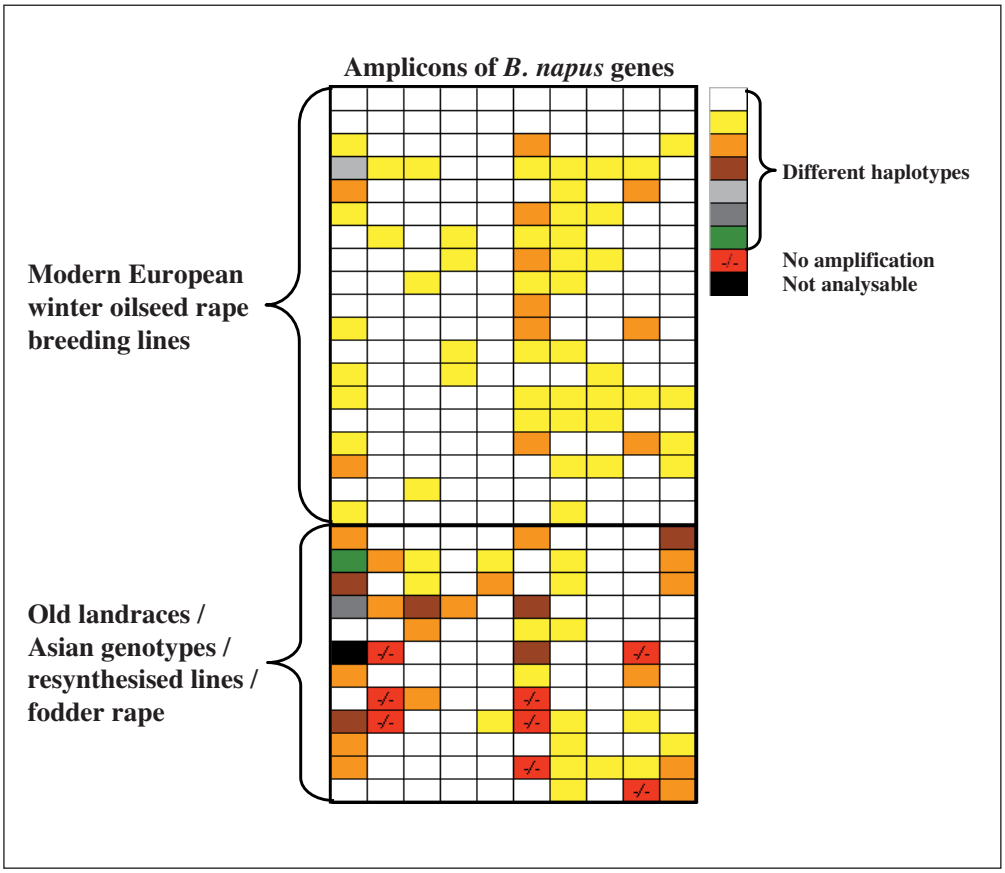

Fig. 25
Analysis of allelic diversity in *Brassica napus* accessions. The different genotypes are represented by rows. Locus-specific amplicons are shown as boxes and each column represents the amplicon for a particular *B. napus* gene. Different colours designate distinct haplotypes (R. Schmidt).

contrast, **higher diversity was noted in twelve accessions comprising of old landraces, Asian genotypes, resynthesised lines and fodder rapeseed**. The results of the allelic diversity studies for ten *B. napus* genes are compiled in Fig. 25 (R. Schmidt).

Future work will encompass comparative quantitative genetics in *A. thaliana* and *B. napus*. These studies will focus on the trait oil content. Novel candidate genes for this trait shall be identified in *A. thaliana* using an eQTL analysis. This work is supported by the BMBF as part of the GABI OIL consortium (A. Boudichevskaia, in collaboration with T. Altmann, research group Heterosis). Furthermore, we plan to exploit the naturally occurring variation in *A. thaliana* to study seed oil accumulation with the aim of identifying and characterising novel regulators of this important process (S. Voigtländer).

Collaborations (selection)

Within the Institute:
Dept. of Cytogenetics and Genome Analysis, Research Group Epigenetics; Dr. M.F. Mette.
Dept. of Molecular Genetics, Research Group Heterosis; Prof. T. Altmann;
Dept. of Molecular Genetics, Research Group Hybrid Wheat; Dr. M. Gils;
Dept. of Physiology and Cell Biology, Research Group Plant Reproductive Biology; Dr. J. Kumlehn.

Outside the Institute:
SW Seed Hadmersleben GmbH, Hadmersleben; Dr. W. Horn;
KWS SAAT AG, Einbeck; Dr. M. Ouzunova, Dr. F. Breuer;
Georg-August University Göttingen, Göttingen; Prof. H. Becker, Dr. W. Ecke;
Universität Bonn; IMBIO Abteilung Molekulare Biotechnologie, Bonn; Prof. P. Dörmann;
Deutsche Saatveredelung AG, Lippstadt; Dr. D. Stelling;
Norddeutsche Pflanzenzucht Hans-Georg Lembke KG, Holtsee; Dr. G. Leckband, Dr. A. Abbadi;
RAPS GbR Grundhof, Grundhof; Dr. P. Duscherer;
Syngenta Seeds GmbH, Bad Salzuflen; Dr. M. Coque.

Publications

Peer Reviewed Papers

2008

Fischer, U., M. Kuhlmann, A. Pecinka, R. Schmidt & M.F. Mette: Local DNA features affect RNA-directed transcriptional gene silencing and DNA methylation. Plant J. 53 (2008) 1-10.

Research Group: Epigenetics

Head: Dr. Michael Florian Mette

Scientists

IPK financed
Bruchmüller, Astrid (0,5 Annex, since 01.08.2009)
Finke, Andreas (0,5 P, since 01.02.2009)
Teo, Chee How, Dr. (Pakt für Forschung und Innovation, since 23.01.2009)

Grant Positions
Borisova-Todorova, Branimira, Dr. (0,5 Saxony-Anhalt, since 11.02.2008)
Kuhlmann, Markus, Dr. (DFG SFB 648)

Goals

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

Research Report

Gene silencing involving double-stranded RNA that is processed into short interfering (si) RNA as a nucleotide sequence-specific signal (RNA silencing) can regulate gene expression at the transcriptional as well as the post-transcriptional level.

By genetic dissection of **RNA-directed transcriptional gene silencing** (RdTGS) in *Arabidopsis thaliana,* several groups identified a considerable number of factors required for RdTGS. The majority of these are involved in siRNA generation and metabolism, DNA methylation or chromatin remodeling. Only a surprisingly small group of the known factors is involved in histone modification. To identify the complete spectrum of factors essential for RdTGS, a screen for EMS-induced mutations showing a "suppressor of silencing" phenotype is being performed in a transgene system showing efficient silencing. A number of mutant lines with a stable release of reporter gene expression could be identified. Crosses of these lines to accession *L-er* were performed and rough mapping was initiated to sort out mutations that co-localise with genes already known to be involved in RdTGS. For novel mutations, the affected genes will be identified by fine mapping and finally confirmed with complementation tests.

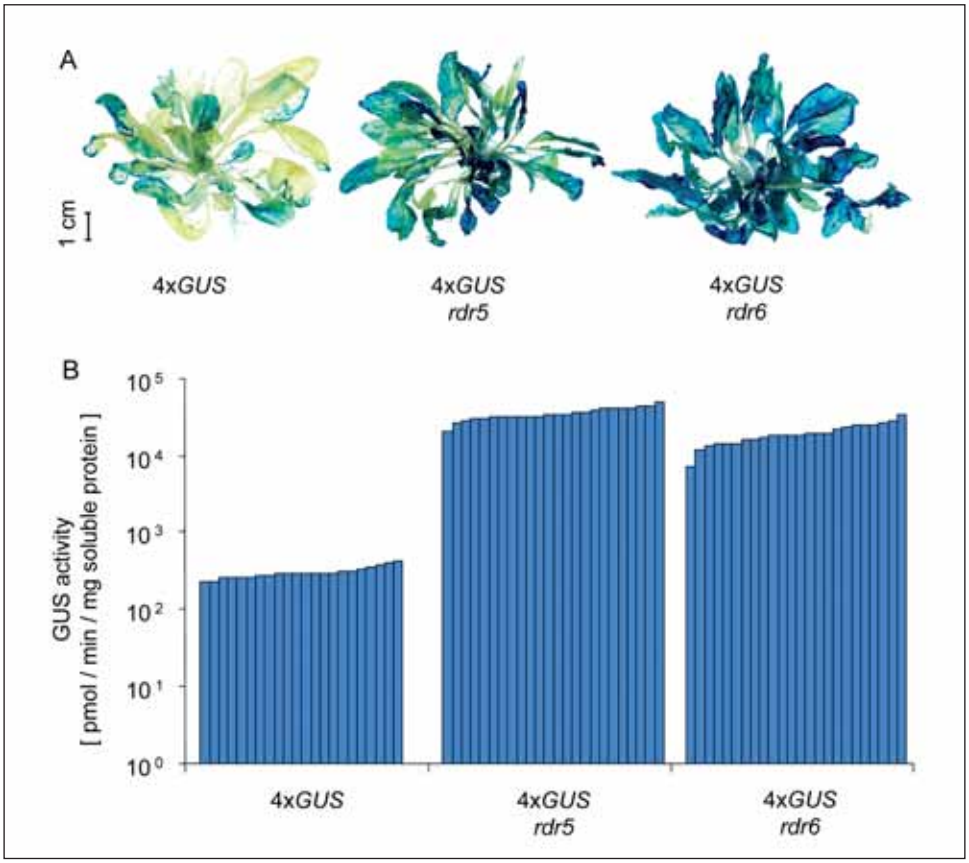

Fig. 26
RNA-dependent RNA polymerases RDR5 and RDR6 are required for transcript level-dependent post-transcriptional gene silencing in *Arabidopsis thaliana*. In *A. thaliana* plants containing four copies of a pro35S-GUS reporter gene (4x*GUS*), frequent onset of silencing of GUS expression was seen in plants grown for nine weeks under a short day regime. In contrast, plants containing the four copies of a pro35S-GUS reporter gene and being homozygous for mutant alleles of *rdr5* (4x*GUS*, *rdr5*) or *rdr6* (4x*GUS*, *rdr6*) showed high GUS expression under the same conditions. A) Histochemical staining to visualise GUS expression patterns (blue) in *A. thaliana* 4x*GUS*, 4x*GUS*, *rdr5* and 4xGUS, *rdr6* plants. B) Quantitative GUS determination in young rosette leaves of 4x*GUS* (n=22), 4x*GUS*, *rdr5* (n=24) and 4x*GUS*, *rdr6* (n=24) plants (A. Bruchmüller).

The mechanism of transcript level-dependent **post-transcriptional gene silencing** (PTGS) is also being analysed in a transgene system in *A. thaliana*. Introgression of mutant alleles demonstrated essential roles for RNA-dependent RNA polymerases RDR5 and RDR6 (Fig. 26, p. 70). Additionally, the potential role of PTGS pathways in limiting expression of recombinant proteins in barley seeds was studied. As in *A. thaliana*, the presence of multiple T-DNA copies can induce PTGS and result in reduced rather than enhanced expression levels (IPK-Ideenwettbewerb, A. Bruchmüller, M. F. Mette, in collaboration with J. Kumlehn, research group Plant Reproductive Biology and R. Schmidt, research group Genome Plasticity).

The presence of transgenic *lacO* tandem repeats, commonly used for chromatin tagging, can alter the **architecture of interphase nuclei** in *A. thaliana*. One of the alterations, enhancement of chromosome pairing at the sites of transgene integration, is dependent on DNA methylation. To probe the potential role of histone H3 lysine 9 dimethylation in mediating DNA methylation, *lacO* tandem repeats were introduced into a triple mutant for histone methyltransferases *suvh4*, *suvh5* and *suvh6*. This resulted in a pronounced reduction of H3K9me2 at *lacO* tandem repeats, but hardly affected the enhanced chromosome pairing. Hence, H3K9me2 does not play a major part in the positional chromosome pairing at *lacO* tandem repeats (Saxony-Anhalt Excellence Cluster, B. Borisova, M.F. Mette, in collaboration with I. Schubert, research group Karyotype Evolution).

In a collaborative approach to harness **minichromosomes as shuttles for recombinant gene expression** in cereals, generation of truncated chromosomes via a transgene-based formation of new telomers in barley is planned (Pakt für Forschung und Innovation; A. Houben, M.F. Mette, J. Schubert, J. Kumlehn). Blocks of *A. thaliana* telomeric repeats were added to a T-DNA construct suitable for *Agrobacterium*-mediated transformation of barley. To allow for a later targeting of expression cassettes into minichromosomes, elements for site-specific Cre/lox recombination were also included. The constructs were finished and transformation of barley was initiated (C.H. Teo, M.F. Mette, in collaboration with J. Kumlehn, research group Plant Reproductive Biology).

A. thaliana accessions Col-0, C24, Cvi, and their reciprocal hybrids were employed as a model system to investigate the relations between **expression of heterosis** and changes in DNA methylation, histone modifications, chromatin structure, and endopolyploidisation (A. Banaei, J. Fuchs, T. Czauderna, A. Houben, M.F. Mette, Theor. Appl. Genet. 2010; see report of the research group Chromosome Structure and Function).

Collaborations (selection)

Within the Institute:

Dept. of Cytogenetics and Genome Analysis, Research Group Karyotype Evolution; Dr. J. Fuchs, Prof. I. Schubert;

Dept. of Cytogenetics and Genome Analysis, Research Group Chromosome Structure and Function; Dr. A. Houben;

Dept. of Cytogenetics and Genome Analysis, Research Group Genome Plasticity; Dr. R. Schmidt;

Dept. of Physiology and Cell Biology, Research Group Plant Reproductive Biology; Dr. J. Kumlehn.

Outside the Institute:

Martin Luther University Halle-Wittenberg, Institute of Genetics, Halle/Saale; Prof. G. Reuter, Prof. K. Breuning;

Université de Genève, Laboratoire de Génétique Végétale, Genève, Switzerland; Prof. J. Paszkowski;

Ecole Normale Supérieure, CNRS UMR 8186, Département de Biologie, Paris, France; Prof. V. Colot.

Publications

Peer Reviewed Papers

2008

Fischer, U., M. Kuhlmann, A. Pecinka, R. Schmidt & M.F. Mette: Local DNA features affect RNA-directed transcriptional gene silencing and DNA methylation. Plant J. 53 (2008) 1-10.

Jovtchev, G., K. Watanabe, A. Pecinka, F.M. Rosin, M.F. Mette, E. Lam & I. Schubert: Size and number of tandem repeat arrays can determine somatic homologous pairing of transgene loci mediated by epigenetic modifications in *Arabidopsis thaliana* nuclei. Chromosoma 117 (2008) 267-276.

Research Group: *In vitro* Differentiation

Head: Prof. Anna M. Wobus

Scientists

IPK financed
Daniel-Wojcik, Anna (0,5 Annex, 01.05.-31.05.2009; 0,25 Annex, since 01.11.2009)
Schroeder, Insa, Dr. (0,75 Annex, 16.06.-31.08.2008)
Sulzbacher, Sabine, Dr. (0,75 Annex, 01.09.-14.09.2008)

Grant Positions
Daniel-Wojcik, Anna (0,5 EU, till 30.04.2009; 01.06.-31.10.2009)
Schroeder, Insa, Dr. (DFG, till 15.06.2008; Overhead, 16.06.-15.08.2008)
Sulzbacher, Sabine, Dr. (BMBF, till 31.08.2008; since 15.09.2008)

Visiting Scientists/Scholars
Chronowska, Ewa, Dr. (DFG, 01.03.2008-31.05.2008)
Kasperczyk, Katarzyna (Individual Grant for PhD students Poland, 09.11-04.12.2009)
Schroeder, Insa, Dr. (Martin Luther University Halle-Wittenberg, since 01.09.2008)
Truong, Thuy Thu (scholarship Vietnam, till 31.01.2008)
Wiese, Cornelia, Dr. (self-financed, 10.11.-31.12.2008)

Goals

Analysis of regulatory mechanisms of *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 are applied to human cord blood-derived cells to enhance their developmental potential.

Research Report

Analysis of pancreatic differentiation by transcriptome analysis: The comparative microchip (Affymetrix), real-time RT-PCR and immunocytochemical analyses of wild type ES cells and ES cells expressing the pancreatic control gene *Pax4* differentiating into the pancreatic lineage and a comparison with *in vivo* pancreas data revealed that ES-derived pancreatic cells resemble an immature embryonic/fetal developmental stage (Schulz et al. 2009; Rolletschek et al., IJDB, in press 2010). To further improve pancreatic differentiation, the selection and enrichment of endoderm progenitor cells was applied.

Selective endoderm differentiation by activin A induction of Sox17-expressing cells: To selectively increase the level of definitive endoderm and early pancreatic progenitor cells, activin A, a member of the TGF-ß superfamily, was applied at high concentrations in a chemically defined medium to differentiating ES cells. 50 and 100 ng/ml activin A induced up-regulation of definitive endoderm-specific Sox17, but down-regulation of extra-embryonic Sox7, mesendoderm-specific Brachyury, and ectoderm-specific Pax6 transcript levels (Sulzbacher et al. 2009).
By using ES cells, which express pSox17-DsRed-puro^r and are differentiated in the presence of 50 ng/ml activin A, the number of Sox17-DsRed-positive cells was increased about 10 to 20 times as measured by flowcytometry (FACS) between day 8 and 10 in comparison to control cells (without activin A induction). Cells differentiating in monolayer or embryoid body culture showed a significant increase in the number of Sox17-positive definitive endoderm cells. The transcriptional profile of FACS-selected Sox17+ cells revealed their potential to develop into pancreatic progenitors as well as into the three subtypes of the pancreas, exocrine, ductal and endocrine cells. The *in vivo* analysis after transplantation of Sox17+ cells into mouse models is ongoing (collaboration with I. Schroeder, Martin Luther University Halle-Wittenberg Halle; M. Solimena, R. Meisterfeld, Technical University Dresden).

Dedifferentiation and reprogramming of cord blood (CB)-derived cells: All efforts to dedifferentiate CB-derived CD14+ cells by growth factors and/or by molecules modifying epigenetic properties of cells (i.e. TSA, 5-azaC) showed only low effects with respect to the maintenance or up-regulation of Oct4 transcript levels (used as a marker of undifferentiated pluripotent cells). Whereas recent data showed reprogramming to pluripotency (to 'induced pluripotent stem cells') of adult mouse and human cells by viral transfection of four pluripotency-associated genes (rev. Rolletschek & Wobus, 2009), we established a new reprogramming strategy without the use of viral vectors: Protein extracts of three or four transcription factors (Oct4, Sox2, Klf4, with or without c-myc, shown to be efficient in reprogramming adult cells to an ES-like state) were prepared and CB-derived mesenchymal stem cells (MCSs) were transfected by 'Chariot'-mediated protein transduction. First data demonstrated that repeated transfections of MSCs by these protein fractions were successful to up-regulate pluripotency markers in CB-derived MSCs (A. Daniel-Wojcik, A.M. Wobus; collaboration with A. Finkensieper, M. Wartenberg; studies are ongoing).

Induction of pacemaker-like cells by Suramin: We showed that Suramin, a naphthylamine derivative of urea, applied to differentiating ES cells specifically induced the formation of pacemaker-like cells when applied at a distinct time point of mesodermal specification. The sequential activation and/or down-regulation of specific mesoderm- and cardiac-specific genes were found to be necessary for the activation of the sinoatrial-specific genes *Tbx2/3* and *HCN4*. The selective

induction of pacemaker-like cells was confirmed by functional studies (patch-clamp analysis). A model of ES-derived pacemaker cell generation *in vitro* was proposed. This is the first report on the specific and selective differentiation induction of pacemaker-like cells, an important subpopulation of the heart (Wiese et al. 2009, in press).

Collaborations (selection)

Within the Institute:

Dept. of Cytogenetics and Genome Analysis, Research Group Karyotype Evolution; Dr. J. Fuchs;

Dept. of Physiology and Cell Biology, Research Group Structural Cell Biology; Dr. M. Melzer.

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Max Planck Institute (MPI) for Molecular Genetics, Berlin; Dr. H. Himmelbauer, Dr. T. Nolden;

Max Delbrück Center of Molecular Biology, Berlin-Buch; Dr. N. Hübner, Dr. H. Schulz;

Dresden University of Technology, Institute of Experimental Diabetology, Dept. of Medicine III, Dresden; Prof. M. Solimena, Dr. R. Meisterfeld;

Friedrich Schiller University of Jena, FZL, Kardiologie, Jena; Prof. M. Wartenberg, Dr. A. Finkensieper;

Forschungszentrum Karlsruhe (FZK), Institut für Biologische Grenzflächen (IBG), Karlsruhe; Dr. A. Rolletschek;

Fraunhofer-Institut für Grenzflächen- und Bioverfahrenstechnik (IGB), Stuttgart; Prof. H. Mertsching;

National Institute on Aging (NIA), NIH, Laboratory of Cardiovascular Science, Baltimore, USA; Prof. K. Boheler;

University of Toronto, Samuel Lunenfeld Research Institute, Toronto, Canada; Dr. A. Nagy, P. Mohseni.

Publications

Peer Reviewed Papers

2008

Hieronymus, T., D. Ruau, J. Ober-Blobaum, J.H. Baek, A. Rolletschek, S. Rose-John, A.M. Wobus, A.M. Müller & M. Zenke: The transcription factor repertoire of Flt$^+$ hematopoietic stem cells. Cells Tissues Organs 188 (2008) 103-115.

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Kuhn, G., O. Brüstle, U. Martens, A. Wobus & K. Unsicker: Stem cells: established facts, open issues, and future directions. Cell Tissue Res. 331 (2008) 1-3.

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Ruau, D., R. Ensenat-Waser, T.C. Dinger, D.S. Vallabhapurapu, A. Rolletschek, C. Hacker, T. Hieronymus, A.M. Wobus, A.M. Müller & M. Zenke: Pluripotency associated genes are reactivated by chromatin-modifying agents in neurosphere cells. Stem Cells 26 (2008) 920-926.

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Books and Book Chapters

2008

Kuhn, G., O. Brüstle, U. Martens, A.M. Wobus & K. Unsicker (Eds.): Stem cells: established facts, open issues, and future directions. Cell Tissue Res. 1, Springer-Verlag, Berlin-Heidelberg (2008) 372 pp.

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Müller-Röber, B., M. Boysen, B. Fehse, F. Hucho, K. Köchy, J. Reich, H.-J. Rheinberger, H. Ropers, K. Sperling & A.M. Wobus (Eds.): Zweiter Gentechnologiebericht – Analyse einer Hochtechnologie in Deutschland, Forschungsberichte der Arbeitsgruppen der Berlin-Brandenburgischen Akademie der Wissenschaften, Bd. 23. Forum W – Wissenschaftlicher Verlag, Dornburg (2009) 464 pp.

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Programme: Genome Analysis

Research Group: Transcriptome Analysis

Head: Dr. Patrick Schweizer

Scientists

IPK financed
Gay, Alexandra, Dr. (Annex, till 14.04.2008)
Himmelbach, Axel, Dr. (1,0/0,25 Annex, till 31.12.2008)
Ihlow, Alexander, Dr. (Annex, till 29.02.2008)
Jorde, Annika (0,25 Annex, 15.11.2008-28.02.2009)
Metzner, Ernst (0,25 Annex, 01.05.-31.07.2009)
Nowara, Daniela (0,5 Annex, 01.06.2008-31.12.2008)

Grant Positions
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Douchkov, Dimitar, Dr. (0,75 Overhead, till 29.02.2008; BMBF, since 01.03.2008)
Himmelbach, Axel, Dr. (0,75 BMBF, since 01.05.2008; 0,25 Overhead, 15.06.-30.11.2009)
Jorde, Annika (0,5 EU, till 14.11.2008)
Marzin, Stefan (0,5 Saxony-Anhalt, till 31.12.2008; 0,5 Overhead, 01.01.-30.06.2009)
Müller, Doreen (0,5 BMBF)
Nowara, Daniela (0,5 EU, till 31.05.2008; Overhead, 01.01.-31.01.2009)
Rajaraman, Jeyaraman (0,5 DFG, since 03.08.2009)

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Aghnoum, Reza (University Wageningen, 26.01.-06.02.2009; 07.11.-12.11.2009)
Delventhal, Rhoda (RWTH Aachen, 07.12.-12.12.2009)
Ihlow, Alexander, Dr. (TH Ilmenau, since 01.06.2008)
Jorde, Annika (self-financed, 01.03.-15.03.2009)
Liu, Luo (self-financed, since 01.01.2008)
Marzin, Stephan (self-financed, 01.07.-31.12.2009)
Metzner, Ernst (Martin Luther University Halle-Wittenberg, till 30.04.2009; self-financed; since 01.08.2009)
Morch, Sara (University of Copenhagen, 02.02.-15.02.2009)
Ramshini, Hosseinali (Ministry of Science of Iran, 01.01.-30.09.2008)
Strauss, Tina (Martin Luther University Halle-Wittenberg, 19.10.-06.11.2009)
Zellerhoff, Nina (self-financed, 03.03.-14.03.2008)

Goals

Gene regulation and -function in stressed barley and wheat.

Research Report

Phenomics of pathogen-attacked barley: The main objective of the first project is **detailed functional analysis and testing of the application potential of barley genes required for nonhost resistance**. The genes of interest were derived from a RNAi high-throughput phenomics screening called TIGS (Transient Induced Gene Silencing, see Annual Report of 2005) in barley epidermal cells attacked by the wheat powdery mildew. Out of 10 identified *RNR* (*Required for Nonhost Resistance*) genes we examined two, *RNR5* encoding part of an U-box ARM-repeat E3 ligase and *RNR6* encoding a cellulose synthase-like protein of the D clade (*CSLD2*) in greater detail by phenotyping transgenic barley RNAi lines. This confirmed that *CSLD2* as an important factor of nonhost- and basal host resistance in barley (see Fig. 27, p. 76). Next steps involve the characterisation of cell-wall changes of selected RNAi lines in non-attacked as well as pathogen-attacked leaves. *RNR5* is another interesting, partly duplicated gene and might represent a decoy of an E3 ligase-encoding effector target for powdery mildew. This hypothesis is supported by enhanced resistance in barley and wheat cells that transiently over-express *RNR5*. To further test this possibility, TILLING mutants of *RNR5* and the ancestral E3 ligase have been obtained in barley cv. Barke in collaboration with the group Genome Diversity, and these will be characterised in ERA-PG project TritNONHOST (D. Douchkov, A. Himmelbach, J. Rajaraman).

The second project is aimed at **identifying genes** from barley that are required **for quantitative host resistance** or **for host susceptibility** in a compatible interaction with barley powdery mildew. This still ongoing RNAi screen includes a set of approx. 500 powdery mildew-induced host genes that we identified previously, plus several hundred genes belonging to important multigene families for plant-pathogen interactions such as peroxidases, WRKY-transcription factors, E3 ligases, and ABC transporters. In addition, we also tested 125 host genes that were mapped to a QTL confidence interval for powdery-mildew resistance on barley chromosome 5HS. At present, we have found 50 candidate genes that affected quantitative host resistance. Most of these candidates as well as several others selected based on literature searches, were re-sequenced for an association-genetic approach by using a worldwide customised barley collection. Sixteen candidates were found to possess single nucleotide polymorphisms or gene haplotypes that were significantly associated with powdery-mildew resistance. Together with the data from gene regulation and co-localisation with resistance QTL, a small number of candidates with

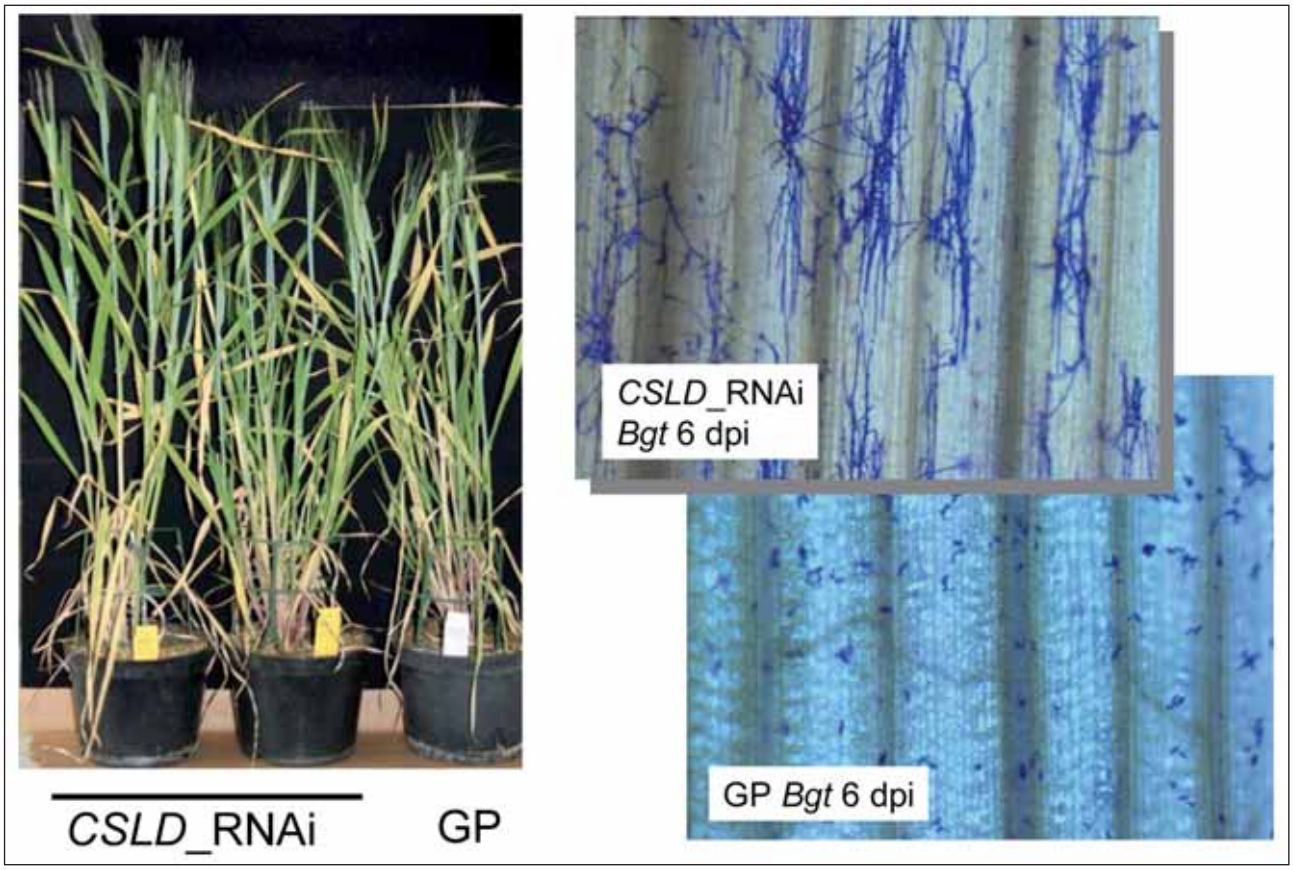

Fig. 27
Normal growth of transgenic barley RNR6 (CSL) RNAi lines compared to wildtype (GP). Under the microscope, strongly enhanced growth (reflected by blue-stained hyphae) of the non-host wheat powdery mildew on RNR6-silenced plant compared to wildtype was observed (D. Douchkov).

strong converging evidence for a role in host quantitative resistance were identified. These will be the starting point for follow-up projects (D. Douchkov, A. Johrde).

The novel phenomenon of "Host-Induced Gene Silencing" (HIGS) in fungal pathogens was further examined in barley and wheat attacked by powdery mildew and *Fusarium* head blight. Moderate to strong protection was observed in several transgenic lines carrying RNAi constructs that target pathogen genes. These results will be further validated and extended in an ERA-PG project "dsRNA-guard" and in a bilateral project with Bayer CropScience AG (D. Nowara, A. Gay).

In two related wheat projects we are searching for host genes that are important for quantitative resistance to *Fusarium* head blight and *Septoria tritici* blotch, currently the most important wheat diseases in Europe. To this aim, we have performed 144 hybridisations of RNA of attacked plants to an in-house developed 13K cDNA array and to the Agilent 44K Wheat Genome Chip, respectively. Preliminary results revealed a small number of genes differentially expressed between susceptible and resistant bulks of either back-cross (BC3) or recombinant-inbred lines. These will be functionally tested by virus-induced gene silencing using the barley-stripe mosaic virus, a transient-assay system recently established in the lab (W. Chen, D. Müller).

Promoter development and analysis: The pathogen-inducible promoter of the barley *HvGER4c* gene was functionally analysed in a transient assay system based on bombardment of barley leaf segments as well as in transgenic barley (see Fig. 19, p. 52). This revealed a number of functionally redundant WRKY-factor binding sites required for strong pathogen-induced expression. We also characterised the complex *HvGER4* locus consisting of nine tandemly duplicated, highly conserved (Ka/Ks < 0.1) genes undergoing repeated birth and death cycles, with a high degree of gene conversion especially spanning WRKY-factor binding sites. This suggests that high transcript dose is the evolutionary driving force for maintenance of the *HvGER4* locus, which deserves further examination in (association) genetic experiments (A. Himmelbach, D. Müller).

Phenomics of drought tolerance: The aim of this project is to identify new candidate genes for osmotic-stress (drought) tolerance in barley by high-throughput RNAi. Therefore, a new transient assay (TIGSa) that quantifies the accumulation of native homotetrameric dsRed reporter protein was developed. In partly dehydrated leaves, DsRed fluorescence was reduced, and the amount of reduction was influenced by RNAi of candidate genes for drought tolerance. In a candidate-gene approach informed by relevant literature, 67 genes were transiently

silenced and 19 were found to reduce DsRed fluorescence. These include genes previously shown to be important for drought tolerance such as mannitol dehydrogenase or the DREB2 transcription factor (S. Marzin).

Collaborations (selection)

Within the Institute:
Dept. of Genebank, Research Group Genome Diversity; Dr. N. Stein, Prof. A. Graner;
Dept. of Cytogenetics and Genome Analysis, Research Group Bioinformatics and Information Technology; Dr. U. Scholz;
Dept. of Molecular Genetics, Research Group Data Inspection; Dr. M. Strickert;
Dept. of Physiology and Cell Biology, Research Group Plant Reproductive Biology; Dr. J. Kumlehn;
Dept. of Physiology and Cell Biology, Research Group Applied Biochemistry; Dr. H.-P. Mock.

Outside the Institute:
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Martin Luther University Halle-Wittenberg, Halle/Saale; Prof. H. Deising;
Lochow-Petkus GmbH, Einbeck; Dr. V. Korzun, Dr. E. Ebmeyer;
Rheinisch-Westfälische Technische Universität, Aachen, Dr. U. Schaffrath;
Technical University Munich; Prof. R. Hückelhoven;
BASF Plant Science, Ludwigshafen; Dr. T. Wetjen, Dr. S. Bieri;
Copenhagen University, Denmark; Dr. H. Thordal-Christensen;
CSIRO, Canberra, Australia; Dr. W. Spielmeyer;
IFA Tulln, Austria; Prof. H. Buerstmayr;
Wageningen University, The Netherlands; Dr. Rients Niks;
University of Iowa, Ames, USA; Prof. R. Wise.

Publications

Peer Reviewed Papers

2008

Göllner, K., P. Schweizer, Y. Bai & R. Panstruga: Natural genetic resources of *Arabidopsis thaliana* reveal a high prevalence and unexpected phenotypic plasticity of *RPW8*-mediated powdery mildew resistance. New Phytol. 177 (2008) 725-742.

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Schweizer, P.: Tissue-specific expression of a defence-related peroxidase in transgenic wheat potentiates cell death in pathogen-attacked leaf epidermis. Mol. Plant Pathol. 9 (2008) 45-57.

Books and Book Chapters

2009

Wise, R., N. Lauter, L. Szabo & P. Schweizer: Genomics of biotic interactions in the Triticeae. In: Feuillet, C. & G. Muehlbauer (Eds.): Genetics and Genomics of the Triticeae. Plant Genetics/Genomics, Vol. 7. Springer Publishers, New York (2009) 559-589.

Patents

2008

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2009

Schweizer, P., G. Hensel, A. Gay & J. Kumlehn: Method for creating broad-spectrum resistance to fungi in transgenic plants. WO 2009/112270, Anmeldetag: 13.03.2008, Anmelder: IPK, Offenlegung: 17.09.2009, IPK Nr. 2008/01.

Research Group: Gene and Genome Mapping

Head: Dr. Marion Röder

Scientists

IPK financed
Hanemann, Anja, Dr. (0,25 P; 0,25/0,75 Pakt für Forschung und Innovation)
Kumar, Uttam, Dr. (Pakt für Forschung und Innovation, since 15.01.2008)
Pietsch, Christof, Dr. (Annex, till 14.01.2008)
Sharma, Shailendra, Dr. (Pakt für Forschung und Innovation, since 01.10.2009)

Grant Positions
Kollers, Sonja, Dr. (BMBF, since 01.08.2008)
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Pietsch, Christof, Dr. (BMBF, 15.01.-14.03.2008)
Worch, Sebastian, Dr. (BMBF, since 01.04.2008)

Visiting Scientists/Scholars
Achtar, Suha (self-financed, 17.02.-17.04.2008)
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Bosse, Verena (BMBF, till 31.01.2009)
Diaz de Leon Alvarez, José Luis, Dr. (BMBF, 20.07.-17.08.2008; 06.08.-05.09.2009)
Garcia-Suarez, Julieta (BMBF, 06.10.-31.12.2008)
Gerstenberg, Fabian (Gründungsprojekt IT-Breeding,15.10.2008-15.01.2009)
Hovhannisyan, Nelli (IFARS-Fellowship Program, 01.10.-09.10.2008)
Kelm, Christiane (self-financed, 28.10.-31.12.2008; 03.02.-28.02.2009)
Kifetew Haile, Jemanesh (DAAD, 25.03.-30.06.2009; since 19.09.2009)
Kordenaeej, Alaeddin, Dr. (self-financed, 02.07.-31.08.2009)
Leonova, Irina, Dr. (DFG, 27.09.-26.12.2008)
Malysheva-Otto, Ludmilla, Dr. (BMBF, till 31.03.2009)
Naji, Amir Mohammad, Dr. (self-financed, 02.07.-31.08.2009)
Paliwal, Rajneesh (DAAD, since 24.09.2008)
Rojas, Adriana (BMBF, 20.07.-17.10.2008; 26.09.-23.12.2009)
Sharma, Shailendra, Dr. (AvH-Foundation, till 30.09.2009)
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Teklu Woldemariam, Yifru, Dr. (AvH-Foundation, till 31.05.2008)

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 genome wide and a candidate gene approach are pursued to obtain detailed information on **marker-trait associations** in *Hordeum vulgare* L. which will facilitate the directed exploitation of the genetic diversity present within the primary gene pool for the allele-based improvement of this crop species. Haplotype patterns of **30 candidate genes involved in nitrogen and carbohydrate-metabolism** and of genes playing a significant role in the phenylpropanoid- and flavonoid-pathway were detected and single nucleotide polymorphisms (SNPs) and insertions-deletions (INDELs) were found to be associated with agronomic traits. These polymorphic sites were converted in high-throughput-markers, applicable as selection tool in barley breeding (I. Matthies, M. Peukert).

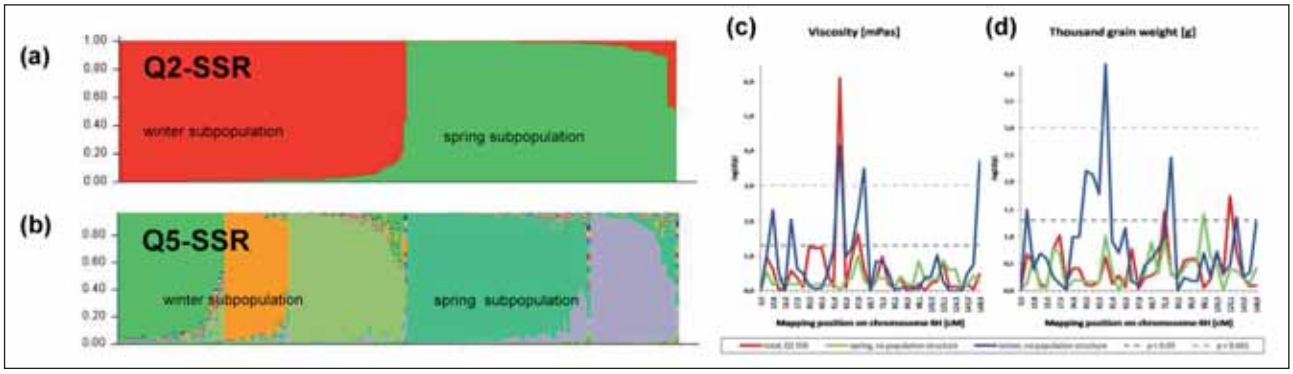

Fig. 28
Population structure of 190 European cultivars studied with 22 SSRs illustrated by bar plots. Q2-SSR (a) is differentiating winter from spring barley and Q5-SSR (b) shows the subclustering in these main groups. Association results with DArT markers on barley chromosome 4H for the traits viscosity (c) and thousand grain weight (d) are shown for the total set of 190 cultivars with correction for population stratification and the subsets of spring and winter barley which are plotted together. Significances of the calculated p-values are shown as –log10 (p-value) (I. Matthies).

Diversity Arrays Technology (DArT) markers and Simple Sequence Repeats (SSRs) were applied to investigate kinship, population structure, extent of linkage disequilibrium (LD) and associations on a genome wide level (see Fig. 28, p. 78). All obtained marker data from the candidate gene and the genome wide approach are used to elucidate **significant associations for important malting and kernel quality parameters** considering population structure and kinship (I. Matthies). The phenotype database "Metabrew" is maintained and actualised in collaboration with the Bioinformatics and Information Technology group (S. Weise, U. Scholz).

Association genetics is used for mapping agronomic traits in wheat. A genome-wide SSR-database consisting of 800 SSR markers is constructed and subsets are used to analyse the population structure of 358 winter wheat varieties, grown in 2008/2009 and 2009/2010 at four locations by breeding companies. Marker-trait relationships for European wheat elite germplasm will be established (S. Kollers).

An introgression line population (BHS584) of the barley spring variety 'Brenda' with the wild barley "*Hordeum vulgare* subsp. *spontaneum* accession 584" as donor parent is used to investigate the **impact of drought stress on the regulatory networks of barley seed development** in particular during the post-anthesis period. More than 600 ESTs, responsive to drought stress or contributing to starch and storage protein synthesis and accumulation, were resequenced from 8 barley genotypes comprising the mapping populations Steptoe × Morex (SM) and Oregon Wolfe Barleys (OWB recessive/dominant) and the introgression populations BHS584 and Scarlett × ISR42_8. Genotyping 141 EST-derived SNP markers and combination with phenotypic data for the BHS584 population (provided by Nordsaat Saatzucht GmbH) revealed two major QTL regions on chromosomes 1H and 2H. Based on these results and including additional expression data from the Seed Development group (N. Sreenivasulu), candidate genes will be selected for a refined expression analysis using a quantitative Real Time PCR approach to identify regulatory genes of signal transduction networks and/or metabolic pathways for knowledge-based breeding strategies to improve yield under drought with minimised side effects on quality parameters (S. Worch).

The **fine mapping of a QTL for grain size** on wheat chromosome 7D was continued together with J. Doležel (Institute of Experimental Botany, Olomouc, Czech Republic). Several BAC clones of a chromosome 7D specific library were fished with flanking markers and fingerprinted. Four BAC clones were sequenced and annotated for their gene content. The syntenic regions in rice and *Brachypodium distachyon* are exploited for candidate gene identification (M. Röder, A. Hanemann).
Previously, the **barley scald resistance gene *Rrs2*** was fine-mapped and the genomic region flanking the resistance gene was obtained by chromosome walking using a barley BAC library. Sequence analysis of six genomic regions of the *Rrs2* locus with 58 different barley genotypes (14 of which carry *Rrs2*) yielded eight diagnostic SNPs for the *Rrs2* phenotype. Based on five such SNPs, eight molecular markers (CAPS and pyrosequencing) were developed which are useful for marker-assisted selection in resistance gene pyramiding programmes for *Rhynchosporium secalis* resistance in barley.
Within the *Rrs2* co-segregating region, eleven genes could be identified; three are considered candidate genes for *Rrs2* based on their functional annotation and are investigated for functional polymorphisms in the coding region as well as for expression in resistant *versus* susceptible cultivars (A. Hanemann, S. Sharma).

Comparative QTL analysis was conducted in three wheat RIL populations segregating for **resistance to spot blotch disease** caused by the pathogen *Bipolaris sorokiniana*. Several markers could be identified which were linked to QTLs present in two or three of the populations. On chromosomes 2BS and 7DS stable QTLs were detected. In the population 'Chirya 3' × 'Sonalika' additionally the trait **stay green,** displaying delayed senescence with green leaves even after seed maturation, was mapped (U. Kumar).
The mapping of quantitative resistance against the devastating **stem rust pathovar UG99** was initiated in a tetraploid wheat population (J.K. Haile).

The QTL analysis for **heat tolerance** in the recombinant inbred population 'NW1014 (tolerant) × HUW468 (susceptible)' of hexaploid wheat (*T. aestivum* L.) was completed by applying composite interval mapping. QTLs were detected on chromosomes 2B, 7B and 7D using three different parameters of heat tolerance viz. heat susceptibility index of grain filling duration and canopy temperature depression. The data are useful for marker-assisted breeding of varieties adapted to global warming to feed a growing world population (R. Paliwal).

The genetic structure of **sucrose phosphate synthase (SPS) gene family II** has been investigated in bread wheat. Using genome-specific primers the SPS gene region (> 4 kb) has been sequenced from 20-30 wheat accessions to detect SNPs and InDels. Orthologous regions were also amplified in the wild wheat progenitors (*Triticum urartu*, *Aegilops speltoides*, *Aegilops tauschii* etc.) and cultivated barley (*Hordeum vulgare*) (S. Sharma).

Collaborations (selection)

Within the Institute:
Dept. of Genebank, Research Group Genome Diversity; Prof. A. Graner;
Dept. of Genebank, Research Group Resources Genetics and Reproduction; Dr. A. Börner;

Dept. of Molecular Genetics, Research Group Seed Development; Prof. U. Wobus, Dr. N. Sreenivasulu;
Dept. of Cytogenetics and Genome Analysis, Research Group Bioinformatics and Information Technology; Dr. U. Scholz, S. Weise.

Outside the Institute:
TraitGenetics GmbH, Gatersleben; Dr. M. Ganal;
Lochow-Petkus GmbH, Einbeck; Dr. V. Korzun, Dr. E. Ebmeyer;
Saaten-Union Biotec GmbH; Leopoldshöhe; J. Förster;
Bavarian State Research Centre for Agriculture (LfL), Freising; Dr. G. Schweizer;
Institute of Experimental Botany, Olomouc, Czech Republic; Dr. J. Doležel;
Institute of Cytology and Genetics (ICG), Novosibirsk, Russia; Dr. E. Salina, Dr. E. Khlestkina;
Landbouw Universiteit Wageningen, The Netherlands; Dr. F. v. Eeuwijk;
Syngenta Seeds S.A.S., Toulouse, France; Dr. O. Argillier;
Universidad Autonoma de Baja California Sur, La Paz, Mexico; Dr. J. de León.

Publications

Peer Reviewed Papers

2008

Elangovan, M., R. Rai, B.B. Dholakia, M.D. Lagu, R. Tiwari, R.K. Gupta, V.S. Rao, M.S. Röder & V.S. Gupta: Molecular genetic mapping of quantitative trait loci associated with loaf volume in hexaploid wheat (*Triticum aestivum*). J. Cereal Sci. 47 (2008) 587-598.

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Books and Book Chapters

2008

Khlestkina, E.K., M.S. Röder, T.A. Pshenichnikova, A.V. Simonov, E.A. Salina & A. Börner: Genes for anthocyanin pigmentation in wheat: review and microsatellite-based mapping. In: Verrity, J.F. & L.E. Abbington (Eds.): Chromosome mapping research developments. NOVA Science Publishers, Inc., New York/USA (2008) 155-175.

Research Group: Bioinformatics and Information Technology

Head: Dr. Uwe Scholz

Scientists

IPK financed
Klapperstück, Matthias (0,25 Annex, 15.02.-15.10.2008; 0,5 P, 01.01.-31.12.2009)
Lange, Matthias, Dr. (P)
Schmutzer, Thomas (0,5 Annex, 15.02.-31.12.2009)

Grant Positions
Colmsee, Christian (BMBF, since 01.04.2009)
Spies, Karl (Industry, till 14.08.2008; Overhead, 15.08.2008-31.05.2009)
Steuernagel, Burkhard (BMBF)
Weise, Stephan, Dr. (BMBF)
Weißbach, Mandy (0,25 Overhead, 15.08.-14.11.2009; 0,5 BMBF, 15.11.-30.11.2009)

Visiting Scientists/Scholars
Klapperstück, Matthias (self-financed, 16.10.-31.12.2008)
Künne, Christian (self-financed, till 29.02.2008)
Spies, Karl (SYNAXON AG Bielefeld, 01.06.-31.12.2009)
Stephanik, Andreas (self-financed, till 30.04.2008)

Goals

Development and maintenance of molecular biological databases, molecular biological data integration, information retrieval) usage and adaptation of bioinformatics tools for *in silico* analysis tasks especially sequence analysis/assembling. Besides its research activities, the group is responsible for the IT infrastructure of the institute.

Research Report

The focus of the research group is integration and persistent storage of large data amounts generated in several projects. In order to share resources in database development and data storage, we developed and implemented the **CropHouse system**. Currently, sequences, marker information, BAC library data, phenotypic and passport data are integrated in our database **to support** the projects, **GABI-GENOBAR, GABI-BARLEX and OPTIMAS**.

Within the **GABI-BARLEX** project we provided the data storage and assembling of 454 sequenced barcoded BAC pools. After evaluation of available assembly tools we chose MIRA to be most useful for our application. Using MIRA an automated pipeline was developed for assembling BACs in a high throughput manner optimising assembly parameters and enhancing assembly output. This pipeline enables to generate phase-1-assemblies as for now for more than 2.000 BACs. All raw- and assembly-data are stored persistently in the CropHouse system (B. Steuernagel).

In the frame of the **GENOBAR** project, we manage the primary data and develop a data warehouse providing information for genome-wide association studies in barley based on phenotypic as well as molecular marker data (SNP, SSR, DArT and Illumina). Therefore, the required database structures were developed and a data integration pipeline was established. All available data were imported; necessary data cleansing was performed. The development of the data warehouse is ongoing (S. Weise).

In 2008 **RYE-EXPRESS** started as a GABI project to explore genomic diversity as to abiotic stress tolerance in rye. More than 2.5 million 454 sequence reads were entered into our genotyping process for *in silico* SNP detection. Since 2009 an automated approach has been developed comprising optimisation of sequence data, assembly, SNP detection and SNP evaluation. The implemented SNP detection system includes verification and validation of each individual SNP candidate and will yield high quality results to establish a high-throughput genotyping platform (T. Schmutzer).

The BMBF funded BioEnergy 2021 project **OPTIMAS** (since 2009) aims to identify metabolic processes and unigenes which correlate with biomass production and yield in the C4-plant maize. We performed a unigene selection for the Agilent Microarray Chip, established a database as an extension of the CropHouse system for all relevant OPTIMAS data and developed an Oracle Application Express based web interface for data retrieval and presentation (C. Colmsee).

In cooperation with BASF Plant Science we developed a **search engine for life science databases**. Goal is the search for novel methods for relevance ranking in life science databases. As result the **LAILAPS** system has been implemented. The concept is to combine relevance ranking, a machine learning approach to model user relevance profiles, ranking improvement by user feedback tracking and an intuitive and slim web user interface that estimates relevance rank by tracking user interactions. Queries are formulated as keyword lists and will be expanded by synonyms. Supporting a flexible text index and a simple data import format, LAILAPS can be used as search engine for comprehensive integrated life science databases and for small in-house project databases. With a set of features,

extracted from each database hit in combination with user relevance preferences, a neural network predicts user specific relevance scores. Using expert knowledge as training data for a predefined neural network or employing users own relevance training sets, a reliable relevance ranking of database hits has been implemented. LAILAPS is used as data retrieval interface in the OPTIMAS project and is publicly available for the SWISSPROT database under http://lailaps.ipk-gatersleben.de (M. Lange, K. Spies, M. Weißbach).

In collaboration with the Plant Bioinformatics group we enhanced the **MetaCrop** information system (http://metacrop.ipk-gatersleben.de). New features have been added in order to compose individual metabolic models and to improve the data exchange via SBML (C. Colmsee, S. Weise).

A study for the implementation of a Laboratory Information Management System (LIMS) was initiated. Aim is the conception of an implementation and establishment of a loadable decision basis. The study is written in cooperation with several research groups at the IPK. The result is a requirement specification of pilot research groups. In this frame, we collected a representative number of IPK laboratory and operating procedures as well as technical and organisational requirements by interviews. After discussions at partner institutes, presentations of commercial LIMS providers and requirement analysis, suggestions as to an IPK-LIMS implementation were made. Because of urgent requirements enfaced during the interviews in the pilot groups, we developed **LIMS-Light**, a database for management of primary lab data (M. Klapperstück, M. Lange, T. Schmutzer, C. Colmsee, see Fig. 29).

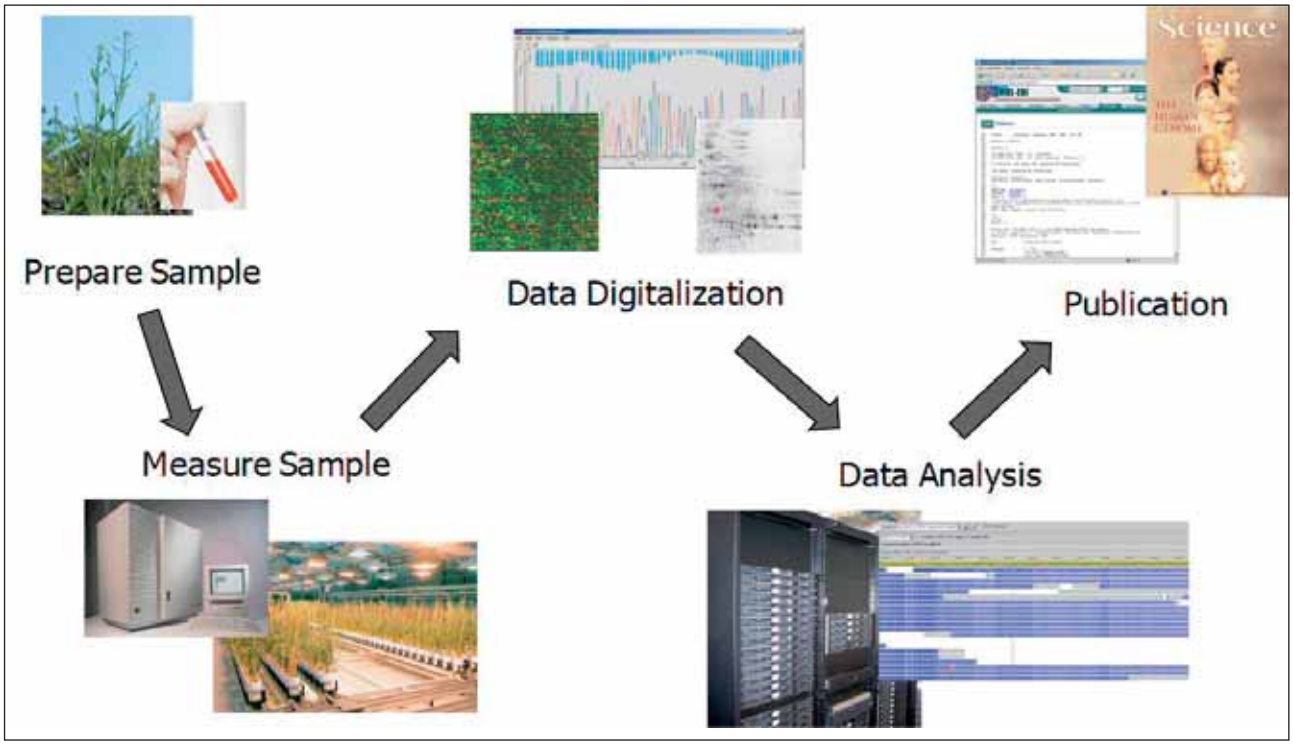

Fig. 29
Typical workflow for the production of primary lab data in a scientific research institute (M. Klapperstück, T. Schmutzer, M. Lange, C. Colmsee).

Collaborations (selection)

Within the Institute:
Dept. of Genebank, Research Group Genome Diversity; Dr. B. Kilian, Dr. D. Schulte, Dr. N. Stein;
Dept. of Genebank, Research Group Genebank Documentation; Dr. H. Knüpffer, M. Oppermann, A. Stephanik;
Dept. of Cytogenetics and Genome Analysis, Research Group Transcriptome Analysis; Dr. P. Schweizer;
Dept. of Cytogenetics and Genome Analysis, Research Group Gene and Genome Mapping; Dr. I. Matthies, Dr. M. Röder;
Dept. of Molecular Genetics, Research Group Plant Bioinformatics; Prof. F. Schreiber, K. Hippe, Ch. Klukas, T. Czauderna, A. Hartmann, E. Grafahrend-Belau.

Outside the Institute:
Otto-von-Guericke University, ITI, Magdeburg; Prof. G. Paul;
University of Bielefeld, Research Group Bioinformatics/ Medical Informatics, Bielefeld; Prof. R. Hofestädt;
Helmholtz Centre Munich, Munich Information Centre for Protein Sequences, Munich; Dr. K.F.X. Mayer;
Technical University Munich, Plant Breeding, Munich; Prof. C.-C. Schön, Dr. E. Bauer, G. Haseneyer;

Friedrich Alexander University of Erlangen-Nuernberg, Biochemistry, Erlangen; Prof. U. Sonnewald, Dr. F. Börnke, Dr. S. Sonnewald;
University of Cologne, Botanical Institute, Cologne; Prof. M. Bucher;
Heinrich-Heine-University, Plant Biochemistry, Düsseldorf; Prof. A. Weber;
University of Regensburg, Cell Biology & Plant Physiology, Regensburg; Prof. T. Dresselhaus;
Hochschule Harz, Dept. of Automation and Computer Science, Wernigerode; Prof. K. Schneider.

Publications

Peer Reviewed Papers

2008

Grafahrend-Belau, E., S. Weise, D. Koschützki, U. Scholz, B.H. Junker & F. Schreiber: MetaCrop: a detailed database of crop plant metabolism. Nucleic Acids Res. 36 (2008) D954-D958.

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Matthies, I.E., S. Weise, J. Förster & M.S. Röder: Association mapping and marker development of the candidate genes (1→3),(1→4)-β-D-Glucan-4-glucanohydrolase and (1→4)-β-Xylan-endohydrolase 1 for malting quality in barley. Euphytica 170 (2009) 109-122.

Matthies, I.E., S. Weise & M.S. Röder: Association of haplotype diversity in the alpha-amylase gene *amy1* with malting quality parameters in barley. Mol. Breed. 23 (2009) 139-152.

Mayer, K.F., S. Taudien, M. Martis, H. Simkova, P. Suchankova, H. Gundlach, T. Wicker, A. Petzold, M. Felder, B. Steuernagel, U. Scholz, A. Graner, M. Platzer, J. Dolezel & N. Stein: Gene content and virtual gene order of barley chromosome 1H. Plant Physiol. 151 (2009) 496-505.

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Schäfer, P., S. Pfiffi, L.M. Voll, D. Zajic, P.M. Chandler, F. Waller, U. Scholz, J. Pons-Kuhnemann, S. Sonnewald, U. Sonnewald & K.H. Kogel: Manipulation of plant innate immunity and gibberellin as factor of compatibility in the mutualistic association of barley roots with *Piriformospora indica*. Plant J. 59 (2009) 461-474.

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Books and Book Chapters

2008

Hofestädt, R., J. Köhler, M. Lange, U. Scholz, F. Schreiber & P. Verrier (Eds.): Integrative Bioinformatics: Proceedings of the 5th International Symposium on Integrative Bioinformatics 2008. IMBio (2008) 345 pp.

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Weise, S., C. Colmsee, E. Grafahrend-Belau, B. Junker, C. Klukas, M. Lange, U. Scholz & F. Schreiber: An integration and analysis pipeline for systems biology in crop plant metabolism. Proc. Int. Workshop "Data Integr. Life Sci." (DILS'09), Lect. Notes Bioinform. 5647 (2009) 196-203.

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Abteilung Molekulare Genetik/
Department of Molecular Genetics

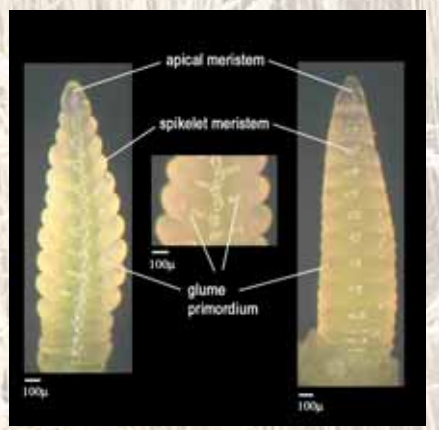
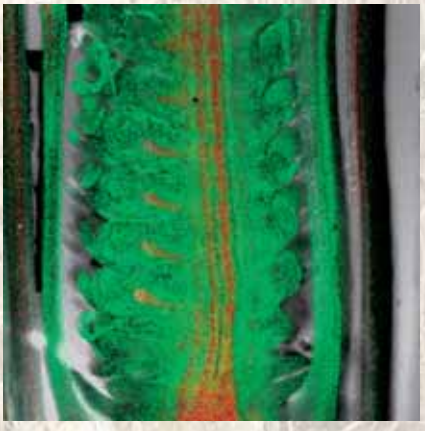
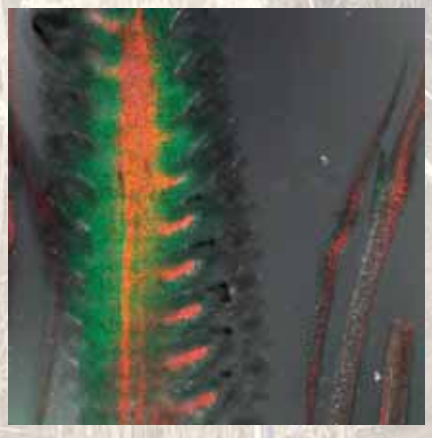


Fig. 30
Aktivität eines Speicherproteingen-Promotors (sp) im Meristem sich entwickelnder Gersten-Ähren. Die Promotoraktivität wurde nachgewiesen mittels Analyse der GFP-Signale in neun Wochen alten transgenen Gerstenpflanzen, die mit einem sp::gfp-Konstrukt transformiert wurden. Promotoren von Speicherprotein-Genen sind als Samen-spezifisch beschrieben. Die Detektion des GFP-Signals im Meristem war deshalb überraschend. Fluoreszenz-Signale wurden in den Regionen des Meristems nachgewiesen, die die Spindel umgeben. In der Spindel verlaufen die vaskulären Gewebe, die später die sich entwickelnden Körner versorgen. Die Expression eines Aminosäuretransporters unter Kontrolle des sp-Promotors beeinflusst die Halmzahl und den Blühzeitpunkt transgener Weizenpflanzen. Wir danken Twan Rutten für die Unterstützung bei der Detektion der GFP-Fluoreszenz und für die Fotografien (W. Weschke).

Activity of a storage protein gene promoter (sp) in the meristem of developing barley spikes. Promoter activity was detected by analysis of GFP signals in 9-weeks old barley plants transformed with a sp::gfp construct. Because storage protein gene promoters are described as being strongly seed-specific, detection of GFP expression in the meristem was surprising. GFP signals label cellular regions flanking the developing rachis, that tissue harbouring the vascular bundle supplying the developing grains later on. Expression of a sp::amino acid transporter construct in transgenic wheat influences tiller number as well as flowering time of the transgenic plants. We thank Twan Rutten for help in GFP fluorescence detection and taking of photographs (W. Weschke).





Abteilung Molekulare Genetik

Leiter: Prof. Dr. Thomas Altmann

Allgemeine Forschungsziele

Die Forschungsarbeiten in der Abteilung Molekulare Genetik gliedern sich überwiegend in den IPK-Forschungsschwerpunkt „Integrative Biologie pflanzlicher Leistungen" ein, bei denen auch Aspekte der Erforschung genetischer Diversität von Pflanzen berücksichtigt werden. 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. Im Vordergrund steht dabei die Untersuchung ertragsbezogener physiologischer Prozesse im Kontext von Entwicklungsprogrammen. Dabei werden sowohl vegetatives Wachstum/Biomasseproduktion und Heterosis (gesteigerte Leistung von Kreuzungsnachkommen gegenüber ihren Eltern) als auch generative Prozesse wie Keimzellbildung, Samenentwicklung und -physiologie und Samenertrag erforscht. Ein wesentliches Ziel der Arbeiten ist die Aufklärung der Regulation zentraler Entwicklungs- und Stoffwechselprozesse, wobei besonders die Rolle von Transkriptionsfaktoren, von Phytohormonen und von neuartigen/komplexen Signalen untersucht werden.

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 und Qualität von Samen und deren Inhaltsstoffe;

Department of Molecular Genetics

Head: Prof. Thomas Altmann

Research Goals

Research performed in the Department of Molecular Genetics is mainly assigned to the IPK research topic "Integrative Biology of Plant Performance" and also addresses aspects of investigating plant genetic diversity. 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 main focus is on the investigation of yield-related physiological processes in the context of developmental programmes. Both areas, 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. 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, of phytohormones, and of novel/complex signals.

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 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; (under development: Image analysis and automated phenotyping) and

- Entwicklung und Anwendung bioinformatischer Verfahren: Integrative Bioinformatik und Netzwerkanalyse (Datenrepresentation und -integration, Visualisierung und Exploration, Analyse und Simulation); Identifizierung von DNA-Motiven, Analyse von RNA- und Proteinexpressionsdaten; (im Aufbau: Bildanalyse und automatisierte Phänotypisierung) und
- Entwicklung experimenteller Ressourcen, Technologien und Methoden (u. a. Mikroprobennahme und -analyse, Mikrosensorik, NMR-basierte Inhaltsstofflokalisierung und -quantifizierung, ChIP-Chip-Verfahren, immunologische Verfahren, SNP-Typisierung, 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 wechselte die Leitung der Abteilung Molekulare Genetik (seit 1. April 2008 Prof. Dr. T. Altmann), es wurde die Arbeitsgruppe „Expressionskartierung" (Leiter Dr. L. Altschmied) in die Abteilung verlagert (aus der Abteilung Cytogenetik und Genomanalyse) und die Arbeitsgruppe „Heterosis" neu in die Abteilung integriert. Innerhalb der Arbeitsgruppe Heterosis wird der Projektbereich „Lipidstoffwechsel und Ölspeicherung" von Dr. L. Borisjuk geleitet.

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 acht Arbeitsgruppen der Abteilung.

Molekularbiologie und Stoffwechselphysiologie pflanzlicher Entwicklungsprozesse
- Aufklärung molekularer Kontrollmechanismen der Gametenentwicklung, der frühen Embryogenese und der Apomixis: Ein wesentlicher Erkenntnisgewinn bzgl. der Bestimmung der Identität pflanzlicher Eizellen wurde mit der Identifizierung von Genen mit Eizell-spezifischer Expression in Weizen und *Arabidopsis* erzielt. Dabei wurde besonders eine bisher nicht charakterisierte Familie pflanzlicher Transkriptionsfaktoren (RKD) untersucht, für die gezeigt werden konnte, dass sie bei Missexpression in der Lage sind, sporophytische Zellen zu reprogrammieren und diesen Aspekte von Eizellidentität zu vermitteln. Ferner wurden Ziel-

- Experimental resource, technology and method development (e.g. microsampling and analysis, microsensorics, NMR-based localisation and quantification of content substances, ChIP-Chip procedures, immunological techniques, SNP typing, 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 in relation 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 the Reporting Period

In the reporting period, the head of the department Molecular Genetics changed (since 1st April 2008 Prof. T. Altmann), the research group "Expression Mapping" (head Dr. L. Altschmied) has been transferred into the Department (from the Cytogenetics and Genome Analysis department), and the research group "Heterosis" was newly integrated into the Department. Within the research group Heterosis, the project area "Lipid metabolism and oil storage" is headed by Dr. L. Borisjuk.

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 eight research groups of the department.

Molecular biology and metabolic physiology of plant developmental processes
- Elucidation of molecular control mechanisms of gamete development, early embryogenesis, and apomixis: Major gain of new knowledge on the determination of plant egg cell determination was achieved through identification of genes that exhibit egg cell-specific expression in wheat and *Arabidopsis.* In particular, a previously uncharacterised family of plant transcription factors (RKD) was investigated that were shown through misexpression to be able to re-program sporophytic cells towards expression of aspects of egg cell identity. Further, target genes were identified of a central regulator of gene expression during embryogenesis (LEC1) induced activation of which in invegetative tissues resulted in ectopic embryo formation. The obtained data gave indications of phytohormone mediated function of this transcription factor. Target genes of a further seed-specific transcription factor (ABI3) were identified using the the ChIP-Chip method and were verified in follow-up experiments. Furthermore, for another family of transcription factors (class A bZip´s) indications were obtained for

gene eines zentralen Regulators der Genexpression während der Embryogenese (LEC1) identifiziert, dessen induzierte Aktivierung in vegetativen Geweben zur ektopischen Ausbildung von Embryonen führt. Über diese Daten wurden Hinweise auf Phytohormon-vermittelte Funktionen dieses Transkriptionsfaktors erhalten. Es wurden Zielgene des Samen-spezifischen Transkriptionsfaktors ABI3 mit Hilfe der ChIP-Chip-Methode identifiziert und in weiterführenden Experimenten verifiziert. Darüber hinaus wurden für eine weitere Familie von Transkriptionsfaktoren (bZip´s der Klasse A) Hinweise auf Kooperation mit ABI3 bei der Regulation Samen-spezifischer Genexpression erhalten. Ein weiterer wichtiger Durchbruch gelang mit der Identifizierung eines Aposporie-Locus (einer genomischen Region, die Embryobildung aus unbefruchteten Zellen verursacht) von *Hypericum perforatum* (Echtes Johanniskraut), der nun einer detaillierten molekularen Charaktierisierung zugänglich ist und wesentliche Informationen zu den molekularen Mechanismen der Apomixis (ungeschlechtliche Fortpflanzung durch Samen) liefern wird.

- Analyse genetischer Ursachen und molekularer Mechanismen der Variation von Stoffwechselleistungen unter günstigen und ungünstigen Umweltbedingungen:
  Vegetatives Wachstum und Biomasseakkumulation, Heterosis: Über die Identifizierung von QTL (genetische Loci, die quantitative Merkmale bestimmen) für Biomasse und Metabolite in *Arabidopsis thaliana* wurden neue Erkenntnisse über die genetischen Faktoren der Steuerung des frühen vegetativen Wachstums und des Stoffwechsels und über einen engen Zusammenhang zwischen pflanzlicher Biomasseproduktion und der physiologischen Konstitution von Pflanzen gewonnen. Mit der Identifizierung von QTL für Biomasse-Heterosis und für Metabolit-Heterosis (gesteigerte Biomasseproduktion bzw. Metabolitgehalte in Kreuzungshybriden gegenüber ihren Eltern) wurden entscheidende Schritte zu Aufklärung der genetischen Ursachen und der molekularen Mechanismen der Heterosis getan. Weiterhin wurden wichtige Beobachtungen über die Vorhersagekraft von genetischen und metabolischen Markern für die Hybridleistung und das Ausmaß der Heterosis gemacht, die ein wertvolles Potenzial für zukünftige Anwendungen in der Pflanzenzüchtung andeuten. Zur Überprüfung ähnlicher Zusammenhänge bei Kulturpflanzen wurden entsprechende Untersuchungen bei Mais initiiert.
  Samenentwicklung und Speicherstoffakkumulation: Über die Analyse transgener Pflanzen, in denen Gene für Transporter von Aminosäuren, organischen Säuren, oder Zuckern, sowie zentralen Enzymen oder Regulatoren in Samen überexprimiert oder reprimiert wurden, ergaben sich wichtige neue Erkenntnisse zur metabolischen Regulation der Samenentwicklung und -füllung sowie Hinweise auf eine Koordination mit hormonellen Signalen (vermittelt durch Auxine, Cytokinine und Abscisinsäure) bei diesem Prozess.

co-operation with ABI3 in regulation of seed-specific gene expression. A further important breakthrough was achieved through identification of an apospory locus (a genomic region conditioning embryo formation from unfertilised cells) in *Hypericum perforatum* (St. John´s wort), which thus is now accessible to a detailed molecular characterisation that will result in major new information on the molecular mechanisms of apomixis (asexual propagation through seeds).

- Analysis of genetic causes and molecular mechanisms of metabolic performance variation under optimal and suboptimal environmental conditions:
  Vegetative growth and biomass accumulation, heterosis: Through identification of QTL (genetic loci that determine quantitative traits) for biomass and for metabolites in *Arabidopsis thaliana* new knowledge was gained on genetic factors that control early vegetative growth and metabolism and on the close relation between plant biomass production and the physiological condition of plants. With identification of QTL for biomass heterosis and for metabolite heterosis (enhanced biomass production or elevated metabolite contents in crossbreds vs. their parental inbreds) important steps were made towards elucidation of genetic causes and molecular mechanisms of heterosis. Furthermore, important observations were made on the predicitive power of genetic and metabolic markers on hybrid performance and the degree of heterosis that indicate a good potential for future applications in plant breeding. To check the existence of similar relations in crop plants corresponding investigations were iniated in maize.
  Seed development and storage compound accumulation: Via analysis of transgenic plants in which genes of transporters of amino acids, organic acids, or sugars as well as central enzymes or regulators were over-expressed or repressed important new knowledge was gained on metabolic regulation of seed development and filling and indications were obtained on coordination with phytohormonal signals (mediated by auxins, cytokinins, and abscisic acid) in this process. Using an integrative approach of molecular, biochemical, and histological analyses in mutants and transgenic plants with altered abscisic acid (ABA) contents, the particular relevance of this phytohormone for seed development and filling was demonstrated. The detailed analysis of genetically diverse barley lines using quantitative genetic, molecular, biochemical and biophysical methods furthermore showed the major importance of ABA for yield stability under drought stress conditions during seed filling. Important methodological advances were made through the development of novel (NMR-based) imaging techniques for the 3-dimensional topology of seeds and seed contents as well as microsampling methods. These techniques open now the opportunity of detailed molecular, biochemical, and physiological investigations of individual tissues or areas especially of seeds but also

Durch eine integrative molekulare, biochemische und histologische Analyse von Mutanten und transgenen Pflanzen mit veränderten Abscisinsäuregehalten in Samen wurde die besondere Bedeutung dieses Phytohormons für die Kontrolle der Samenentwicklung und -füllung belegt. Durch eine detaillierte Analyse genetisch diverser Gerstenlinien mittels quantitativ genetischer, molekularer, biochemischer und biophysikalischer Verfahren wurde ferner die besondere Bedeutung von Abscisinsäure (ABA) für die Ertragsstabilität unter Trockenstressbedingungen während der Samenfüllung belegt. Wichtige methodische Fortschritte wurden über die Entwicklung neuartiger (NMR-basierter) bildgebender Verfahren für die dreidimensionale Topologie von Samen und Sameninhaltsstoffen sowie von Methoden der Mikroprobennahme erzielt. Diese erlauben es nun, detaillierte molekulare, biochemische und physiologische Untersuchungen einzelner Gewebe, wie z.B. Meristeme (s. Fig. 30, S. 85) bzw. Bereiche von Samen während verschiedener Entwicklungsphasen durchzuführen und deren spezifische Funktionen aufzuklären. Neben seiner wichtigen Rolle bei der programmierten Degradierung des Nucellargewebes während der Entwicklung von Gerstensamen wurde für das *JEKYLL*-Gen auch eine essentielle Rolle bei der Degradierung des Tapetums über programmierten Zelltod und die Pollenfertilität nachgewiesen.

Biotechnologische, anwendungsorientierte Forschung

- „Phyto-F(Ph)arming“:
  Im Berichtszeitraum gelang die Produktion verschiedener Formen von Spinnenseidenproteinen in Pflanzen und deren nachfolgende Isolierung und Charakterisierung mittels Rasterkraftmikroskopie. Ferner wurde die Produktion und Reinigung einer besonderen Form von Antikörpern (V_HH-Moleküle) gegen den Tumornekrosisfaktor α (TNFα, spielt eine wichtige Rolle bei einer Reihe von chronischen Entzündungserkrankungen) erzielt und deren hohe biologische Aktivität nachgewiesen. Schließlich wurden diverse Proteine als Fusionen mit ELP (Elastin-ähnliches Polypeptid) in Pflanzen produziert und partiell gereinigt, die sich zur Immunisierung u.a. gegen Tuberkulose oder Vogelgrippe (H5N1) eignen.
- Entwicklung von Hybridtechnologien:
  Als Alternative zu chemischer Pollenabtötung wurde ein hoch effizientes Verfahren zur Erzeugung von Hybridsaatgut bei Pflanzen entwickelt, 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 Funktionameristems (see Fig. 30, p. 85), respectively, during various developmental phases und to uncover their specific functions. For the *JEKYLL* gene an important role was demonstrated to be played in degradation via programmed cell death of the tapetum and in pollen fertility in addition to its action in programmed degradation of nucellar tissue during the development of barley seeds.

Biotechnological, application-oriented research

- “Phyto-F(Ph)arming”:
  In the reporting period, the production in plants of various forms of spider silk proteins and their isolation and characterisation using atomic force microscopy was achieved. In addition, the production and purification of a particular form of antibodies (V_HH molecules) against tumor necrosis factor α (TNFα, plays an important role in several chronic inflammatory disorders) was achieved and their high biological activity was demonstrated. Finally, various other proteins that are suitable for vaccinations e.g. against tuberculosis or against avian flue were produced in plants as fusions to ELP (elastin-like protein) and partially purified.
- 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 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 produced through cross-pollination, which on its own is inactive, the produced hybrids are fully fertile. During the reporting period the functionality of the system was verified, both, in transgenic dicot model plants and in transgenic wheat. This represents a major breakthrough towards development of a commercially viable hybrid wheat system.
- Yield and quality of seeds and their constituents:
  Confirming prior results from greenhouse experiments, increased seed protein content and protein yield was demonstrated for transgenic winter wheat plants over-expressing amino acid and sugar transporter genes in developing seeds that were cultivated in field-like conditions in “mini greenhouses”. These results show that information derived from systems-oriented analyses of seed development and molecular physiology can be effectively used to achieve improvements in crops via transgenic approaches that are highly relevant to plant breeding.

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.

lität dieses Systems sowohl in transgenen zweikeimblättrigen Modellpflanzen als auch in transgenen Weizenpflanzen nachgewiesen werden und damit ein entscheidender Durchbruch erzielt werden, der die Weiterentwicklung dieses Verfahrens zu einem kommerziellen Hybridweizensystem ermöglicht.
- Ertrag und Qualität von Samen und deren Inhaltsstoffe: Mit Hilfe der Überexpression von Aminosäure- und Zuckertransportern in sich entwickelnden Samen von Winterweizen konnten nach früheren Gewächshausexperimenten nun auch in feldnahen Kulturverfahren in Minigewächshäusern erhöhte Proteingehalte in Samen und ein gesteigerter Proteinertrag nachgewiesen werden. Damit wird bestätigt, dass Informationen, die aus system-orientierten Analysen der Samenentwicklung und der molekularen Physiologie gewonnen wurden, herangezogen werden können, um züchtungsrelevante Verbesserungen durch Einsatz gentechnischer Verfahren bei Kulturpflanzen zu erzielen.

Entwicklung und Anwendung bioinformatischer Verfahren

Als generische Verfahren gehören bioinformatische Methoden zum unverzichtbaren Repertoire moderner pflanzenbiologischer Forschung und finden abteilungsübergreifend Anwendung in vielfältigen Projekten.
- Koordination der Bioinformatikarbeiten am IPK (Prof. Dr. F. Schreiber)
- Integrative Bioinformatik und Netzwerkanalyse: Eine zentrale Plattform für die Analyse experimenteller Daten im Kontext biologischer Netzwerke und Klassifizierungshierarchien (VANTED), das als open source Software System implementiert ist, wurde durch weitere Komponenten ergänzt und erweitert und in vielfältigen Projekten eingesetzt. Auf dessen Basis wurde eine neue Plattform für die Erstellung räumlicher, struktureller und kinetischer Modelle entwickelt, die die Integration vielfältiger Informationen erlaubt. Ferner wurde das MetaCrop-Informationssystem für Stoffwechselwege weiterentwickelt und für zusätzlich Pflanzenarten und weitere Stoffwechselwege anderer Organismen ergänzt. Diese Plattformen bzw. deren gespeicherte Informationen dienten der Erstellung von Stoffwechselmodellen und Analysen von Stoffflüssen. Weiterhin wurden ein Informationssystem für das Management biologischer Experimentdaten (DBE2) und ein auf internationalen Konventionen (SBGN) beruhendes System zur Darstellung und Handhabung biologischer Netzwerke etabliert, das für die Darstellung regulativer Prozesse und genetischer Interaktionen während der pflanzlichen Embryo- und Samenentwicklung herangezogen wird. Schließlich wurde eine Bildanalysepipeline für die Verarbeitung von Daten aus automatisierten Phänotypisierungsanlagen entwickelt und diverse neue Algorithmen für die strukturelle Netzwerkanalyse und die Netzwerkdarstellung entwickelt, implementiert und angewendet.

- Coordination of bioinformatics research at IPK (Prof. F. Schreiber)
- Integrative bioinformatics and network analysis: A central platform for the analysis of experimental data in the context of biological networks and hierarchies (VANTED) that has been implemented as an open source software system was extended by further components and used in numerous projects. On its basis, a new platform for the establishment of spatial, structural, and kinetic models has been developed that allows integration of various types of data. Furthermore, the MetaCrop information system for metabolic pathways has been further developed and has been expanded for additional plant species and metabolic pathways of other organisms. These platforms and the information stored therein were used to develop metabolic models and to analyse metabolic fluxes. Moreover, an information system for the management of biological experiment data (DBE2) and an international convention-based system (SBGN) to display and handle biological networks have been developed. The latter is currently used to create a display of regulatory processes and genetic interactions occurring during plant embryo and seed development. Finally, an image analysis pipeline for the analysis of data produced by automated phenotyping facilities has been implemented and various novel algorithms for the structural network analysis and display were developed, implemented, and used.
- DNA motif identification, RNA and protein expression data analysis: Factor analyses were carried out on numerous large data sets of expression analyses (time series and stress response experiments) for the identification of genes differentially expressed on the RNA or protein level. A Hidden Markov Models-based platform for analysis of array-CGH and ChIP-Chip data sets was developed and used for comparative genome analysis and epigenetic chromatin modification of diverse *Arabidopsis thaliana* accessions and hybrids thereof. Finally, novel graph-based algorithms have been developed for the *de novo* motif detection and the re-analysis of transcription factor binding sites and were used in analyses on *Arabidopsis thaliana*.

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, January 2010

- Identifizierung von DNA-Motiven, Analyse von RNA- und Proteinexpressionsdaten: Für umfangreiche Expressionsanalysedatensätze (Zeitreihen und Stressexperimente) wurden Faktorenanalyseverfahren zur Identifizierung differentiell exprimierter Gene auf RNA- und Protein-Ebene angewendet. Eine auf Hidden Markov-Modellen basierte Plattform zur Analyse von Array-CGH und ChIP-Chip-Datensätzen wurde entwickelt und für die vergleichende Genomanalyse einschließlich epigenetischer Chromatinmodifikationen verschiedener *Arabidopsis thaliana*-Akzessionen und deren Hybriden eingesetzt. Schließlich wurden neue Graphen-basierte Algorithmen zur *de novo*-Motiverkennung und zur Re-Analyse von Transkriptionsfaktorbindestellen in DNA-Sequenzen entwickelt und für Analysen bei *Arabidopsis thaliana* eingesetzt.

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

Thomas Altmann, Januar 2010

Research Group: Heterosis (since 1st April 2008)

Head: Prof. Thomas Altmann

Scientists

IPK financed
Borisjuk, Lioudmilla, Dr. (P, since 22.10.2008)
Günther, Torsten (0,25 Annex, 01.06.-31.08.2008)
Meyer, Rhonda, Dr. (P, since 01.04.2008)
Riewe, David, Dr. (P, since 15.09.2008)

Grant Positions
Ernst, Michaela, Dr. (BMBF, since 10.07.2008)
Fuchs, Johannes (0,5 BMBF, since 22.10.2008)
Heinzel, Nicolas, Dr. (Industry, since 01.07.2009)
Jasik, Jan, Dr. (Industry, since 01.08.2009)
Melkus, Gerd (0,5 BMBF, since 22.10.2008)
Müller, Margarete, Dr. (BMBF, since 01.05.2008)
Muraya, Moses Mahugu (BMBF, since 15.08.2009)
Radchuk, Ruslana, Dr. (Industry, 01.06.-31.10.2009)
Rajesh, Kalladan (0,5 BMBF, since 22.10.2008)
Rolletschek, Hardy, Dr. (BMBF, 22.10.-31.10.2008; Industry, since 01.11.2008)
Rosso, Mario, Dr. (BMBF, since 01.08.2008)
Schiebold, Silke (Industry, since 22.10.2008)
Seyfarth, Monique (Saxony-Anhalt, since 01.10.2009)
Thiel, Johannes, Dr. (0,5 DFG, 22.10.2008-31.05.2009)
Tschiersch, Henning, Dr. (0,5 Industry, since 22.10.2008)
Weigelt, Kathleen (0,5/1,0 BMBF, since 10.01.2009)

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 of oil storing seeds is investigated using topographical biochemical, biophysical, and molecular analysis procedures (mainly applied to oilseed rape) to uncover determinants and limiting factors of oil yield.

Research Report

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

Identification of biomass and metabolite QTL in *Arabidopsis thaliana*

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 have been cultivated and analysed for their early vegetative growth/biomass accumulation and for their metabolic composition (in collaboration with L. Willmitzer and co-workers at MPI-MP, Golm) using a mass spectrometry-based metabolic profiling approach (Lisec et al. 2008). Analysis of the data on the RILs resulted in the identification of six and 157 quantitative trait loci (QTL) for biomass and metabolite contents, respectively. The observation of coincidence of significantly more metabolic QTL (mQTL) with two biomass QTL than expected for a random distribution and the ability of simulating three out of six biomass QTL purely on the basis of metabolic composition indicates a close link between plant biomass production and metabolic constitution. Five out of six biomass QTL and 55 % of the mQTL were independently identified and thus verified through similar analysis of 97 ILs. Metabolic reaction or metabolic pathway-derived (enzyme encoding) candidate genes were identified for 24 % or 67 % of the mQTL, respectively. These data open the opportunity of molecular identification of vegetative growth and metabolism-controlling genes through map-based cloning of QTL and they provide a comprehensive basis for the detection of functionally relevant variation in known genes encoding metabolic factors.

Identification of QTL for biomass heterosis and metabolite heterosis in *Arabidopsis thaliana*

Using the aforementioned *Arabidopsis* RILs and ILs jointly with their respective testcrosses (TCs) in analyses of their dry matter yield and of their metabolite profiles (in collaboration with Prof. L. Willmitzer and co-workers at MPI-MP, Golm) allowed the identification of genomic regions, that condition heterosis for vegetative growth/biomass accumulation (see Fig. 31, p. 93) or metabolite content, respectively, in crosses of the *Arabidopsis* Col-0 and C24 accessions (Meyer et al. 2009, in press; Lisec et al. 2009). Biomass (dry weight) and leaf area mid-parent heterosis in RILs/RIL-TCs ranged from -31 to 99 % and from -58 to 143 %, respectively (Meyer et al., in press). Including data on ILs/IL-TCs, ten genomic regions were detected that are involved in seedling stage biomass heterosis and that individually explained between 2.4 % and 15.7 % of the phenotypic variation. While overdominant gene action was prevalent in heterotic QTL, the results indicate that a combination of dominance, overdominance and epistasis is involved in biomass heterosis in this *Arabidopsis* cross.

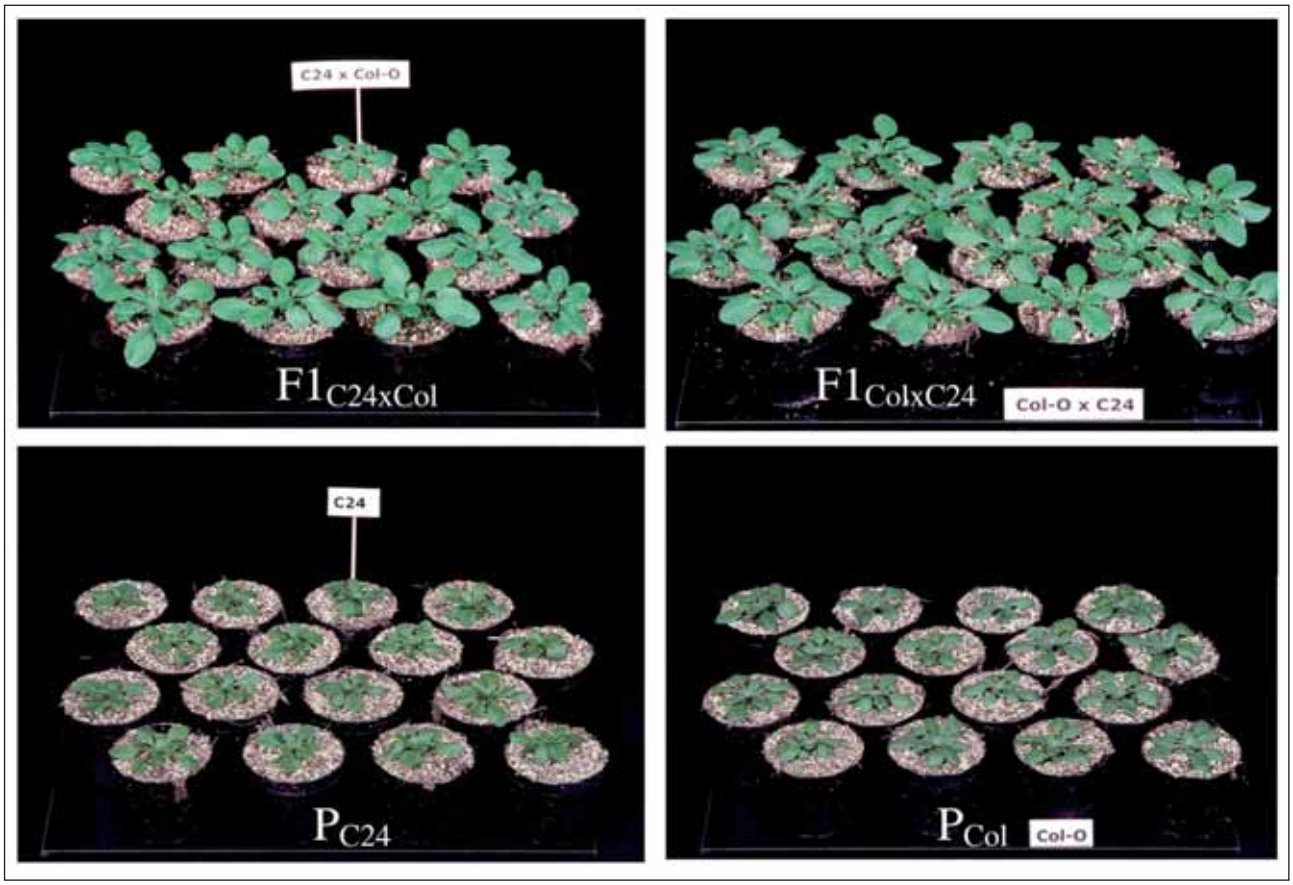


Fig. 31
Heterosis of vegetative growth in the *Arabidopsis thaliana* cross of accessions Col-0 and C24: Enhanced growth of F1 hybrids (top) in comparison to the parental inbreds (bottom) (T. Altmann).

Analysis of the contents of 181 metabolites in RILs/RIL-TCs allowed the identification of 147 heterotic metabolite (hm)QTL and 634 significant differences in metabolite levels were observed in ILs/IL-TCs (Lisec et al. 2009). The obtained results indicate epistasis to be a major contributor to metabolite heterosis in *Arabidopsis*.

Identification of predictors of hybrid performance and heterosis and molecular network analyses in the *Arabidopsis thaliana* Col-0×C24 cross

In collaboration with Prof. J. Selbig and co-workers (Potsdam University; MPI-MP, Golm) and D. Repsilber and co-workers (FBN, Dummerstorf) the genetic marker data, metabolite profiles and transcript profiles of parents, F1 hybrids, or RILs and RIL-TCs were subjected to advanced statistical and network analysis procedures. It was shown that hybrid performance (Steinfath et al. 2009, in press) and mid-parent heterosis (Gärtner et al. 2009) can be predicted purely based on parental genetic marker and metabolic marker information, in particular when both marker types are used jointly upon application of variables/feature selection in combination with regression and dimensionality reduction. Using a systems biological approach, enhanced connectivity of metabolome (Andorf et al. 2009a) and transcriptome (Andorf et al. 2009b) networks, respectively, was observed on the basis of partial correlations. This hints towards increased numbers of regulatory interactions in hybrids versus parents possibly leading to enhanced adaptability of the hybrids.

Analysis of metabolism – growth relations in *Arabidopsis thaliana* accesssions

In collaboration with M. Stitt and co-workers (MPI-MP, Golm), previous analyses that indicated a close relationship between metabolic composition and plant biomass in the *Arabidopsis* Col-0/C24 RIL/RIL-TC population (Meyer et al. 2007) were expanded to investigations of a diverse set of 94 *Arabidopsis* accessions (Sulpice et al. 2009): Metabolite profiling revealed negative correlations of biomass with many metabolites, especially starch that appears to act as an integrator of the overall metabolic response. Through transcript profiling across 21 accessions two candidate genes potentially involved in the regulation of growth and metabolism were identified whose expression correlates with biomass and DNA polymorphisms and that are significantly associated with biomass and other metabolic traits.

Characterisation of a highly diverse maize inbred line collection

In the frame of the GABI-ENERGY co-operation project (jointly with Prof. A. Melchinger and co-workers, University of Hohenheim; Profs. L. Willmitzer and M. Stitt and co-workers, MPI-MP, Golm; J. Selbig and co-

workers, Potsdam University), a detailed characterisation of a collection of 300 diverse maize inbred lines ('Dent panel') and testcrosses thereof has been initiated for vegetative growth performance under controlled (green house) conditions, for metabolite composition and transcript profiles, and for genetic diversity (M. Ernst et al., unpublished data).

Project area *Lipid Metabolism in Oil-storing Seeds*

Modelling lipid metabolism using a systems biology approach

Using rapeseed (*Brassica napus*), a systems biology approach is followed to gain knowledge for maximisation of oil yield. A comprehensive analysis of lipid metabolism and seed filling, including histological and metabolic modelling has been initiated through combination of the lipid imaging tool (see below) and laser-microdissection for the analysis of metabolites, storage products and gene expression (L. Borisjuk et al., unpublished results). The projects rely on extensive collaboration with partners from University Hannover, Brookhaven National Lab (USA) and Bayer CropScience (Belgium). The bioanalytical tools were also used in other collaborations (e.g. GABI-Grain, K. Rajesh; SysSeed, G. Melkus) and resulted in several publications (Tiedemann et al. 2008; Akhani et al. 2009; Melkus et al. 2009; Radchuk et al. 2009).

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

NMR-based methods have been developed that allow rapid and non-invasive detection and quantitative visualisation of lipids in living seeds (Neuberger et al. 2008, see Fig. 32). The method provides 3-dimensional "lipid maps", and was applied to a variety of species (rapeseed, tobacco, soybean, barley, maize and others). This *in vivo* technology represents a significant breakthrough in oilseed research with high biotechnological relevance (Neuberger et al. 2009).

To study the distribution and flow of metabolites non-invasively and *in vivo,* methods have been developed based on $^{1}H/^{13}C$-NMR (in collaboration with University of Würzburg, Prof. P. Jakob). In seeds of pea, the levels of key metabolites could be monitored and visualised (L. Borisjuk et al., unpublished). The NMR method, combined with laser micro-dissection, isotope labelling, HPLC, *in situ* hybridisation and electron microscopy, allowed re-evaluation of the role of the transient endosperm in dicots (Melkus et al. 2009).

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

Oxygen deficiency is commonplace in the seed (Borisjuk & Rolletschek, 2009; Rolletschek et al. 2009). Oxygen limitation of energy- and storage metabolism was shown to be linked with nitric oxide (NO) – an important signalling molecule in both the plant and animal kingdom – and the role of NO for dynamic adjustment of seed metabolism to environmental and developmental changes was demonstrated (Benamar et al. 2008; Borisjuk & Rolletschek, 2008).

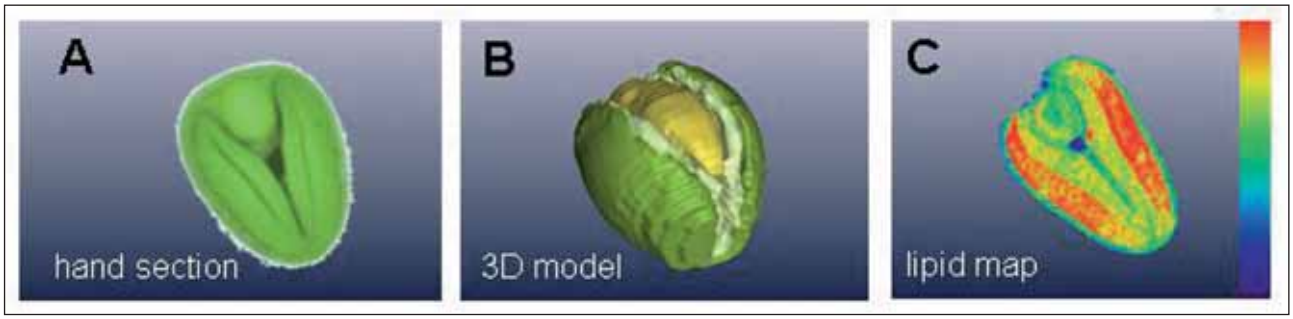


Fig. 32
NMR-based modelling of *Brassica napus*. (A) seed structure. (B) 3-dimensional digital model of embryo. (C) lipid map showing oil deposition across the seed (virtual section); the color bar indicates lipid content (max in red) (L. Borisjuk, H. Rolletschek) .

Collaborations (selection)

Within the Institute:

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Dept. of Cytogenetics and Genome Analysis, Research Group Epigenetics; Dr. M.F. Mette, Dr. M. Kuhlmann;

Dept. of Cytogenetics and Genome Analysis, Research Group Genome Plasticity; Dr. R. Schmidt, S. Voigtländer;

Dept. of Cytogenetics and Genome Analysis, Research Group Bioinformatics and Information Technology; Dr. U. Scholz, T. Schmutzer;

Dept. of Molecular Genetics, Research Group Seed Development; Dr. W. Weschke, Dr. N. Sreenivasulu, Dr. V.V. Radchuk, R. Radchuk;

Dept. of Molecular Genetics, Research Group Plant Bioinformatics; Prof. F. Schreiber, A. Hartmann;

Dept. of Physiology and Cell Biology, Research Group Molecular Plant Nutrition; Prof. N. v. Wirén, Dr. M.R. Hajirezaei;
Dept. of Physiology and Cell Biology, Research Group Structural Cell Biology; Dr. M. Melzer; Dr. T. Rutten
Dept. of Physiology and Cell Biology, Research Group Plant Reproductive Biology; Dr. J. Kumlehn, K. Plasun.

Outside the Institute:
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Metanomics GmbH, Berlin; Dr. H. Schön;
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University of Würzburg; Prof. P. Jacob;
Pennsylvania State University, Dept. Bioengineering, USA; Prof. A. Webb, Dr. T. Neuberger;
Brookhaven National Lab, Upton, USA; Dr. J. Schwender, Dr. A. Rogers;
INRA/University of Angers, France; Prof. D. Macherel.

Publications

(All publications with a "*" are based on work that has been carried out when Thomas Altmann and Rhonda Meyer were at the University of Potsdam, Germany, when David Riewe was at the Max Planck Institute of Molecular Plant Physiology, Golm, Germany and when Mario Rosso was at the University of Bielefeld, Germany)

Peer Reviewed Papers

2008

*Balazadeh, S., S. Parlitz, B. Mueller-Roeber & R.C. Meyer: Natural developmental variations in leaf and plant senescence in *Arabidopsis thaliana*. Plant Biol. 10 (2008) 136-147.

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Radchuk, V.V., L. Borisjuk, N. Sreenivasulu, K. Merx, H.P. Mock, H. Rolletschek, U. Wobus & W. Weschke: Spatiotemporal profiling of starch biosynthesis and degradation in the developing barley grain. Plant Physiol. 150 (2009) 190-204.

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Books and Book Chapters

2009

Neuberger, T., H. Rolletschek, A. Webb & L. Borisjuk: Non-invasive mapping of lipids in plant tissue using Magnetic Resonance Imaging. In: Armstrong, D. (Ed.): Lipidomics, Vol. 2 (Methods Mol. Biol. 579). Humana Press, Totowa/USA (2009) 485-496.

Research Group: Seed Development

Head: Dr. Winfriede Weschke

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Riebeseel, Erik (0,25 Annex, 01.02.2008-30.06.2008; 01.10.2008-30.06.2009)
Rolletschek, Hardy, Dr. (P, till 28.02.2008)
Schiebold, Silke (0,25 Annex, till 30.09.2008)
Tewes, Annegret, Dr. (P, till 30.06.2008)
Weber, Hans, Dr. (P)
Weigelt, Kathleen (0,25 Annex, 10.11.2008-09.01.2009)
Wobus, Ulrich, Prof. (P, till 31.03.2008; 0,5 Annex, since 01.04.2008)

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Kohl, Stefan (0,5 DFG, since 01.04.2009)
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Nguyen, Thuy Ha (0,5 DFG, till 29.02.2008)
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Schiebold, Silke (0,5 Industry, 01.10.-21.10.2008)
Seiler, Christiane (0,5/1,0 BMBF)
Sreenivasulu, Nese, Dr. (BMBF)
Staroske, Nicole (0,5 BMBF)
Thiel, Johannes, Dr. (DFG, till 21.10.2008; 0,5 Overhead, 01.03.-31.05.2009; DFG, 01.06.-31.08.2009; Overhead, 01.09.-31.10.2009; DFG, since 01.11.2009)
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Weichert, Nicola, Dr. (Saxony-Anhalt, till 30.06.2009)
Weier, Diana, Dr. (DFG)
Weigelt, Kathleen (0,5 EU, till 09.02.2008; 0,25 Overhead, 10.02.-09.11.2008)

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Lata, Charu (DLR, 22.11.-11.12.2009)
Potokina, Elena, Dr. (DFG, 01.10.-30.11.2009)
Prasad, Manoj, Dr. (DLR, 01.03.-15.03.2009)
Riebeseel, Erik (self-financed, 01.07.-31.12.2009)
Weichert, Nicola, Dr. (self-financed, 01.07.-31.12.2009)

Goals

Understanding and influencing regulatory networks determining composition and yield of crop seeds.

Research Report

Composition and yield of crop seeds depend on: (i) source capacity (ii) sink strength and (iii) transport capacity. Genetic and metabolic networks regulating assimilate supply from source organs, assimilate distribution and establishment of sink strength are analysed. Comparing regulatory pathways within different tissues sink-source interactions are studied. Using -omics and analytical micro technologies transgenic models and mutants are analysed to answer the questions: Can seed composition be changed in favour of N? Can sink strength and sink-source interactions be modulated in favour of seed size and yield?

Metabolic regulation of seed development
Over-expression of **amino acid permease VfAAP1** in pea seeds increases amino acids, seed N and protein as revealed by field trials. Higher ABA levels, involved in storage-associated gene expression and N-dependent stimulation of sucrose mobilisation indicate signalling networks of C, N and ABA operating during seed maturation. Results demonstrate high capacities to regulate N to C ratios and the importance of mitochondrial control of N to C balance and amino acid homeostasis (Weigelt et al. 2008). Repression of **2-oxoglutarate/ malate translocator** (PsOMT) in pea seeds revealed that OMT is important for protein-storing crop seeds and necessary for amino acid biosynthesis in plastids. Gene expression analysis demonstrated delayed differentiation into storage plastids indicating that C supply mediated by OMT controls plastid differentiation (Riebeseel et al., in press). Over-expression of **sucrose transporter HvSUT1** caused higher sucrose uptake capacity into wheat grains. Grain sucrose levels are not altered indicating effects on sucrose fluxes rather than steady state levels. HvSUT1-overexpression increases grain protein content but deregulates the metabolic status. Alternate stimulation of positive and negative regulators causes oscillatory patterns in gene expression pattern and highlights capacities and flexibilities to adjust storage metabolism in response to metabolic alterations (Weichert et al., in press). **ADP-glucose pyrophosphorylase**-repression in pea seeds causes excess sugar accumulation following

carbohydrate oxidation and stress responses. Enhanced provision of C precursors activates amino acid and storage protein biosynthesis and leads to N limitation. Pea seeds effectively circumvent stress-signalling to avoid cellular damage and premature senescence or apoptosis (Weigelt et al. 2009). **SnRK1 kinase**-antisense pea seeds (Radchuk et al. 2006) show lower cytokinin levels, deregulated cotyledonary establishment and growth and downregulated gene expression related to cell proliferation, meristem maintenance and differentiation, leaf formation and polarity. SnRK1 regulates coordinated early cotyledon emergence and growth via cytokinin-mediated auxin transport and/or distribution. SnRK1 communicates nutrient and hormonal signals from auxins, cytokinins and ABA with metabolism and development (Radchuk et al., in press).

Hormonal influences on seed development

Development of the maternally effected barley shrunken endosperm mutant *seg8* was analysed by comprehensive molecular, biochemical and histological means. The most obvious finding was deregulation of ABA levels. Inversely correlated ploidy levels and ABA amounts suggest influences of ABA on cell cycle regulation (Sreenivasulu et al., resubmitted). Transgenic pea and barley lines were produced with increased ABA levels in seeds due to anti-ABA antibody gene expression (Phillips et al. 1997, GABI-GRAIN, N. Staroske, unpubl.). RNAi-suppression of the major ABA catabolism enzyme (ABA 8'-hydroxylase2) in barley caused vegetative and generative phenotypes (GABI-SysSEED, V. Radchuk, unpubl.). The barley anti-ABA-antibody and RNAi-suppression lines are analysed in ongoing DFG projects (partner B. Hause, IPB Halle/Saale). Methods for microdissection of specific grain tissues were established and combined with subsequent expression profiling and amino acid analysis at the atomolar scale. Analysis of nucellar projection (NP) and endosperm transfer cells (ETC) of young barley grains unravel the network of hormonal regulation of cellular differentiation and function related to GA in NP and ethylene in ETC (Thiel et al. 2008; Thiel et al. 2009). For more details see Fig. 33.

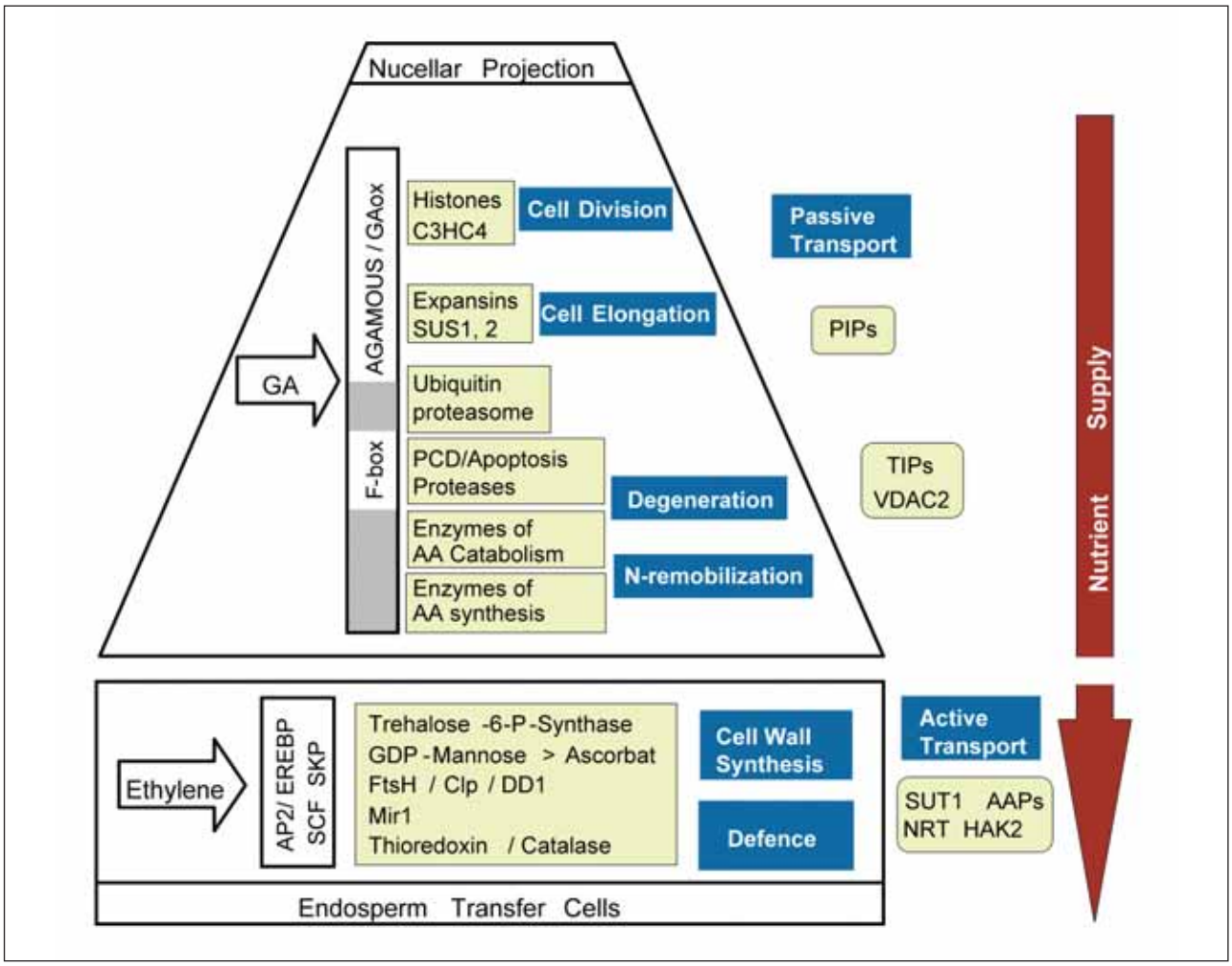

Fig. 33
Model of cellular processes in nucellar projection and endosperm transfer cells of developing barley grains at 8 DAF (days after flowering). Tissue sections were prepared by laser pressure catapulting-based microdissection and subsequent transcript profiling. AA, amino acid; AAP, amino acid permease; C3HC4, C3HC4 ubiqutin ligase; FtsH, Clp, DD1, Mir1, specific types of proteases; GDP, glucose diphosphate; HAK, potassium transporter; NRT, nitrate transporter; PIP, plasma membrane intrinsic protein; SUS, sucrose synthase; SUT, sucrose transporter; TIP, tonoplast intrinsic protein; VDAC, voltage-dependent anion channel (J. Thiel).

Sink-source interactions
The relationship between senescence-induced N remobilisation are analysed together with N transporters and regulators/signals mediating sink-source relationship in relation to grain filling (DFG Forschergruppe 948, S. Kohl and F. Andersch, unpubl.).

Functional analysis of selected genes and gene families
The JEKYLL-protein degrades nucellar tissues during barley seed development (Radchuk et al. 2006). *Jekyll* is expressed in tapetum but not pollen. Its repression negatively affects pollen fertility indicating crucial roles for tapetum degradation and PCD (V. Radchuk, R. Radchuk, L. Borisjuk, in prep.). Analysis of temporal and spatial gene expression patterns and activities of starch metabolism enzymes suggest a role for starch degradation in maternal and filial grain tissues and two different pathways for starch degradation in maternal tissues. DNA degradation and fragmentation, a hallmark of PCD, increased with pericarp age (Radchuk et al. 2009). Distribution of degrading nuclei coincided temporally and spatially with tissue degeneration in nucellus, nucellar projection and pericarp. In early development, TUNEL-positive nuclei were detected in nucellus until tissue degeneration. Later, degenerating nuclei were detected in pericarp, spreading from inner to outer cell layers and from dorsal and lateral towards ventral regions of the caryopsis (V. Radchuk, D. Weier, in prep.).

The barley atlas
16 ^{1}H-NMR datasets were acquired covering barley grain development and combined using warping algorithms forming a virtually growing grain (Pielot et al. 2008). Striking proton-rich cellular structures within specific tissues were identified by integration of ^{1}H-NMR signals into structural 3-D models, which were created based on serial transverse sections at five developmental stages (Bollenbeck et al. 2009). Inter-individual models representing biological variability between individuals of one stage are available (F. Bollenbeck, IFF Magdeburg, R. Pielot, Univ. Magdeburg, D. Weier). The 4-D barley atlas opens possibilities to integrate mRNA *in situ* patterns and peptide distributions established by MALDI imaging (Pielot et al. 2009; Bollenbeck et al. 2009). Presently, data are prepared for web presentation.

Drought stress and seed filling (project GABI-GRAIN, N. Sreenivasulu)
Complementary genomics approaches have been used to explore natural genetic variation among introgression line populations with wild barley accession as donors in an attempt to understand mechanisms of reaching enhanced yield stability and uncompromised seed quality under terminal drought stress during seed filling within GABI-GRAIN consortium (Project coordinator N. Sreenivasulu and co-coordinator: U. Wobus). 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 and 2 were detected (in collaboration with M. Röder). 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, C. Seiler, H. Rolletschek and M. Strickert, research group Data Inspection). 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 by manipulating different nodes of ABA biosynthesis and degradation pathways using a set of drought inducible promoters (V.T. Harshavardhan and C. Seiler).

Collaborations (selection)

Within the Institute:
Dept. of Genebank, Research Group Genome Diversity; Prof. A. Graner;
Dept. of Genebank, Research Group Resouces Genetics and Reproduction; Dr. A. Börner;
Dept. of Cytogenetics and Genome Analysis, Research Group Gene and Genome Mapping; Dr. M. Röder, Dr. S. Worch;
Dept. of Cytogenetics and Genome Analysis, Research Group Bioinformatics and Information Technology, Dr. U. Scholz;
Dept. of Molecular Genetics, Research Group Heterosis; Dr. H. Rolletschek, Dr. L. Borisjuk, Prof. T. Altmann;
Dept. of Molecular Genetics, Research Group Gene Regulation; Dr. H. Bäumlein;
Dept. of Molecular Genetics, Research Group Phytoantibodies; Dr. U. Conrad;
Dept. of Molecular Genetics, Research Group Data Inspection; Dr. M. Strickert;
Dept. of Physiology and Cell Biology, Research Group Structural Cell Biology; Dr. T. Rutten, Dr. M. Melzer;
Dept. of Physiology and Cell Biology, Research Group Plant Reproductive Biology; Dr. J. Kumlehn, Dr. G. Hensel;
Dept. of Physiology and Cell Biology, Research Group Systems Biology; Dr. B.H. Junker.

Outside the Institute:
Leibniz Institute of Plant Biochemistry (IPB), Halle/Saale; Dr. B. Hause;
Martin Luther University Halle-Wittenberg, Plant Breeding, Halle/Saale; Prof. K. Pillen;

Max Planck Institute of Molecular Plant Physiology, Golm; Prof. J. Kopka; Dept. 2, Research Group System Regulation, Prof. M. Stitt; Research Group Integrative Carbon Biology, Dr. B. Usadel;
Nordsaat Saatzucht GmbH, Böhnshausen; Dr. L. Kuntze;
KWS Lochow GmbH, Bergen-Wohlde; Dr. V. Korzun;
Humboldt University Berlin; Institute of Crop Science, Dept. of Crop Production in Tropical and Subtropical Areas, Berlin; Dr. K.-P. Götz;
Vavilov Institute of Plant Industry (VIR), Laboratory of Molecular and Ecological Genetics, St. Petersburg, Russia; Dr. E. Potokina;
Natl. Academy of Sciences of Ukraine, Institute of Food Biotechnology and Genomics, Kiev, Ukraine; Prof. Ya. Blume, Dr. A. Yemets, Dr. V. Korkhovoy;
National Institute of Agrobiological Sciences, Tsukuba, Japan; Dr. T. Komatsuda.

Publications

Peer Reviewed Papers

2008

Balyan, H.S., N. Sreenivasulu, O. Riera-Lizarazu, R. Azhaguvel & S.F. Kianian: Mutagenesis and high-throughput functional genomics in cereal crops: Current status. Adv. Agron. 98 (2008) 357-414.

Benamar, A., H. Rolletschek, L. Borisjuk, M.H. Avelange-Macherel, G. Curien, H.A. Mostefai, R. Andriantsitohaina & D. Macherel: Nitrite-nitric oxide control of mitochondrial respiration at the frontier of anoxia. Biochim. Biophys. Acta 1777 (2008) 1268-1275.

Borisjuk, L. & H. Rolletschek: Nitric oxide is a versatile sensor of low oxygen stress in plants. Plant Signalling Behav. 3 (2008) 391-393.

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Sreenivasulu, N., A. Graner & U. Wobus: Barley genomics: an overview. Int. J. Plant Genomics (2008) 13 pp, doi:10.1155/2008/486258.

Sreenivasulu, N., B. Usadel, A. Winter, V.V. Radchuk, U. Scholz, N. Stein, W. Weschke, M. Strickert, T.J. Close, M. Stitt, A. Graner & U. Wobus: Barley grain maturation and germination: metabolic pathway and regulatory network commonalities and differences highlighted by New MapMan/PageMan profiling tools. Plant Physiol. 146 (2008) 1738-1758.

Thiel, J., D. Weier, N. Sreenivasulu, M. Strickert, N. Weichert, M. Melzer, T. Czauderna, U. Wobus, H. Weber & W. Weschke: Different hormonal regulation of cellular differentiation and function in nucellar projection and endosperm transfer cells - a microdissection-based transcriptome study of young barley grains. Plant Physiol. 148 (2008) 1436-1452.

Tiedemann, J., T. Rutten, G. Mönke, A. Vorwieger, H. Rolletschek, D. Meissner, C. Milkowski, S. Petereck, H.-P. Mock, T. Zank & H. Bäumlein: Dissection of a complex seed phenotype: novel insights of *FUSCA3* regulated developmental processes. Dev. Biol. 317 (2008) 1-12.

Weigelt, K., H. Küster, R. Radchuk, M. Müller, H. Weichert, A. Fait, A.R. Fernie, I. Saalbach & H. Weber: Increasing amino acid supply in pea embryos reveals specific interactions of N and C metabolism and highlights the importance of mitochondrial metabolism. Plant J. 55 (2008) 909-926.

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Govind, G., V.T. Harshavardhan, J.K. Patricia, R. Dhanalakshmi, M. Senthil Kumar, N. Sreenivasulu & M. Udayakumar: Identification and functional validation of a unique set of drought induced genes preferentially expressed in response to gradual water stress in peanut. Mol. Genet. Genomics 281 (2009) 591-605.

Melkus, G., H. Rolletschek, R. Radchuk, J. Fuchs, T. Rutten, U. Wobus, T. Altmann, P. Jakob & L. Borisjuk: The metabolic role of the legume endosperm: a noninvasive imaging study. Plant Physiol. 151 (2009) 1139-1154.

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Radchuk, V.V., L. Borisjuk, N. Sreenivasulu, K. Merx, H.P. Mock, H. Rolletschek, U. Wobus & W. Weschke: Spatiotemporal profiling of starch biosynthesis and degradation in the developing barley grain. Plant Physiol. 150 (2009) 190-204.

Rolletschek, H., A. Stangelmayer & L. Borisjuk: Methodology and significance of microsensor-based oxygen mapping in plant seeds - an overview. Sensors 9 (2009) 3218-3227.

Thiel, J., M. Müller, W. Weschke & H. Weber: Amino acid metabolism at the maternal-filial boundary of young barley seeds: a microdissection-based study. Planta 230 (2009) 205-213.

Weigelt, K., H. Küster, T. Rutten, A. Fait, A.R. Fernie, O. Miersch, C. Wasternack, R.J. Emery, C. Desel, F. Hosein,

M. Müller, I. Saalbach & H. Weber: ADP-glucose pyrophosphorylase-deficient Pea embryos reveal specific transcriptional and metabolic changes of carbon-nitrogen metabolism and stress responses. Plant Physiol. 149 (2009) 395-411.

Yemets, A.I., O.A. Bayer, V.V. Radchuk & Y.B. Blume: *Agrobacterium*-mediated transformation of flax with mutant tubulin genes encoding resistance to the dinitroaniline herbicides. Russ. J. Genet. 45 (2009) 1215-1222.

Books and Book Chapters

2008

Radchuk, V.V.: Multiple gene transfer to plants. In: Rao, G.P., Y. Zhao, V.V. Radchuk & S.K. Bhatnagar (Eds.): Advances in plant biotechnology. Studium Press LLC, Houston/USA (2008) 1-37.

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Bollenbeck, F. & U. Seiffert: Computational intelligence in biomedical image processing. In: Abraham, A., A.-E. Hassanien & V. Snášel (Eds.): Foundations of Computational Intelligence Vol. 5, SCI 205. Springer-Verlag, Berlin-Heidelberg (2009) 197-222.

Weber, H., R. Radchuk, K. Weichert & I. Saalbach: Changing metabolic pathways to manipulate legume seed maturation and composition. In: Krishnan, H.B. (Ed.): Modification of seed composition to promote health and nutrition. American Society of Agronomy Madison, WI/USA (2009) 55-78.

Research Group: Gene Regulation

Head: Dr. Helmut Bäumlein

Scientists

IPK financed
Johnston, Amal Joseph, Dr. (0,75 Annex, 01.08.-31.10.2009)
Junker, Astrid (0,5 Annex, till 31.12.2008)
Köszegi, David, Dr. (P, since 15.07.2008)
Mildner, Maria (0,5 Pakt für Forschung und Innovation)
Mohr, Michaela (0,75 Annex, 01.01.-31.01.2008)
Schallau, Anna (0,5 Pakt für Forschung und Innovation)
Winter, Hendrik, Dr. (P, 01.01.-31.03.2008)

Grant Positions
Gryczka, Corina, Dr. (BMBF, since 01.09.2008)
Johnston, Amal Joseph, Dr. (DFG, since 01.11.2009)
Junker, Astrid (0,5 BMBF, 01.01.-30.06.2009)
Köszegi, David, Dr. (BMBF, till 14.07.2008)

Visiting Scientists/Scholars
Johnston, Amal Joseph, Dr. (EMBO Heidelberg, 30.04.-31.07.2009)
Lee Hong, Diep (Ministry of Education & Training, Vietnam)

Goals

Analysis of gene networks during gametophyte development and embryogenesis.

Research Report

The group deals with the characterisation of gene regulation during various forms of plant embryogenesis including zygotic, apomictic, somatic and androgenetic processes. Previous genetic studies in *Poa pratensis* suggest at least five loci as essential for the control of **apomixis**, challenging efforts to identify the corresponding genes at the molecular level.

Thus, we have identified and characterised an **apospory**-linked locus of ***Hypericum perforatum*** (A. Schallau, D. Köszegi). Genetic and molecular analyses of sexual and aposporous alleles demonstrate similarity to ring finger proteins of the ARIADNE class known to be involved in protein degradation. BAC sequencing and allele quantifications suggest a structural model of the locus based on dominance and hemizygosity of the aposporous allele. Ongoing work tries to determine the size of the locus by characterisation of flanking genes in the aposporous allele using genomic walking and BAC clone sequencing (collaboration with research group Apomixis and research group Expression Mapping).

Sexual and parthenogenetic wheat egg cells have been used to study molecular processes important for egg cell activation and parthenogenesis (A. Czihal). Complex subtractive approaches have identified candidate genes with egg cell-specific expression in wheat and *Arabidopsis*. Work has been focused on a novel class of transcription factors, the **RKD family** (D. Köszegi). The plant-specific occurrence, egg cell-specific expression (collaboration with U. Grossniklaus, A. Johnston), the mis-expression phenotype and evolutionary conservation strongly suggest the idea that RKD factors are key regulators of female gamete identity and, when mis-expressed, are able to reprogram sporophytic cells into cells with aspects of egg cell identity. Currently, single and double mutants with T-DNA insertions in AtRKD genes are analysed. Using RKD gene promoter deletions and motif mutations, a promoter region was shown to be required for egg cell-specific expression (A. Czihal, M. Mildner). **Transgenic wheat** lines carrying RNAi constructs directed against *TaRKD* have been investigated and suggest an increased abortion rate due to egg cell distortions (D. Köszegi, in collaboration with research group Plant Reproductive Biology). Other focuses are the identification of interacting proteins using yeast two hybrid systems and the identification of downstream target genes of RKD factors using ChIP-on-chip techniques (M. Mildner, D. Köszegi, in collaboration with research group Phytoantibodies). A novel approach concerns the interaction between RKD factors and retinoblastoma-related (RBR) functions (A. Johnston).

Another research focus concerns the regulation of gene expression during late **embryogenesis** (A. Junker). Two experimental approaches for TF gene regulation have been applied: a) TF fusion to the glucocorticoid receptor (GR) domain and b) the estradiol-regulated XVE-system. The regulated subcellular localisation of a *35S::LEC1::GR* gene product leads to impaired growth of transgenic seedlings (see Fig. 34, p. 103), ectopic embryo formation between root and hypocotyl and embryo-like structures on root tips similar to the *pkl* mutant. To isolate downstream gene involved in **LEC1** dependent early embryogenesis induction an array analysis has been performed based on inducible *35S::LEC1::GR* lines (collaboration with J.P. Renou, Evry). In addition ChIP-on-chip experiments using a LEC1-specific antibody have been performed and putative target genes have been identified (A. Junker, in collaboration with research group Phytoantibodies). The results suggest novel phytohormone-mediated functions of LEC1 during embryogenesis and skotomorphogenic growth.

An extensive transcriptome analysis using regulated expression of ABI3, FUS3 and LEC1 was completed; the data analysis is currently ongoing (A. Junker, in collaboration with research group Phytoantibodies and research group Data Inspection). The recently described *Systems Biology Graphical Notation (SBGN)* (LeNovere et al. 2009) has been applied to display the regulatory interactions underlying Arabidopsis seed development and led to the establishment of a corresponding web site (**RIMAS**-Regulatory Interaction Maps of Arabidopsis Seed Development) (A. Junker, in collaboration with research group Plant Bioinformatics).

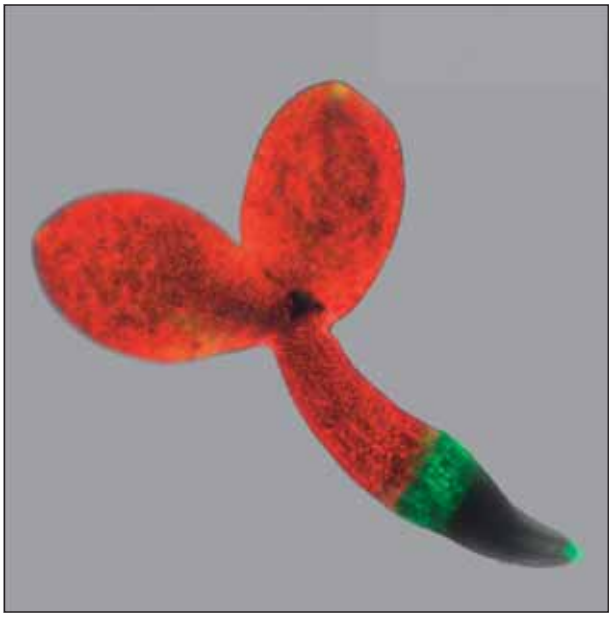

Fig. 34
DR5 Marker-basierte Visualisierung von Auxinmaxima in der Elongationszone (Collet) von LEC1-induzierten embryonalen Keimlingen (A. Junker).

Pollen embryogenesis (POEM) is considered to be a most promising pathway to generate doubled haploid plants suitable for a variety of breeding purposes. During POEM, immature pollen switch their normal microgametophytic development towards an embryogenic pathway. Using 1-30 barley microspores of precisely defined developmental stages, we apply linear mRNA amplification to generate cDNA libraries sufficient for *de novo* sequencing with the Illumina Genome Analyser platform (C. Gryzcka, A. Czihal, collaboration with research group Plant Reproductive Biology).

The molecular analysis of **ET factors** containing an UVRC-like domain putatively involved in gene regulation has been continued and includes the expression in *E. coli,* the hormone-regulated expression in transgenic plants and the characterisation of ET1/ET2 double mutants as a prerequisite for the identification of target genes (Le Hong Diep, A. Junker).
The work on embryonic functions of **BURP proteins** has been concluded and published (Son et al. 2009). A more detailed mutant analysis suggests that BURP proteins are involved in drought stress response and possibly act as an interface between embryogenesis and stress responses (collaboration with research group Seed Development).

Collaborations (selection)

Within the Institute:
Dept. of Cytogenetics and Genome Analysis, Research Group Apomixis; Dr. T. Sharbel;
Dept. of Molecular Genetics, Research Group Phytoantibodies; Dr. U. Conrad, Dr. G. Mönke;
Dept. of Molecular Genetics, Research Group Expression Mapping; Dr. L. Altschmied, Dr. U. Hähnel;
Dept. of Molecular Genetics, Research Group Data Inspection; Dr. M. Strickert, M. Seifert, J. Keilwagen;
Dept. of Physiology and Cell Biology, Research Group Applied Biochemistry; Dr. H.-P. Mock, Dr. A. Matros;
Dept. of Physiology and Cell Biology, Research Group Structural Cell Biology; Dr. M. Melzer, Dr. T. Rutten;
Dept. of Physiology and Cell Biology, Research Group Plant Reproductive Biology; Dr. J. Kumlehn, Dr. I. Saalbach.

Outside the Institute:
Technical University, Brunswick; Dr. R. Hänsch;
Technical University, Brunswick; Prof. L. Beerhues;
University of Regensburg; Prof. Th. Dresselhaus;
University of Göttingen, Göttingen; Dr. W. Dröge-Laser;
University of Zurich, Zurich, Switzerland; Prof. U. Grossniklaus;
INRA, Versailles, France; Prof. M. Caboche, Dr. L. Lepiniec, Dr. B. Debreucq;
INRA, Evry, France; Dr. J.P. Renou.

Publications

Peer Reviewed Papers
2008

Ivanov, R., J. Tiedemann, A. Czihal, A. Schallau, L. Diep, H.-P. Mock, B. Claus, A. Tewes & H. Bäumlein: EFFECTOR OF TRANSCRIPTION2 is involved in xylem differentiation and includes a functional DNA single strand cutting domain. Dev. Biol. 313 (2008) 93-106.

Schallau, A., I. Kakhovskaya, A. Tewes, A. Czihal, J. Tiedemann, M. Mohr, I. Grosse, R. Manteuffel & H. Bäumlein: Phylogenetic footprints in fern spore- and seed-specific gene promoters. Plant J. 53 (2008) 414-424.

Takacs, I., D. Koszegi & B. Barnabas: cDNA library preparation from a single wheat kernel. Acta Biol. Cracov. Bot. 50 (2008) 105-109.

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2009

van Son, L., J. Tiedemann, T. Rutten, S. Hillmer, G. Hinz, T. Zank, R. Manteuffel & H. Bäumlein: The BURP domain protein AtUSPL1 of *Arabidopsis thaliana* is destined to the protein storage vacuoles and overexpression of the cognate gene distorts seed development. Plant Mol. Biol. 71 (2009) 319-329.

Research Group: Phytoantibodies

Head: Dr. Udo Conrad

Scientists

IPK financed
Floß, Doreen, Dr. (0,75 Annex, 01.04.-31.12.2008)
Giersberg, Martin, Dr. (Annex, till 31.07.2009)
Herrmann, Isabella (0,25 Annex, 01.07.-31.12.2009)
Mönke, Gudrun, Dr. (P)
Tran My, Linh (Annex, till 29.02.2008)

Grant Positions
Floß, Doreen, Dr. (0,5 EU, till 31.03.2008)
Hauptmann, Valeska (0,5 Saxony-Anhalt, since 01.11.2008)
Schallau, Kai, Dr. (0,5 Overhead, 01.01.-29.02.2008)

Visiting Scientists/Scholars
Floß, Doreen, Dr. (self-financed, 01.05.-22.05.2009)
Herrmann, Isabella (Martin Luther University Halle-Wittenberg, till 30.06.2009)
Hoang, Phan Trong (DLR, till 31.03.2008; since 29.05.2009)
Huynh, Thi Thu Hue (Biotechnological Institute Hanoi, 05.09.-28.11.2008)
Lubomir, Janda, Dr. (ERASMUS scholarship, 17.11.-12.12.2008)
Tran My, Linh (self-financed, 01.03.-14.03.2008)

Goals

Tissue- and development-specific immunmodulation of phytohormone functions in transgenic plants and molecular analysis of seed development by chromatin IP method with recombinant and classical antibodies for the molecular analysis of seed development as well as production of recombinant fiber proteins and recombinant therapeutic antibodies and vaccines in transgenic plants.

Research Report

Molecular Farming experiments were performed with **recombinant spider silk proteins** to develop new materials for technical and medical purposes in plants. Spider silk proteins with a dimerisation tag were purified from transgenic plants and post-translationally dimerised with bacterial transglutaminase. These proteins have been characterised by atomic force microscopy and atomic force microscopy based nanointendation (V. Hauptmann, F. Junghans, M. Menzel, U. Spohn, IWM Halle). Four different spider silk genes, encoding characteristic repetitive consensus repeats, have been synthesised to combine these different genes on a genetic base in a variable number. One repeat of FLAG, MASPII and SO1 protein has been produced in transgenic tobacco plants (V. Hauptmann).
The **tumour necrosis factor-alpha** (TNFα) plays an important role in a number of chronic inflammatory disorders. A strategy to obtain **functional dimeric anti-TNF-V_HH molecules**, based on the C-terminal fusion of a k light chain domain to the anti-TNF-V_HH has been devloped. The resulting fusion protein was transiently expressed in tobacco leaves and purified. Competitive ELISA and cell cytotoxicity assays revealed that the **dimerised anti-TNF-$V_HH_{Cκ}$ proteins** blocked **TNFα-activity more effectively** than either the monomeric *Escherichia coli* produced anti-TNF-V_HH or the monomeric anti-TNF-V_HH_{Ck} was able to. We suggest that **enhanced inhibition** shown by **dimeric anti-TNF-$V_HH_{Cκ}$** proteins is achieved by **an increase in avidity** (M. Giersberg, U. Conrad, D. Floß, J. Scheller, Christian-Albrechts-University at Kiel). The anti-TNF-V_HH has been further engineered for prolonged serum half-life as well as for optimal biomanufacturing in a plant protein expression system. The antibody component (TNF-V_HH) was linked to an elastin-like polypeptide (ELP). We demonstrate that **ELP fusion to the TNF-V_HH enhances accumulation** of the fusion protein during biomanufacturing in transgenic tobacco plants. With this study, we showed for the first time that this plant-derived anti-human TNF-V_HH antibody was biologically active *in vivo*. Therefore, **therapeutic application of TNF-V_HH_{ELP}** was tested in humanised TNF mice, and was shown to be **effective in preventing death due to septic shock**. The ***in vivo* persistence** of the **ELPylated antibody** was **~20 fold longer** than that of non-ELPylated TNF-V_HH (U. Conrad, I. Plagmann, S. Malchow, D. Floß, J. Scheller, Christian-Albrechts-University at Kiel, A.A. Kruglov, S. Nedospasov, German Rheumatism Research Center Berlin, M. Sack, RWTH Aachen). Further work is dealing with the use of ELP to overexpress and to partly purify antigens for vaccination from transgenic plants. 13 mg **TB fusion antigens with ELP** have been produced in transgenic tobacco plants and purified via an optimised ITC (inverse transition cycling) procedure and size exlusion chromatography. An immunisation experiment with a mouse model has been started (U. Conrad, in collaboration with D. Floß, Christian-Albrechts-University at Kiel, Ch. Hölscher, Leibniz-Zentrum Borstel). Different antigens from the **bird flu virus H5N1** (haemagglutinin, neuraminidase, matrix protein) with and without ELP have been stably expressed in tobacco leaves and seeds. ITC has been optimised for the haemagglutinin-ELP fusion. ScFv and VH against haemagglutinin and matrix protein have been identified and characterised (Phan Trong Hoang, U. Conrad).

In *Arabidopsis thaliana* the seed-specific transcription factor ABI3 is a key regulator of seed maturation. By **ChIP-chip technology** several target genes of ABI3 were identified and verified by transient GUS-activation assay. Based on the analysis of the promoter architecture und expression profile of these target genes further **genome-wide candidate genes of the ABI3-regulon** were predicted. The prediction was proven by qRT-PCR analysis of transcripts using an **ABI3::GR inducible system**. Many genes were identified to be regulated by ABI3 (G. Mönke, in collaboration with L. Altschmied, Expression Mapping group).
New **synthetic Phage Display Libraries** based on **cameloid VHH** were constructed and tested by screening against different antigens (M. Giersberg, U. Conrad).

Collaborations (selection)

Within the Institute:
Dept. of Cytogenetics and Genome Analysis, Research Group Chromosome Structure and Function; Dr. A. Houben;
Dept. of Molecular Genetics, Research Group Seed Development; Dr. W. Weschke;
Dept. of Molecular Genetics, Research Group Gene Regulation; Dr. H. Bäumlein;
Dept. of Molecular Genetics, Research Group Expression Mapping; Dr. L. Altschmied;
Dept. of Molecular Genetics, Research Group Data Inspection; M. Seifert;
Dept. of Physiology and Cell Biology, Research Group Plant Reproductive Biology; Dr. J. Kumlehn.

Outside the Institute:
Martin Luther University Halle-Wittenberg, Institute of Pharmaceutical Biology, Halle/Saale; Prof. W. Roos;
IWM, Halle/Saale; Dr. U. Spohn;
Leibniz-Zentrum Borstel; Dr. C. Hölscher;
RWTH, Aachen; Dr. E. Stöger, M. Sack;
Fraunhofer IME, Aachen; Dr. S. Schillberg;
BOKU, Vienna, Austria; Prof. E. Stöger;
VTT Helsinki, Finland; Dr. J. Joentsuu;
IBT, Hanoi, Vietnam; Prof. Le Tran Binh.

Publications

Peer Reviewed Papers
2008
Floss, D.M., M. Sack, J. Stadlmann, T. Rademacher, J. Scheller, E. Stöger, R. Fischer & U. Conrad: Biochemical and functional characterisation of anti-HIV antibody-ELP fusion proteins from transgenic plants. Plant Biotechnol. J. 6 (2008) 379-391.

Frutos, R., H. Denise, C. Vivares, J.M. Neuhaus, S. Vitale, E. Pedrazzini, J. Ma, P. Dix, J. Gray, M. Pezzotti, U. Conrad & D. Robinson: Pharmaceutical proteins in plants: a strategic genetic engineering approach for the production of tuberculosis antigens. Ann. N. Y. Acad. Sci. 1149 (2008) 275-280.

Irons, S.L., J. Nuttall, D.M. Floss, L. Frigerio, A.M. Kotzer & C. Hawes: Fluorescent protein fusions to a human immunodeficiency virus monoclonal antibody reveal its intracellular transport through the plant endomembrane system. Plant Biotechnol. J. 6 (2008) 649-662.

Tiedemann, J., T. Rutten, G. Mönke, A. Vorwieger, H. Rolletschek, D. Meissner, C. Milkowski, S. Petereck, H.-P. Mock, T. Zank & H. Bäumlein: Dissection of a complex seed phenotype: novel insights of *FUSCA3* regulated developmental processes. Dev. Biol. 317 (2008) 1-12.

Urakami, E., I. Yamaguchi, T. Asami, U. Conrad & Y. Suzuki: Immunomodulation of gibberellin biosynthesis using an anti-precursor gibberellin antibody confers gibberellin-deficient phenotypes. Planta 228 (2008) 863-873.

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Floss, D.M., M. Sack, E. Arcalis, J. Stadlmann, H. Quendler, T. Rademacher, E. Stoger, J. Scheller, R. Fischer & U. Conrad: Influence of elastin-like peptide fusions on the quantity and quality of a tobacco-derived human immunodeficiency virus-neutralizing antibody. Plant Biotechnol. J. 7 (2009) 899-913.

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Zimmermann, J., I. Saalbach, D. Jahn, M. Giersberg, S. Haehnel, J. Wedel, J. Macek, K. Zoufal, G. Glünder, D. Falkenburg & S.M. Kiprijanov: Antibody expressing pea seeds as fodder for prevention of gastrointestinal parasitic infections in chickens. BMC Biotechnol. 9 (2009) 79.

Books and Book Chapters
2009
Gahrtz, M. & U. Conrad: Immunomodulation of plant function by *in vitro* selected single-chain Fv intrabodies. In: Faye, L. & V. Gomord (Eds.): Recombinant pharmaceutical proteins from plants. Methods and protocols. Meth. Mol. Biol. 483, Humana Press, New York/USA (2009) 289-312.

Research Group: Expression Mapping

Head: Dr. Lothar Altschmied

Scientists

IPK financed
Hähnel, Urs, Dr. (P, till 31.03.2008)
Witkowicz, Justyna, Dr. (P, since 15.07.2008)
Zierold, Annchristin (0,5/0,25 Annex, till 31.07.2008)

Visiting Scientists/Scholars
Hähnel, Urs, Dr. (Julius Kühn-Institute, Quedlinburg, since 01.04.2008)

Goals

Characterisation of genes and their regulation, which are involved in female reproductive development in Triticeae, *Arabidopsis*, and *Hypericum*. Analysis of promoter structure and transcription factors responsible for seed-specific gene expression.

Research Report

cDNA sequences of clones selected by subtractive hybridisation from **sexual and parthenogenetic egg cell** libraries of "Salmon" wheat had indicated an almost completely **different expression programme** for both egg cell types. Hybridisation of 20 different cDNA clones with 18,000 cDNA clones from each library confirmed this difference in the unselected library (L. Altschmied). In co-operation with D. Köszegi (Gene Regulation group) and J. Kumlehn (Plant Reproductive Biology group) we attempted to prove this expression difference by single cell RT-PCR on sexual and parthenogenetic egg cells, but failed, since parthenogenetic egg cells could not be isolated in sufficient quantity. Two genes available as full-length cDNA clones (L. Altschmied) could be shown to be expressed specifically in sexual egg cells (D. Köszegi, Gene Regulation group).

Genes from these wheat egg-cell libraries, which do not show significant sequence homology to *Arabidopsis* proteins or which show undistinguishable homologies to various members of a gene family were identified. A **pool of 60 cDNA clones** was hybridised to 83,000 gene containing BAC clones of barley (L. Altschmied) spotted on a set of two high-density colony membranes (R. Ariyadasa, Genome Diversity group). 119 positive BAC clones were identified and hybridised with the 60 cDNA clones individually. 25 cDNA probes gave reliable signals on 103 of these BAC clones, which map to 31 contigs defined by fingerprinting (D. Schulte, Genome Diversity group). Four BACs overlapping the gene-location within the respective contig had been sequenced and assembled (B. Steuernagel, Bioinformatics and Information Technology group). Three of them contain sequences similar to the cDNA probe and await gene annotation. **14 BACs which represent 13 genes will be sequenced** within the current barley sequencing programme run by N. Stein and D. Schulte (Genome Diversity group).

In cooperation with A. Schallau (Gene Regulation group) a BAC clone of approx. 140 kbp containing the sexual allele of at least a **part of the apomeiosis locus of *Hypericum perforatum* has been identified, sequenced, and assembled completely** (U. Hähnel).

Chromatin immuno-precipitation experiments were performed to identify binding sites of the transcription factor ABI3, a master regulator of seed development in *Arabidopsis thaliana*. On a nylon array with almost 12,000 intergenic regions (U. Hähnel), 37 genomic regions containing 51 promoters were identified (M. Seifert, Data Inspection group), which were enriched by immuno-precipitation with an antiABI3-antibody (G. Mönke, Phytoantibodies group). To distinguish binding from activation, especially for intergenic regions containing two divergent promoters, 32 promoters were cloned in front of a GUS reporter (G. Mönke, Phytoantibodies group; U. Hähnel) and tested for activation in transiently transformed *Arabidopsis* protoplasts (G. Mönke, Phytoantibodies group). **21 ABI3 activated promoters were enriched for ABRE- and RY-like sequence motifs** (see Fig. 35, p. 108). Regulatory models with ABI3 binding to RY-like motifs and one or more hypothetical bZIP trancription factors binding to ABRE-like motifs (G. Mönke, Phytoantibodies; L. Altschmied) were tested using *Arabidopsis* promoters obtained by genome-wide classification (L. Altschmied). For that purpose, more than 120 promoters were analyzed by qRT-PCR (G. Mönke, Phytoantibodies) in seedlings of a transgenic *Arabidopsis* line carrying an ABI3 gene fused to a glucocorticoid receptor domain (A. Junker, Gene Regulation group). This system allows controlled activation of ABI3 and synthesis of a required bZIP factor by an independent inducer. These tests demonstrate, that **ABI3 target promoters in *Arabidopsis* can be predicted** with high confidence by their combination of sequence motifs and an additional parameter most likely dependent on the general sequence context (L. Altschmied). Three bZIP transcription factors predicted to co-operate with ABI3 (L. Altschmied) were tested on several ABI3 target promoters in transiently transformed protoplasts (A. Kretzschmar, G. Mönke, Phytoantibodies group) and confirmed to participate in regulation.

Similar investigations in monocot crops, such as barley, require knowledge of the respective transcription factor families. For that reason barley cDNA clones with homology to transcription factors of rice were selected from the available EST collections, re-sequenced, pooled, and hybridised with BAC clones gridded at high density (L. Altschmied). A pool of **27 cDNAs representing the AUX/IAA and ARF families** yielded 169 BAC clones and a pool of **56 cDNAs representing the bZIP and Myb families** identified 487 BAC clones. These BACs were collected, spotted, and hybridised with inserts of individual cDNA clones. Hybridisation with a transcription factor cDNA could be confirmed for 547 BAC clones. 430 BACs for 74 different cDNA probes reside in 148 contigs defined by fingerprinting (D. Schulte, Genome Diversity group). 13 BAC clones had been sequenced already (D. Schulte, N. Stein, Genome Diversity group) and their assembled sequences (B. Steuernagel, Bioinformatics and Information Technology group) contain regions of high homology with the respective transcription factor cDNA in 11 cases (L. Altschmied). 32 additional BAC clones will be sequenced in the near future (D. Schulte, N. Stein, Genome Diversity group).

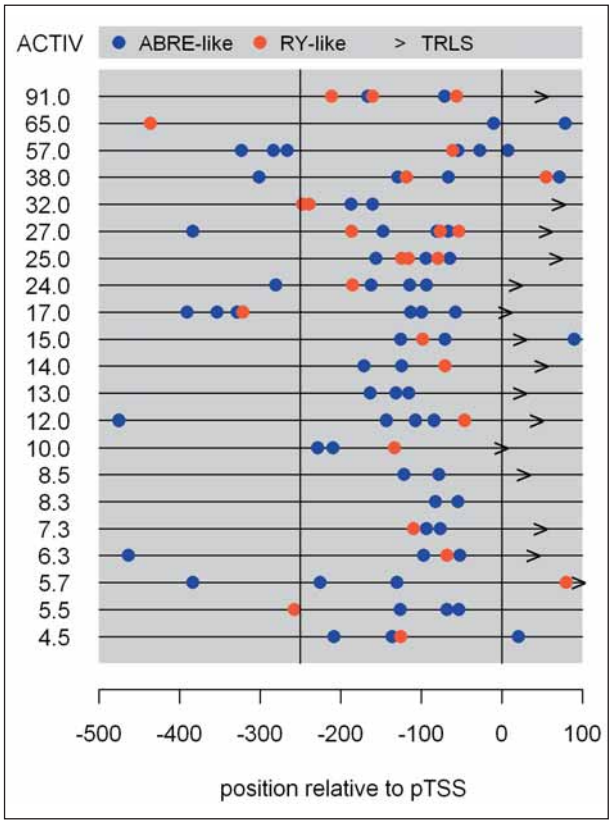

Fig. 35
Sequence motifs in 21 promoter regions of *Arabidopsis*, which were enriched by chromatin immuno-precipitation and activated by the B3-domain transcription factor ABI3 in transiently transformed protoplasts (G. Mönke, Phytoantibodies group; M. Seifert, Data Inspection group; U. Hähnel, L. Altschmied). 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.

Collaborations (selection)

Within the Institute:
Dept. of Genebank, Research Group Genome Diversity; Dr. R. Ariyadasa, Dr. D. Schulte, Dr. N. Stein;
Dept. of Cytogenetics and Genome Analysis, Research Group Transcriptome Analysis; Dr. P. Schweizer, Dr. A. Himmelbach, S. König;
Dept. of Cytogenetics and Genome Analysis, Research Group Bioinformatics and Information Technology; Dr. U. Scholz;
Dept. of Molecular Genetics, Research Group Heterosis; Prof. T. Altmann, Dr. M. Müller, Dr. R. Meyer;
Dept. of Molecular Genetics, Research Group Gene Regulation; Dr. H. Bäumlein, A. Czihal, D. Köszegi;
Dept. of Molecular Genetics, Research Group Phytoantibodies; Dr. U. Conrad, Dr. G. Mönke;
Dept. of Molecular Genetics, Research Group Data Inspection; M. Seifert, J. Keilwagen;
Dept. of Physiology and Cell Biology, Research Group Plant Reproductive Biology; Dr. J. Kumlehn, R. Paride.

Outside the Institute:
Friedrich Schiller University, Institute of General Botany, Jena; Dr. C. Milkowski;
University of Bielefeld, Institute for Genome Research, Bielefeld; Prof. B. Weisshaar, Dr. P. Viehöver;
INRA, Laboratoire de Biologie des Semences, Versailles, France; Dr. B. Dubreucq, Dr. C. Rochat, Dr. M. Miquel, Dr. L. Lepiniec, Prof. M. Caboche;
ETSI Agronomos, Dept. of Biotechnology, Madrid, Spain; Dr. I. Diaz, Dr. V. Carbajosa;
University of Zurich, Institute of Plant Biology, Zurich, Switzerland; Prof. U. Grossniklaus, A.J. Johnston;
ETH Zurich, Plant Biotechnology, Zurich, Switzerland; Dr. P. Zimmermann.

Research Group: Plant Bioinformatics

Head: Prof. Falk Schreiber

Scientists

IPK financed
Czauderna, Tobias (1,0 /0,75 Annex, 01.03.2008-23.01.2009)
Grafahrend-Belau, Eva (0,75 Annex, 01.01.-30.06.2008)
Ihlow, Alexander, Dr. (Annex, 01.03.-31.03.2008)
Klukas, Christian, Dr. (Annex, 01.01.-29.02.2008, P, since 01.03.2008)
Koschützki, Dirk, Prof. (P, till 29.02.2008)
Schallau, Kai, Dr. (0,25/0,75 Annex, 01.03.-30.06.2008)

Grant Positions
Bollenbeck, Felix (BMBF, 01.03.-30.09.2008)
Czauderna, Tobias (BMBF, since 01.02.2009)
Grafahrend-Belau, Eva (BMBF, since 01.07.2008)
Hartmann, Anja (BMBF, since 15.08.2009)
Hippe, Klaus (BMBF, 01.06.-30.06.2009; Industry, 01.07.-31.12.2009)
Ihlow, Alexander, Dr. (Overhead, 01.04.-31.05.2008)
Junker, Astrid, Dr. (BMBF, since 01.07.2009)
Mehlhorn, Hendrik (BMBF, since 01.03.2009)
Pielot, Rainer, Dr. (DFG, 01.03.-31.12.2008)
Rohn, Hendrik (BMBF, since 01.05.2008)

Visiting Scientists/Scholars
Czauderna, Tobias (self-financed, 24.01.-31.01.2009)
Koschützki, Dirk, Prof. (University of Furtwangen/self-financed, 01.03.2008-01.03.2009)
Pielot, Rainer, Dr. (self-financed, 01.01.-30.06.2009)
Schwöbbermeyer, Henning (self-financed, till 31.12.2008)

Goals

Representation, modelling, analysis and visualisation of biological networks and related multimodal and multidimensional data in their spatial and temporal embedding.

Research Report

We continued the development of methods for analysing experimental data in context of biological networks and classification hierarchies and their implementation in the open source software system **VANTED** (C. Klukas). Novel methods allow easy visual data exploration and statistical functions support filter operations, e.g., to identify over-representation of significantly expressed genes in pathways. Furthermore, VANTED has been extended to support add-ons, software components that can be loaded at runtime and provide new programme functionality and database access. VANTED has been used in several in-house and external collaborations, e.g., with the research groups Apomixis and Plant Reproductive Biology to investigate *Boechera holboellii*, the research group Applied Biochemistry to analyse pathways in *Beta vulgaris* and the research group Heterosis to investigate *Brassica napus*.

Based on VANTED, a novel **platform for spatial, structural and kinetic models** has been developed with users from the research group Heterosis and applied to barley seed metabolism (H. Rohn). It allows integration of experimental data from several domains and spatial information such as 2D and 3D data (e.g. derived from NMR imaging). Data from these domains (*omics, networks, images and volumes) can be mapped onto each other, resulting in a unique combination providing novel insight into biological systems. For the 3D visualisation of data and mappings a volume rendering algorithm has been implemented in Java3D allowing rendering volumetric data, surface models, images and networks at the same time.

The development of the **MetaCrop information system** for metabolic pathway information has been continued in collaboration with the research group Bioinformatics and Information Technology. For example, new features of MetaCrop are an interoperable, open and flexible service-oriented architecture, which is realised with web services and a MetaCrop add-on, which enables the user to access all MetaCrop functionalities and data in VANTED (K. Hippe). Based on an intensive survey of scientific literature and online databases, the **content of MetaCrop** has been extended by three model and crop plants (*Arabidopsis thaliana*, *Medicago truncatula* and *Beta vulgaris*) and further metabolic pathways of primary metabolism (e.g., photosynthesis and lipid degradation) of different species (E. Grafahrend-Belau, A. Hartmann, A. Junker).

Information in MetaCrop is the basis for **stoichiometric models**, and a stoichiometric, compartmented model of primary metabolism in the developing endosperm of *Hordeum vulgare* has been constructed. The model provides a framework for studying cereal seed storage metabolism *in silico* and was subjected to flux balance analysis (FBA) to study grain yield and metabolic flux distributions in response to environmental conditions and genetic backgrounds. Additionally, to provide an interactive, visual analysis of FBA results the VANTED add-on *FBASimVis* was implemented (E. Grafahrend-Belau, see Fig. 36, p. 110). In collaboration with the research group Systems Biology **multiscale modelling of metabolism** combining different modelling approaches has been started, and together with the RGs Systems Biology and Bioinformatics and Information Technology

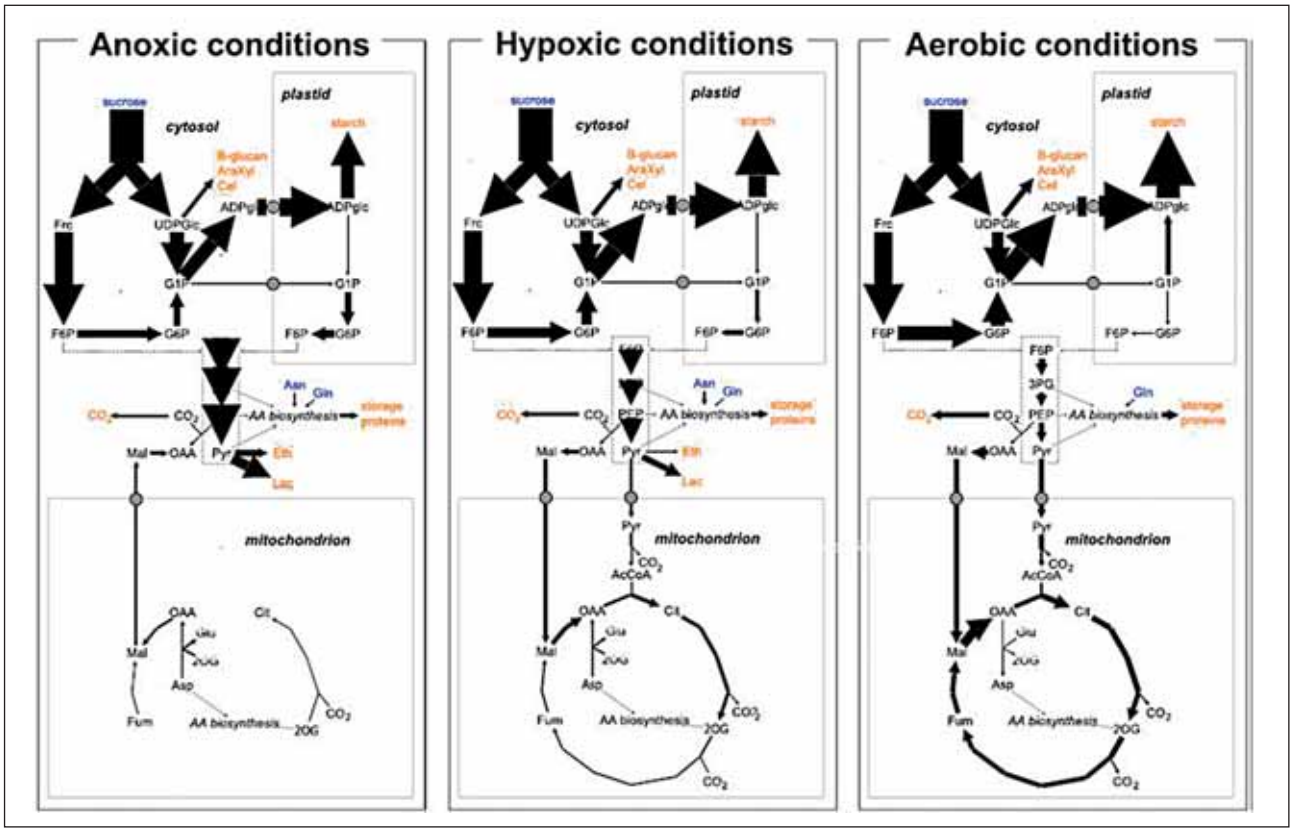

Fig. 36
Carbon flux maps generated by FBASimVis which depict the key uptake/excretion rates and fluxes within central metabolism of the developing endosperm of barley under anoxic conditions (A), hypoxic conditions (B), and aerobic conditions (C) (E. Grafahrend-Belau).

an **integration and analysis pipeline for systems biology** in crop plant metabolism has been established.
The **DBE2 information system** for managing biological experiment data has been derived from DBE (H. Mehlhorn). It provides persistent data storage and the opportunity to access, save, load and modify the data worldwide. The database schema, a web service, and a VANTED add-on were implemented. In addition the **OlsUpdater** tool was developed. It allows the automated update of the local ols database schema which provides various ontologies that will be used by several programmes (such as the LIMS light system) in the institute.

In an international collaboration with various partners we were involved in the development of the **Systems Biology Graphical Notation (SBGN)** representing an agreed-upon convention for the display and handling of biological networks. Several **tools and resources** were established in the group which will facilitate and exemplify the use of SBGN. The VANTED system has been extended to support the emerging standard for drawing biochemical pathways using SBGN (C. Klukas). A VANTED add-on (SBGN-ED) has been developed which allows creating and editing all three types of SBGN maps, validating their syntactical and semantical correctness and translating already existing non-SBGN diagrams from KEGG and MetaCrop automatically into SBGN (T. Czauderna).

RIMAS was developed as a web-based information portal which provides a comprehensive regularly updated overview of regulatory pathways and genetic interactions during *Arabidopsis* embryo and seed development (A. Junker). The RIMAS service provides access to standardised (SBGN) network maps, linked literature databases and possibilities to export maps in common exchange formats for modifying them according to individual purposes and further application using tools, e.g. VANTED.
For the non-destructive high-throughput phenotyping system LemnaTec we developed in collaboration with the research group Genome Diversity an **image analysis pipeline** implemented as a plug-in for ImageJ to improve colour image analysis of barley plants and compute several phenotypic parameters such as plant height, plant width and leaf area (A. Hartmann). The results of the analysis can be used to derive biological insights in current projects such as drought stress during plant development.
Several novel **algorithms for structural network analysis and automatic network layout** have been developed in collaboration with external partners and have been/are currently implemented in tools such as VANTED (D. Koschützki, T. Czauderna, C. Klukas). These methods have been successfully applied to biological questions such as the identification of key regulators in *E. coli* and the visual analysis of integrated networks (e.g. integration

of metabolic and protein interaction networks). Highly efficient **algorithms using parallel architectures** such as the Cell processor or GPGPUs for multimodal alignment (R. Pielot) and in collaboration with the research group Data Inspection for several bioinformatics analysis and visualisation methods have been developed.

Collaborations (selection)

Within the Institute:
Dept. of Genebank, Research Group Genome Diversity; Dr. N. Stein;
Dept. of Genebank, Research Group Genebank Documentation; Dr. H. Knüpffer;
Dept. of Cytogenetics and Genome Analysis, Research Group Chromosome Structure and Function; Dr. A. Houben, A.M. Banaei;
Dept. of Cytogenetics and Genome Analysis, Research Group Apomixis; Dr. T. Sharbel;
Dept. of Cytogenetics and Genome Analysis, Research Group Bioinformatics and Information Technology; Dr. U. Scholz, Dr. M. Lange, S. Weise;
Dept. of Molecular Genetics, Research Group Heterosis; Prof. T. Altmann, Dr. L. Borisjuk, Dr. H. Rolletschek;
Dept. of Molecular Genetics, Research Group Seed Development; Dr. W. Weschke, Dr. V. Radchuk, Dr. J. Thiel;
Dept. of Molecular Genetics, Research Group Gene Regulation; Dr. H. Bäumlein;
Dept. of Molecular Genetics, Research Group Data Inspection; Dr. M. Strickert;
Dept. of Physiology and Cell Biology, Research Group Molecular Plant Nutrition; Dr. M. Hajirezaei;
Dept. of Physiology and Cell Biology, Research Group Applied Biochemistry; Dr. H.-P. Mock, Dr. K. Witzel;
Dept. of Physiology and Cell Biology, Research Group Plant Reproductive Biology; Dr. J. Kumlehn, Dr. G. Hensel, S. Goedeke;
Dept. of Physiology and Cell Biology, Research Group Systems Biology; Dr. B.H. Junker.

Outside the Institute:
SunGene Gatersleben; Dr. R. Lemke, Dr. R. Wünschiers;
Martin Luther University Halle-Wittenberg, Halle/Saale; Prof. T. Hollemann, Prof. R. Horstkorte, Prof. J. Müller, Prof. S. Posch, Prof. A. Simm, Prof. W. Zimmermann;
Leibniz Institute for Neurobiology, Magdeburg; Dr. R. Pielot;
Humboldt University, Berlin; Dr. K.P. Götz, Dr. R. Steuer;
Technical University of Applied Sciences, Berlin; Prof. I. Koch;
Max Planck Institute for Molecular Plant Physiology, Dept. Metabolic Networks, Golm; Dr. B. Usadel;
University of Bielefeld, Research Group Bioinformatics/Medical Informatics, Bielefeld; Prof. R. Hofestädt;
University of Düsseldorf, Division of Biology, Düsseldorf; Prof. A. Weber, Dr. A. Bräutigam;
Friedrich Alexander University Erlangen-Nürnberg, Institute of Biology, Erlangen; Prof. U. Sonnewald;
University of Passau, Faculty of Mathematics and Informatics, Passau; Prof. F.J. Brandenburg, Dr. C. Bachmaier;
University of Sydney, Sydney, Australia; Prof. P. Eades, Prof. S. Hong;
Växjö University, School of Mathematics and Systems Engineering, Växjö, Sweden; Prof. A. Kerren;
Teheran University, Teheran, Iran; Prof. A. Masoudi Nejad;
Monash University, Melbourne, Australia; Dr. T. Dwyer, Prof. K. Marriot, Dr. M. Wybrow.

Publications

Peer Reviewed Papers
2008
Dwyer, T., K. Marriott, F. Schreiber, P. Stuckey, M. Woodward & M. Wybrow: Exploration of networks using overview+detail with constraint-based cooperative layout. IEEE Trans. Vis. Comput. Graph 14 (2008) 1293-1300.

Fung, D.C.Y., S.-H. Hong, D. Koschützki, F. Schreiber & K. Xu: 2.5D visualisation of overlapping biological networks. J. Integr. Bioinformatics 5 (2008) 90.

Grafahrend-Belau, E., F. Schreiber, M. Heiner, A. Sackmann, B.H. Junker, S. Grunwald, A. Speer, K. Winder & I. Koch: Modularization of biochemical networks based on classification of Petri net t-invariants. BMC Bioinformatics 9 (2008) 90.

Grafahrend-Belau, E., S. Weise, D. Koschützki, U. Scholz, B.H. Junker & F. Schreiber: MetaCrop: a detailed database of crop plant metabolism. Nucleic Acids Res. 36 (2008) D954-D958.

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Schreiber, F.: Visualization. Methods Mol. Biol. 453 (2008) 441-450.

Thiel, J., D. Weier, N. Sreenivasulu, M. Strickert, N. Weichert, M. Melzer, T. Czauderna, U. Wobus, H. Weber & W. Weschke: Different hormonal regulation of cellular differentiation and function in nucellar projection and endosperm transfer cells - a microdissection-based transcriptome study of young barley grains. Plant Physiol. 148 (2008) 1436-1452.

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del Rio, G., D. Koschützki & G. Coello: How to identify essential genes from molecular networks? BMC Syst. Biol. 3 (2009) 102.

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approach to study systemic properties of central metabolism. Plant Physiol. 149 (2009) 585-598.

Kashani, Z.R., H. Ahrabian, E. Elahi, A. Nowzari-Dalini, E.S. Ansari, S. Asadi, S. Mohammadi, F. Schreiber & A. Masoudi-Nejad: Kavosh: a new algorithm for finding network motifs. BMC Bioinformatics 10 (2009) 318.

Le Novere, N., M. Hucka, H. Mi, S. Moodie, F. Schreiber, A. Sorokin, E. Demir, K. Wegner, M.I. Aladjem, S.M. Wimalaratne, F.T. Bergman, R. Gauges, P. Ghazal, H. Kawaji, L. Li, Y. Matsuoka, A. Villeger, S.E. Boyd, L. Calzone, M. Courtot, U. Dogrusoz, T.C. Freeman, A. Funahashi, S. Ghosh, A. Jouraku, S. Kim, F. Kolpakov, A. Luna, S. Sahle, E. Schmidt, S. Watterson, G. Wu, I. Goryanin, D.B. Kell, C. Sander, H. Sauro, J.L. Snoep, K. Kohn & H. Kitano: The Systems Biology Graphical Notation. Nat. Biotechnol. 27 (2009) 735-741.

Schreiber, F.: Analyse und Visualisierung biologischer Netzwerke. Informatik Spektrum 32 (2009) 301-309.

Schreiber, F., T. Dwyer, K. Marriott & M. Wybrow: A generic algorithm for layout of biological networks. BMC Bioinformatics 10 (2009) 375.

Books and Book Chapters

2008

Hofestädt, R., J. Köhler, M. Lange, U. Scholz, F. Schreiber & P. Verrier (Eds.): Integrative Bioinformatics: Proceedings of the 5th International Symposium on Integrative Bioinformatics 2008. IMBio (2008) 345 pp.

Junker, B.H. & F. Schreiber (Eds.): Analysis of biological networks. Wiley Book Series on Bioinformatics: Computational techniques and engineering, John Wiley & Sons, Hoboken, NJ/USA (2008) 368 pp.

Koschützki, D.: Network centralities. In: Junker, B.H. & F. Schreiber (Eds.): Analysis of biological networks. Wiley Book Series on Bioinformatics, John Wiley & Sons, Hoboken, NJ/USA (2008) 65-84.

Schreiber, F.: Graph theory. In: Junker, B.H. & F. Schreiber (Eds.): Analysis of biological networks. Wiley Book Series on Bioinformatics, John Wiley & Sons, Hoboken, NJ/USA (2008) 15-28.

Schwöbbermeyer, H.: Network motifs. In: Junker, B.H. & F. Schreiber (Eds.): Analysis of biological networks. Wiley Book Series on Bioinformatics, John Wiley & Sons, Hoboken, NJ/USA (2008) 85-111.

2009

Fester, T., F. Schreiber & M. Strickert: CUDA-based multi-core implementation of MDS-based bioinformatics algorithms. Proc. Ger. Conf. Bioinform. (GCB09), Lect. Notes Inform. 157 (2009) 67-79.

Grafahrend-Belau, E., B.H. Junker, C. Klukas, D. Koschützki, F. Schreiber & H. Schwöbbemeyer: Topology of plant metabolic networks. In: Schwender, J. (Ed.): Plant Metabolic Networks. Springer, New York (2009) 173-209.

Kormeier, B., K. Hippe, T. Töpel & R. Hofestädt: CardioVINEdb: a data warehouse approach for integration of life science data in cardiovascular diseases. In: Fischer, S., E. Maehle & R. Reischuk (Eds.): INFORMATIK 2009, Lect. Notes Inform. P-154 (2009) 704-708.

Rohn, H., C. Klukas & F. Schreiber: Integration and visualisation of multimodal biological data. Proc. German Conf. Bioinformatics (GCB09), Lect. Notes Inform. 157 (2009) 105-115.

Weise, S., C. Colmsee, E. Grafahrend-Belau, B. Junker, C. Klukas, M. Lange, U. Scholz & F. Schreiber: An integration and analysis pipeline for systems biology in crop plant metabolism. Proc. Int. Workshop "Data Integr. Life Sci." (DILS'09), Lect. Notes Bioinform. 5647 (2009) 196-203.

Weise, S., C. Colmsee, E. Grafahrend-Belau, B. Junker, C. Klukas, M. Lange, U. Scholz & F. Schreiber: Datenaustausch und Datenintegration zur Modellierung und Analyse metabolischer Netzwerke am Beispiel von Kulturpflanzen. In: Fischer, S., E. Maehle & R. Reischuk (Eds.): INFORMATIK 2009, Lect. Notes Inform. P-154 (2009) 693-697.

Wheelock, C.E., S. Goto, L. Yetukuri, F.L. D'Alexandri, C. Klukas, F. Schreiber & M. Oresic: Bioinformatics strategies for the analysis of lipids. In: Armstrong, D. (Ed.): Lipidomics, Vol. 2 (Methods Mol. Biol. 580). Humana Press, Totowa/USA (2009) 339-368.

Research Group: Data Inspection

Head: Dr. Marc Strickert

Scientists

IPK financed
Friedel, Svetlana, Dr. (Annex, since 15.12.2009)

Grant Positions
Haldemann, Berit (0,25 Saxony-Anhalt, 01.10.-31.12.2008)
Keilwagen, Jens (Saxony-Anhalt)
Seifert, Michael (Saxony-Anhalt)

Visiting Scientists/Scholars
Soto, Axel (BMBF, 05.08.-03.09.2009)
Vazquez, Gustavo, Dr. (BMBF, 31.03.-21.04.2009)

Goals

Processing and statistical analysis of massive array data and DNA sequences using probabilistic and data-driven computer models.

Research Report

A large number of gene expression data sets was analysed ranging from macroarray technology to microarray technology including Affymetrix, Agilent and NimbleGen, and also protein data from 2D gels was analysed. Typical tasks were related to the preprocessing and normalisation of raw data files and to the clustering and **identification of differentially expressed genes and proteins** from temporal and stress related experiment designs. In addition to standard approaches new methods were developed for overcoming some existing limitations. For example, the restrictions of linear and variance-based principal component projections were addressed by improving a multidimensional scaling approach for massive data sets, thereby utilising highly parallel computer graphics hardware. For data labelled by their experimental condition a new type of linear projection method was established to further improve the label-specific separation by the optimisation of a robust discriminant function that allows the identification of specifically regulated genes and proteins as well as the tentative derivation of network information. Collaborations in this area comprise analyses of drought stressed barley introgression lines together with their parents 'Brenda' and HS584, barley lines from KWS Lochow (GABI GRAIN, N. Sreenivasulu), HOSUT transgenics of wheat (H. Weber, W. Weschke), salt stressed plant proteome of Steptoe and Morex barley lines (H.-P. Mock) and trichome gene expression data of *Nicotiana tabacum* (H.-P. Mock, M. Strickert).

The area of **computational genome comparison and epigenetics** is addressed by using the Array-CGH and the ChIP-chip technology in combination with the genome annotation available for *Arabidopsis thaliana* (A. Banaei, A. Houben, M.F. Mette). By exploiting correlations between adjacent probes on the chromosomes, refined models for comparative genome analysis of different ecotypes of *Arabidopsis* were created based on extensions and adaptations of Hidden Markov Models (HMMs). Based on this, polymorphic regions in the ecotypes C24 and Cvi have been identified in relation to the reference genome of ecotype Col. The mapping of polymorphic regions to the TAIR8 genome annotation of Col revealed a strong implication of transposable elements. These findings are currently complemented by array-based chromatin immunoprecipiation (ChIP-chip) experiments by studying the distribution of specific histone marks in C24, Cvi, Col, and their hybrid offsprings. Higher order correlations in sequential hybridisation data and characteristic correlation modes in different partitions of chromosomal distances are currently integrated into extended HMMs in order to further improve the data analysis (M. Seifert).

In the domain of **DNA sequence analysis** the research group contributed to two important fields. On the one hand, important theoretical results including an improved learning of statistical models were obtained that step from widely used plain representation models of functional motifs to active discrimination models. The new formalisms are made available in the open-source Java framework Jstacs (http://www.jstacs.de/) in cooperation with the Martin Luther University Halle-Wittenberg. On the other hand, these results have been used to build better computational tools for the prediction of transcription factor binding sites. One of these tools, called MotifAdjuster, is related to the automatic curation of sequence databases of transcription factor binding sites, where entries can be proposed for removal, shift, and switch of strand annotations (see Fig. 37, p. 114). Another tool improves the *de novo* motif discovery and classification of functionally relevant DNA sites. This tool is developed for the identification of transcription factor binding sites in the genome of *Arabidopsis thaliana* at the IPK (J. Keilwagen).

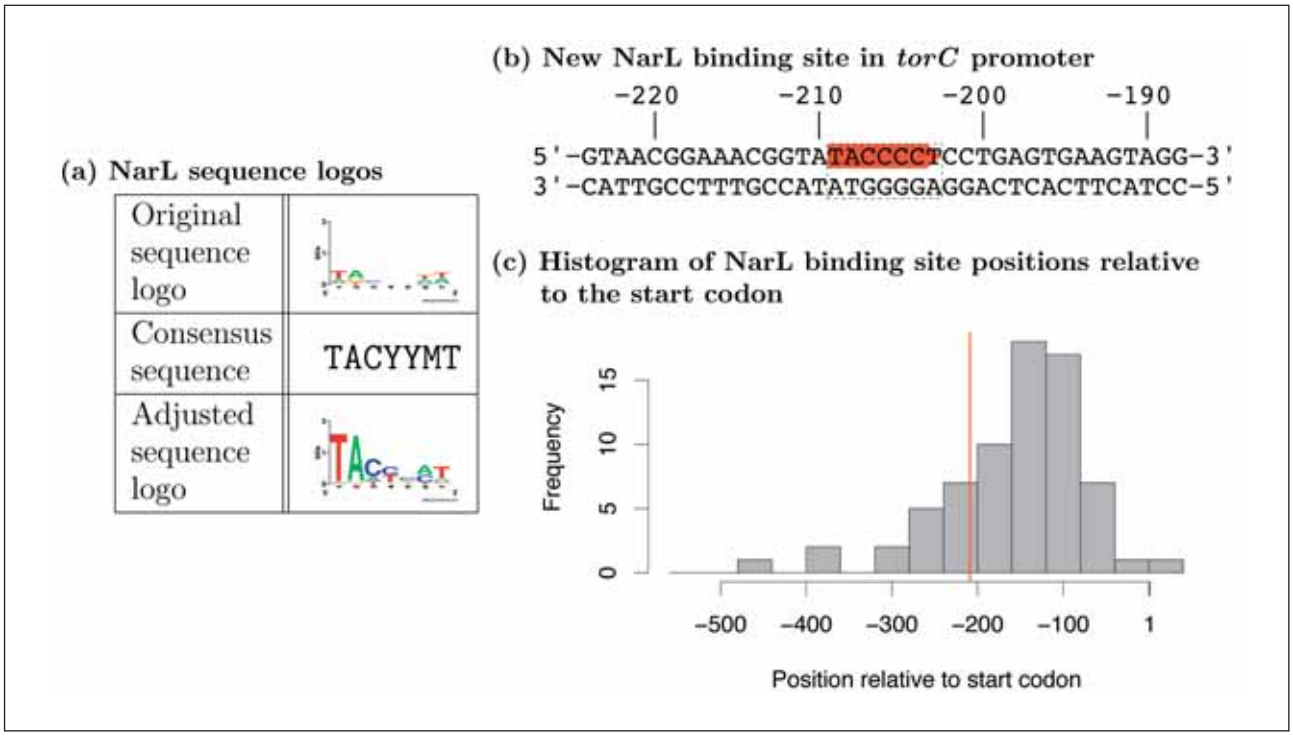

Fig. 37
Results of MotifAdjuster. (a) Illustrates the comparison of the original and the adjusted sequence logos to the consensus sequence extracted from literature. (b) Shows the binding site of NarL that can now be found in the upstream region of torC. (c) Indicates that the distance of this binding site (red line) relative to the start codon is in good agreement with the common distances of known binding sites (peak of histogram) (J. Keilwagen).

Collaborations (selection)

Within the Institute:
Dept. of Cytogenetics and Genome Analysis, Research Group Chromosome Structure and Function; A. Banaei, Dr. A. Houben;
Dept. of Cytogenetics and Genome Analysis, Research Group Epigenetics; Dr. M.F. Mette;
Dept. of Cytogenetics and Genome Analysis, Research Group Transcriptome Analysis; Dr. P. Schweizer;
Dept. of Molecular Genetics, Research Group Seed Development; Dr. N. Sreenivasulu, Dr. H. Weber, Dr. W. Weschke, Dr. J. Thiel;
Dept. of Molecular Genetics, Research Group Gene Regulation; Dr. H. Bäumlein;
Dept. of Molecular Genetics, Research Group Phytoantibodies; Dr. U. Conrad, Dr. G. Mönke;
Dept. of Molecular Genetics, Research Group Expression Mapping; Dr. L. Altschmied;
Dept. of Molecular Genetics, Research Group Plant Bioinformatics; Prof. F. Schreiber, A. Junker;
Dept. of Physiology and Cell Biology, Research Group Applied Biochemistry; Dr. H.-P. Mock, K. Witzel.

Outside the Institute:
Martin Luther University Halle-Wittenberg, Halle/Saale; Prof. I. Große, Prof. S. Posch, J. Grau, M. Porsch, I. Lemnian;
Mittweida University of Applied Sciences, Mittweida; Prof. T. Villmann;
Technical University, Clausthal; Prof. B. Hammer;
Bielefeld University, Centre for Biotechnology, Bielefeld; T. Kohl;
University of Leipzig; Dr. F.-M. Schleif;
Max Planck Institute for Molecular Genetics, Berlin; Dr. A. Schliep;
University of Groningen, The Netherlands; Prof. M. Biehl, P. Schneider;
International Computer Science Institute, Berkeley, USA; Dr. J. Baumbach;
Ecole Normale Supérieure, Paris, France; F. Roudier, V. Colot.

Publications

Peer Reviewed Papers
2008

Sreenivasulu, N., B. Usadel, A. Winter, V. Radchuk, U. Scholz, N. Stein, W. Weschke, M. Strickert, T.J. Close, M. Stitt, A. Graner & U. Wobus: Barley grain maturation and germination: metabolic pathway and regulatory network commonalities and differences highlighted by New MapMan/PageMan profiling tools. Plant Physiol. 146 (2008) 1738-1758.

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Thiel, J., D. Weier, N. Sreenivasulu, M. Strickert, N. Weichert, M. Melzer, T. Czauderna, U. Wobus, H. Weber & W. Weschke: Different hormonal regulation of cellular differentiation and function in nucellar projection and endosperm transfer cells - a microdissection-based transcriptome study of young barley grains. Plant Physiol. 148 (2008) 1436-1452.

2009

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Books and Book Chapters

2008

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2009

Fester, T., F. Schreiber & M. Strickert: CUDA-based multi-core implementation of MDS-based bioinformatics algorithms. Proc. Ger. Conf. Bioinform. (GCB09), Lect. Notes Inform. 157 (2009) 67-79.

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Strickert, M., F.M. Schleif, T. Villmann & U. Seiffert: Unleashing Pearson correlation for faithful analysis of biomedical data. In: Villmann, T., M.M. Biehl, B. Hammer & M. Verleysen (Eds.): Similarity-based clustering - recent developments and biomedical applications, Lect. Notes Comp. Sci. 5400. Springer (2009) 70-91.

Research Group: Hybrid Wheat

Head: Dr. Mario Gils

Scientists

Grant Positions
Kempe, Katja, Dr. (BMBF)
Rubtsova, Myroslava, Dr. (BMBF)

Goals

The work of our group is focussed on the development of a transgenic method that provides a significant simplification of the hybrid seed production procedure. The work is carried out in tight cooperation with an industry partner (Nordsaat GmbH, Böhnshausen).

Research Report

For commercial **hybrid seed production**, the female crossing partner must be male-sterile in order to circumvent self-fertilisation. In the system developed by the group "Hybrid Wheat", a technique is used that has several advantages over the conventional chemical sterilisation method. The technology is based on splitting a **tapetum-expressed *barnase* gene** (from *Bacillus amyloliquifaciens*), which causes male-sterility by pollen ablation, into two fragments (A_1 and A_2, see Fig 38). Eventually, it allows growing the female crossing partners as male-sterile plants, whereas the hybrid progeny is fully fertile.
In a commercial process, plants of genotype $A_1 \times A_2$ will be used as the male-sterile (female) crossing partner for the final hybridisation step with any desired line of interest (Fig. 38a). As a consequence of the isoallelic position of loci A_1 and A_2, 100 % of the seeds/plants derived from this cross will be fully fertile. The isoloci are produced by a **site-specific recombination system** (Fig. 38b).
The genetic design of the male-sterile line provides the opportunity for an efficient strategy for unlimited maintenance of the sterile lines, which is a prerequisite for a commercial application of the technique (Fig 38c). Finally, rapid introgression of the genetic components into new varieties (line conversion) can be accomplished by repetitive backcrossing of A_1 and A_2 loci independently to a new line of interest using standard marker-assisted breeding (Fig. 38d).
Summary - Advantages of the system:

1. Only one parent has to be manipulated
2. No restorer/fertility gene needed; simple conceptual solution
3. No external induction by chemicals
4. 100 % restoration guaranteed in T_1, T_2, T_x...
5. Trait control - only inactive fragments can be distributed

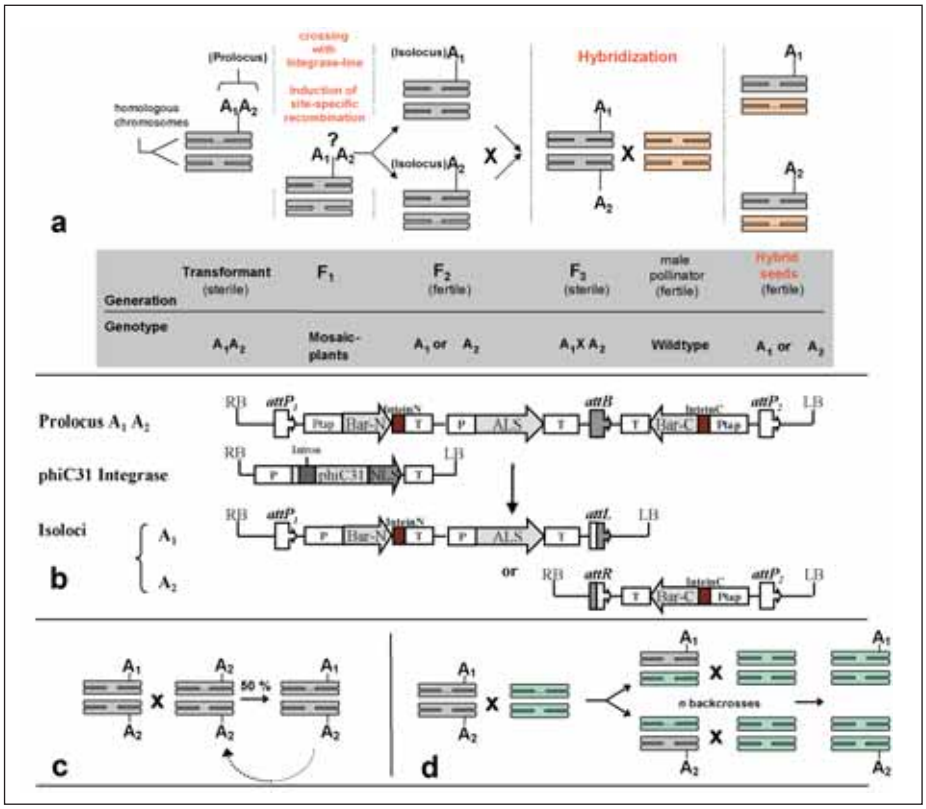

Fig. 38
Split Gene Approach. a: General scheme of hybrid seed production via the "split gene approach", b: Vector constructs, c: Maintenance and propagation of the male-sterile crossing partner, d: Introgression of isoloci in elite-wheat varieties. Abbreviations: Bar-N, Bar-C, N- and C-terminal fragments of the *Bacillus amyloliquifaciens* Barnase Gene; ALS, mutated acetolactate synthase gene from rice; DnaB IntN, DnaB IntC, N- and C-terminal intein sequences from the gene DnaB of the green blue algae *Synechocystis* sp.; attL and attR, hybrid products of the site-specific recombination between attP and attB; attP, attB, *Streptomyces* phage phiC31 target sites; P, constitutive promoter, Ptap, tapetum-specific promoter osg6B from rice; Tocs, octopine synthase terminator; phiC31, phage phiC31 recombinase; Pspm, maize spm promoter; Pubi, maize ubiquitin promoter; T, terminator; NLS, SV40 T-antigene nuclear localisation signal (M. Gils).

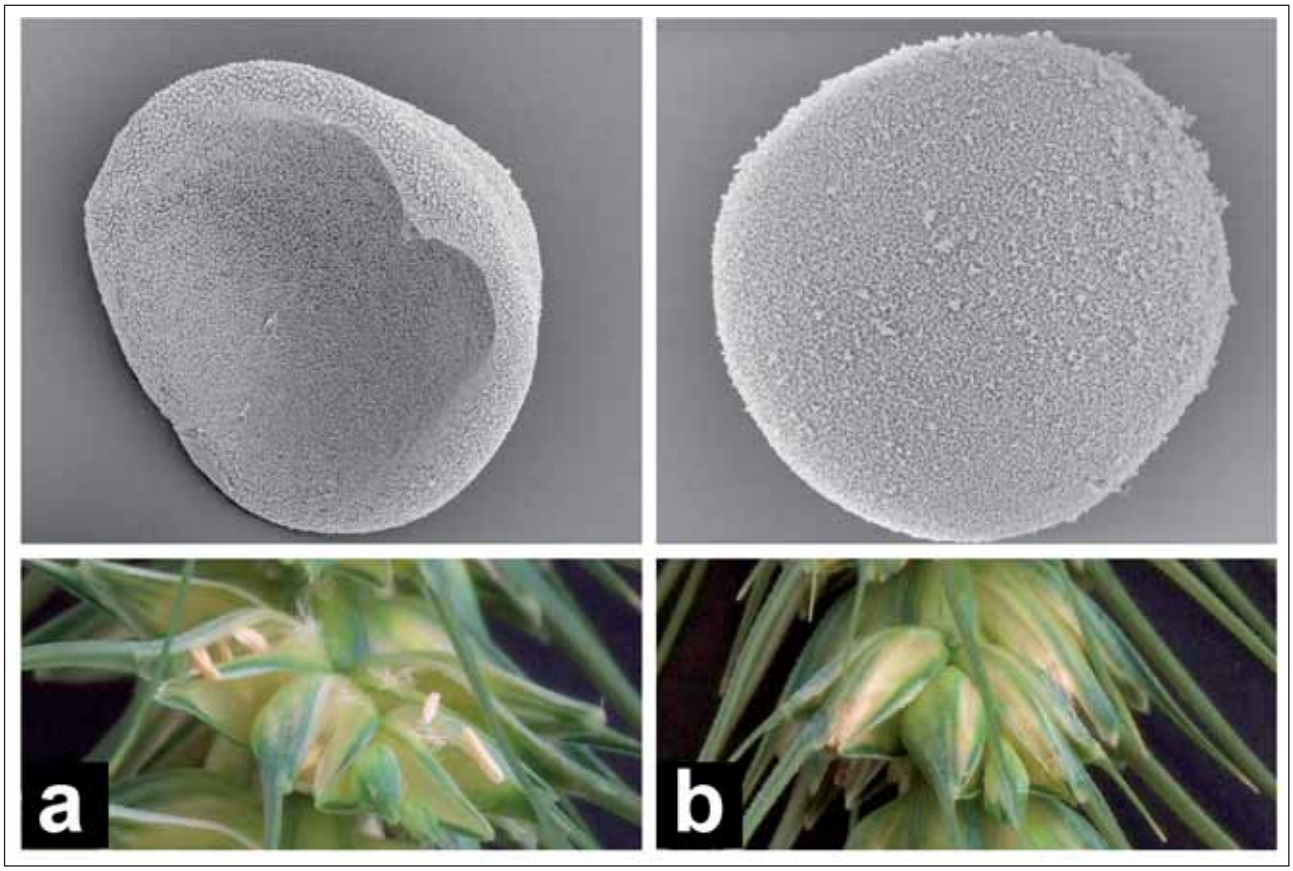

Fig. 39
Morphology of pollen and florets of a wheat plant that carries a split barnase transgene (a, male sterile) compared to a wild-type wheat plant (b) (K. Hoffie, Structural Cell Biology group).

6. No risk of leakiness
7. Isoloci can be introduced into elite lines
8. The system is expected to be applicable in different plant species (with fine-tuning)
9. Mixed-breeding is possible (by removal of the "father" carrying no ALS gene through herbicides)

State of the project:

The complete system was proven to be functional in dicotyledonous plant species (Gils et al. 2008). In stably transformed wheat plants, male-sterility could be established by complementing inactive precursor protein fragments of the barnase through **intein-mediated *trans*-splicing** (Kempe et al. 2009). Depending on the vector version that was transformed, up to 51 % of primary transformed plants produced sterile pollen (see Fig. 39). The phenotype was stable under high temperatures, making an application in open-field conditions realistic.

Additionally, a highly operable site-specific recombination technology based on the ***Streptomyces* phiC31 integrase system** was established for deleting alternative sequences from the provector constructs that are stably integrated in the wheat chromosomes (Rubtsova et al. 2008).

Currently, the derivative loci A_1 and A_2 that resulted from the recombination process are under analysis.

Collaborations (selection)

Within the Institute:

Dept. of Cytogenetics and Genome Analysis, Research Group Genome Plasticity; Dr. R. Schmidt;
Dept. of Molecular Genetics, Research Group Phytoantibodies; Dr. U. Conrad;
Dept. of Physiology and Cell Biology, Research Group Structural Cell Biology; Dr. T. Rutten;
Dept. of Physiology and Cell Biology, Research Group Plant Reproductive Biology; Dr. J. Kumlehn.

Outside the Institute:

Nordsaat Saatzucht GmbH, Saatzucht Langenstein, Böhnshausen; W. von Rhade;
SAATEN-UNION BIOTEC GmbH, Betriebsstätte Biopark Gatersleben; Dr. H. Schmuths;
SAATEN-UNION BIOTEC GmbH, Leopoldshöhe; Dr. J. Weyen;
Icon Genetics GmbH, Halle/Saale; Prof. Y. Gleba.

Publications

Peer Reviewed Papers

2008

Gils, M., S. Marillonnet, S. Werner, R. Grützner, A. Giritch, C. Engler, R. Schachschneider, V. Klimyuk & Y. Gleba: A novel hybrid seed system for plants. Plant Biotechnol. J. 6 (2008) 226-235.

Rubtsova, M., K. Kempe, A. Gils, A. Ismagul, J. Weyen & M. Gils: Expression of active *Streptomyces* phage phiC31 integrase in transgenic wheat plants. Plant Cell Rep. 27 (2008) 1821-1831.

2009

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Abteilung Physiologie und Zellbiologie/
Department of Physiology and Cell Biology

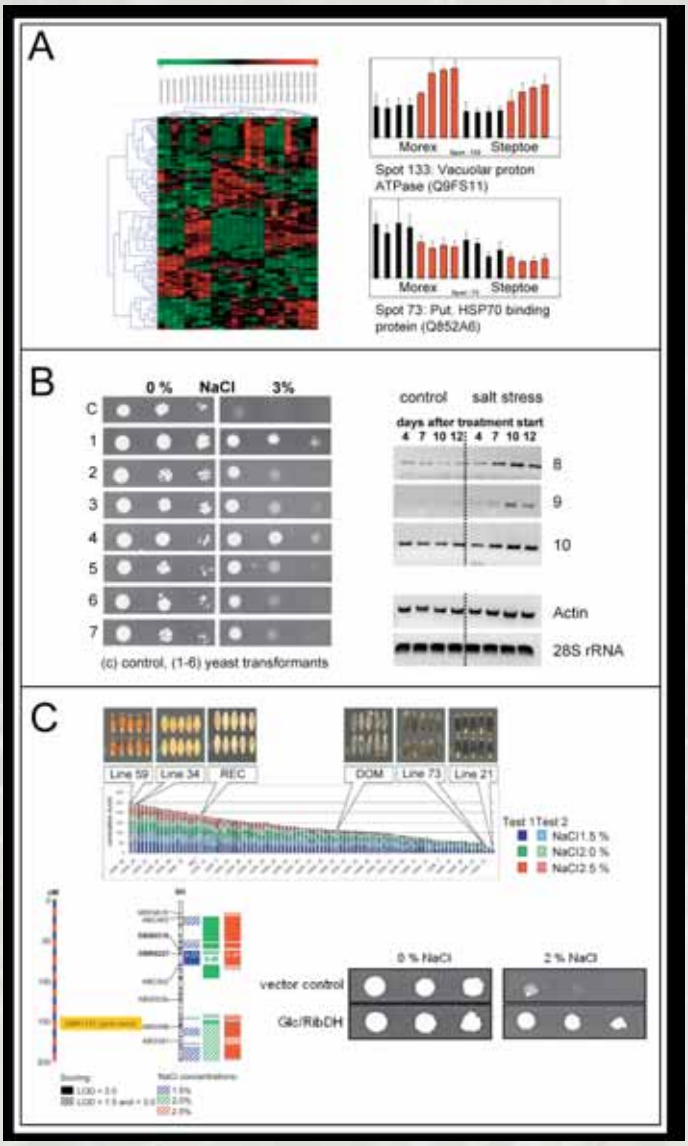

Fig. 40
Untersuchungen von Gerstenlinien mit kontrastierender Salztoleranz durch komplementäre biochemische und molekularbiologische Methoden. A: Genotypspezifische und salzstressinduzierte Proteinexpression in Wurzeln in der vergleichenden Analyse der salztoleranten Gerstenlinie Morex und der salzsensitiven Linie Steptoe. Unter Verwendung von hierarchischem Clustering erfolgte eine Gruppierung dieser Proteine nach den Expressionsmustern. Normalisierte Spotvolumina zeigen den Anstieg einer vakuolären ATPase und die Reduktion eines HSP70-bindenden Proteins unter Salzstress (schwarze Balken: Kontrolle, rote Balken: 150 mM NaCl). B: Isolierung von Genprodukten aus Gerste, die den salzsensitiven Phänotyp der *Saccharomyces cerevisiae Dhog1*-Mutante komplementieren. Nach der Transformation von Hefezellen mit einer cDNA-Bank, welche aus salzgestressten Wurzeln der toleranten Morex-Linie hergestellt wurde, erfolgte das Ausplattieren der Zellen auf salzhaltigem Medium und die Isolierung toleranter Transformanten. Die Genexpression einzelner Kandidaten wurde mittels semiquantitativer RT-PCR überprüft. C: Untersuchung von Samen kontrastierender Gerstengenotypen anhand kombinierter Proteomanalysen und quantitativer genetischer Studien. In Keimungstests konnten tolerante und sensitive Akzessionen der Oregon Wolfe Kartierungspopulation von Gerste identifiziert werden. QTL-Analyse und funktionelle heterologe Komplementationsstudien dienen zur Charakterisierung von Proteinen, welche eine höhere Expression in toleranten Akzessionen aufzeigen (K. Witzel, H.-P. Mock).

Investigation of barley genotypes with contrasting response towards salinity using complementary molecular and biochemical approaches. A: The comparative proteome analysis of roots from the salt-tolerant Morex and the salt-sensitive barley genotype Steptoe resulted in the detection of genotype-specific or time-dependent salinity-induced protein expression. Hierarchical clustering was applied to group the proteins based on expression patterns. Normalised spot volumes display an induction of vacuolar proton ATPase and a down-regulation of a putative HSP70-binding protein upon salt treatment (black bars: controls, red bars: 150 mM NaCl treatment). B: Functional screen for barley gene products complementing the salt-sensitive phenotype of the *S. cerevisiae Dhog1* mutant. Yeast cells were transformed with a cDNA library from roots of the salt-adapted Morex genotype and plated onto salt-containing media. Gene expression of selected cDNAs was analysed by semi-quantitative RT-PCR. C: Combined proteomic and quantitative genetics approach for the analysis of grains from contrasting genotypes. A germination assay of the Oregon Wolfe Barley mapping population under salt stress identified tolerant and sensitive accessions. Proteins showing a higher abundance in grains of tolerant lines were subjected to QTL analysis and functional complementation studies (K. Witzel, H.-P. Mock).

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

Mit der Namensänderung zur „Abteilung Physiologie und Zellbiologie" soll neben den zellbiologischen Arbeiten eine verstärkte Orientierung der inhaltlichen und methodischen Ausrichtung der Abteilung hin zu physiologischen Fragestellungen und Ansätzen ausgedrückt werden. Impulse dafür sollen von der neu gegründeten Arbeitsgruppe „Molekulare Pflanzenernährung" ausgehen, die die vorhergehende Ag „Molekulare Pflanzenphysiologie" ablöst. Mit der Einrichtung einer neuen Arbeitsgruppe „Systembiologie", die durch BMBF-Fördermittel getragen wird, wurde zudem eine neue Verbindung zwischen den biochemischen Plattformen der Abteilung und der Bioinformatik geschaffen, indem Modellierungsansätze in der Pflanzenbiochemie implementiert werden.
Als abteilungsübergreifendes Projekt hat die Herstellung salztoleranter Pflanzen nun zu ersten Publikationen geführt. Dazu wurden Proteomansätze zur Identifizierung von Kandidatenproteinen in Kartierungspopulationen von Gerstenlinien durchgeführt, die sich in der Salztoleranz unterscheiden. Die korrespondierenden Gene wurden in salzsensitiven Hefezellen sowie in transgenen *Arabidopsis*- und Gerstenpflanzen funktional exprimiert (s. Fig. 40, S. 119).

Hervorzuheben sind folgende Entwicklungen:

Aufklärung der Biosynthese und Funktion von Sekundärmetaboliten. Die Arbeitsgruppe „Angewandte Biochemie" hat im Rahmen des EU-Projekts FLORA phytochemische Untersuchungen zur gesundheitsfördernden Wirkung von Flavonoiden in der menschlichen Ernährung angestellt. Das Hauptaugenmerk lag auf der Bestimmung verschiedener Phenylpropanoide in transgenen Tomatenfrüchten. Die fruchtspezifische Expression bestimmter Transkriptionsfaktoren führte dabei zu einer Akkumulation von Anthocyaninen ohne bedeutende Veränderungen bei den Phenylpropanoiden auszulösen. Die Strukturen

Department of Physiology and Cell Biology

Head: Prof. Nicolaus von Wirén

Research Goals

Common research goals are the regulation of metabolic pathways and developmental processes in plants and their cellular expression systems aiming at the improvement of agronomically relevant traits in crops or biotechnological applications.

Developments in the Reporting Period

With the change of its name the "Department of Physiology and Cell Biology" intends to emphasise its future focus on physiological research questions and approaches besides those already set in cellular biology. A major driving force in physiology is expected from the topics brought in by the newly established group "Molecular Plant Nutrition" which replaces the former one on "Molecular Plant Physiology". With the establishment of a new BMBF-granted research group on "Systems Biology" a link has been created between the various biochemical platforms within the department and bioinformatics by implementing modelling approaches in plant biochemistry.
The department-wide project on the generation of salt-tolerant plants has now led to first publications. Proteome approaches have been conducted to identify candidate proteins related to salt stress tolerance in barley mapping populations with contrasting tolerance of the parental lines. The corresponding genes are functionally expressed in salt-sensitive yeast strains as well as in *Arabidopsis* mutants and transgenic barley lines (see Fig. 40, p. 119).

Some highlights that deserve particular attention are the following:

Elucidating the biosynthesis and function of secondary metabolites. The "Applied Biochemistry" group has performed phytochemical research within the frame of the EU project FLORA dedicated to research on beneficial health effects of flavonoids as part of the human diet. A major aspect was the profiling of phenylpropanoids of transgenic tomato lines. The fruit-specific expression of selected transcription factors resulted in the accumulation of anthocyanins, with minor effects on the levels of other phenylpropanoids. The structures of the main anthocyanins were elucidated by ESI-MS/MS and NMR.

der hauptsächlichen Anthocyanine konnten über ESI-MS/MS und NMR aufgeklärt werden. Fütterungsversuche in Tierversuchen zeigten, dass anthocyaninangereichertes Futter gesundheitsfördernd wirkt.
Über das Screening von „activation-tagged" *Arabidopsis*-Linien wurden Gene gesucht, die an der Biosynthese von Coumarin beteiligt sind. Ein Kandidatengen wurde charakterisiert, das wahrscheinlich einen regulatorischen Faktor kodiert. Des Weiteren wurde über Fluoreszenzmikroskopie der Wurzeln von Wildtyppflanzen und einer Insertionslinie mit defekter Biosynthese das Coumarin Scopolin in der Endodermis und im Cortex lokalisiert.

Erweiterung der Transformationsplattform für Gramineen. Die für kleinkörnige Getreidearten bereits seit einigen Jahren außerordentlich leistungsfähige Transformationsplattform der Arbeitsgruppe „Pflanzliche Reproduktionsbiologie" wurde durch die Etablierung einer effizienten und reproduzierbaren Methode für Mais erweitert. Diese Methode wird bereits für erste experimentelle Ansätze zur Erhöhung der Resistenz von Mais gegenüber phytopathogenen Pilzen angewendet. Durch Kombination von Transformations- und Haploidentechniken wurde eine neue Methode entwickelt, die bei vergleichsweise geringem Aufwand die Herstellung reinerbiger Selektionsmarker-freier Gerstenlinien gestattet. Diese Methode basiert auf der Co-Integration unabhängiger DNA-Fragmente mit Effektor- bzw. Markergenen und der nachfolgenden Segregation dieser ungekoppelten Gene in Populationen doppelhaploider Pflanzen, die mittels embryogener Pollenkulturen hergestellt werden. Die Herstellung vollkommen reinerbiger, doppelhaploider Linien aus primärtransgenen Pflanzen hat sich auch für zahlreiche andere wissenschaftliche Vorhaben als sehr nützlich erwiesen, da selbst subtile Effekte transgener Ereignisse aufgrund einer geringen Variabilität innerhalb der Nachkommenschaft und der unlimitierten Menge genetisch identischen Pflanzenmaterials belegt werden können. Mit dieser Strategie ist es beispielsweise gelungen, die Erhöhung der Mehltauresistenz in transgenen Weizenlinien nachzuweisen, bei denen die Expression des Suszeptibilitätsfaktors *Mlo* mittels RNA-Interferenz reprimiert wurde.

Methodischer Fortschritt bei der Konservierung von Pollen-Ultrastrukturen. Im Rahmen des Verbundvorhabens zur Aufklärung früher Mechanismen der Pollen-Embryogenese für die Entwicklung von Methoden zur Herstellung reinerbiger Rekombinanten (GABI-POEM) hat die Arbeitsgruppe „Strukturelle Zellbiologie" ultrastrukturelle Unterschiede bei der gametophytischen und embryogenen Pollenentwicklung unter Anwendung verschiedener Fixierungsmethoden untersucht. Morphologische Analysen und 3D-Rekonstruktionen von Semidünnschnittserien chemisch fixierter, isolierter, unreifer Pollen zeigten, dass vor allem in den ersten vier Tagen nach Initiation der Pollenembryogenese signifikante Strukturveränderungen auftreten (s. Fig. 43 A-B, S. 133).

Feeding experiments in an animal model system demonstrated beneficial health effects of a diet enriched in anthocyanins.
Furthermore, the elucidation of the coumarin biosynthetic pathway and its regulation was addressed by screening of a collection of activation-tagged *Arabidopsis* lines. A candidate gene representing a putative regulatory factor was identified and will be functionally characterised. Preferential localisation of the coumarin scopolin in the endodermis and the cortex of roots has been shown by comparative fluorescence microscopy of wild-type and of a knock-out mutant blocked in one step of the biosynthetic pathway.

Extension and improvement of the transformation platform for cereal crops. The cereal transformation platform run by the group "Plant Reproductive Biology" has been extended by the development of an efficient and reproducible transformation method for maize. This method is already being applied for first experimental approaches to the improvement of maize in terms of its resistance to pathogenic fungi. By coupling transformation and haploid technology, a further method has been established which enables us to produce true-breeding transgenic, selectable marker-free barley lines with a significantly reduced requirement of resources and time. This method combines the co-integration of independent DNA-fragments carrying the effector and selection marker genes, respectively, with the segregation of these uncoupled genes in populations of doubled haploid plants, which are produced by embryogenic pollen cultures. The generation of entirely true-breeding, doubled haploid lines from primary transgenic plants proved very beneficial for other scientific approaches as well, since even subtile effects of transgenicity can be experimentally elucidated thanks to the low background variability and the availability of unlimited amounts of genetically identical plant material. Using this strategy, we have been able to verify an increased resistance of transgenic wheat lines towards powdery mildew upon down-regulating the expression of the susceptibility factor *Mlo* by means of RNA interference.

Methodological improvements in the preservation of pollen ultrastructure. Within the research consortium Initial Mechanisms of Pollen Embryogenesis (GABI-POEM), the "Structural Cell Biology" group carried out comparative analyses on ultrastructural changes during gametophytic and embryonic pollen development. Morphological and ultrastructural aspects of pollen differentiation in wild-type plants were investigated by light and transmission electron microscopy (TEM). 3-D reconstructions of semi-thin sections of chemically fixed immature pollen or comparable pollen from gametophytic development showed significant structural changes within the first 4 days after the initiation of pollen embryogenesis (see Fig. 43 A-B, p. 133). Ultrastructural analysis was significantly improved by replacing chemical fixation by high pres-

Zur Immobilisierung aller Moleküle und zelldynamischer Prozesse innerhalb weniger Millisekunden wurde erfolgreich ein Protokoll zum Hochdruckgefrieren (HPF) von Pollen entwickelt. Hierbei werden Nitrozelluloseschläuche mit einem Gemisch aus isolierten Pollen und Zellen des wesentlich kleineren Cyanobakteriums *Synechocystis* (ø 5 µm) gefüllt, um die wässrigen Freiräume zwischen den Pollen auszufüllen. Das HPF führt dann zu einer exzellenten Ultrastrukturerhaltung unter physiologischen Bedingungen bei weitgehender Vermeidung von Fixierartefakten (s. Fig. 43 C-D, S. 133).

Expression bakterieller Flavodoxine zur Erhöhung der Stresstoleranz in Pflanzen. In vielen nicht-wirtsspezifischen und inkompatiblen Pathogen-Wirtsbeziehungen wird die Expression von Abwehrgenen induziert sowie eine Form des programmierten lokalen Zelltods, um die Ausbreitung des Pathogens zu verhindern. Diese hypersensitive Antwort folgt der Bildung reaktiver Sauerstoffspezies (ROS). Um die Rolle von ROS in der hypersensitiven Abwehrreaktion aufzuklären, hat die Arbeitsgruppe „Molekulare Pflanzenernährung" transgene Tabakpflanzen hergestellt, die ein Flavodoxingen aus Cyanobakterien exprimieren. In Prokaryoten und Algen wirkt Flavodoxin als Überträger von Elektronen und reduziert v.a. in Chloroplasten die Bildung von stressinduzierten ROS. Infiltration von Tabakblättern von Wildtyppflanzen mit einem hohem Titer an *Xanthomonas campestris* cv. *vesicatoria* (*Xcv*), einem nicht-wirtsspezifischem Pathogen, führte zur Akkumulation von ROS in Chloroplasten und dem Auftreten von Läsionen, typisch für die hypersensitive Abwehrreaktion. In transgenen Tabaklinien mit chloroplastidiärer Expression von Flavodoxin waren diese Symptome dagegen stark verringert. Stoffwechselwege, die durch das Pathogen normalerweise gehemmt werden, waren in diesen Pflanzen unverändert, auch wenn andere Aspekte der hypersensitiven Antwort, wie die Expression von Abwehrgenen oder die Bildung von Salicylsäure und Jasmonat, wie in inokulierten Wildtyppflanzen ablief. Das heißt, dass die Bildung von ROS in Chloroplasten Voraussetzung ist für die nicht-wirtsspezifische Abwehr und für das Fortschreiten des lokalen Zelltods, aber nicht zur Induktion von Pathogenese-typischen Genen oder anderen Signalkomponenten beiträgt.

Untersuchungen zur Salztoleranz in Hefe. Zur Aufklärung von Faktoren der Salztoleranz werden von der Arbeitsgruppe „Hefegenetik" *Saccharomyces cerevisiae* und nicht-*saccharomycete* Hefen wie *Arxula adeninivorans* und *Hansenula polymorpha* als zelluläre Expressionssysteme eingesetzt. Am Beispiel der osmotoleranten Hefe *A. adeninivorans* konnte gezeigt werden, dass im Gegensatz zu osmosensitiven Hefen die Aktivierung des sog. HOG-Pathways neben einer Phosphoylierungsreaktion über eine induzierbare Expression der entsprechenden Gene erfolgt. Die Aktivierung des HOG-Pathways induziert wiederum die Expression von Genen, die für die Synthese von Schutzsubstanzen („compatible solu-

sure freezing (HPF). This method is less prone to artifacts and allows obtaining an immediate immobilisation of all molecules and cell dynamic processes under physiological conditions. A key feature of this method is the loading of nitrocellulose tubes with a mixture of pollen (ø 50 µm) and cells of the much smaller cyanobacteria *Synechocystis* (ø 5 µm) which fill out the liquid space between pollen. Under these conditions HPF allows an excellent structural preservation of pollen structures (see Fig. 43 C-D, p. 133).

Expression of bacterial flavodoxins to boost stress tolerance in transgenic plants. In many non-host and incompatible host interactions, defense responses induce the expression of defense-associated genes and trigger a form of localised cell death (LCD) designed to restrict pathogen distribution and known as the hypersensitive response (HR). It is preceded by an oxidative burst generating reactive oxygen species (ROS). To elucidate the role of reactive oxygen species (ROS) during the hypersensitive response the "Molecular Plant Nutrition" group generated tobacco plants that express cyanobacterial flavodoxin. Flavodoxin is an electron shuttle present in prokaryotes and algae that, when expressed in chloroplasts, specifically prevents ROS formation in plastids during abiotic stress. Infiltration of tobacco wild-type leaves at high titers of *Xanthomonas campestris* cv. *vesicatoria* (*Xcv*), a non-host pathogen, resulted in ROS accumulation in chloroplasts, followed by the appearance of localised lesions typical of the HR. In contrast, chloroplast ROS build-up and LCD were significantly reduced in *Xcv*-inoculated plants expressing plastid-targeted flavodoxin. Metabolic routes normally inhibited by pathogens were protected in the transformants, while other aspects of the HR, including induction of defense-associated genes and synthesis of salicylic and jasmonic acid, proceeded as in inoculated wild-type plants. Therefore, ROS generated in chloroplasts during this non-host interaction are essential for the progress of LCD, but do not contribute to induction of pathogenesis-related genes or other signaling components of the response.

Investigations on salt tolerance in yeast. Employing *Saccharomyces cerevisiae* and non-*Saccharomyces* yeasts like *Arxula adeninivorans* and *Hansenula polymorpha* as cellular expression systems to elucidate salt tolerance, the "Yeast Genetics" group found out that the osmo-tolerant yeast *A. adeninivorans* activates phosphorylation reactions and the so-called HOG pathway for expression of salt tolerance genes. The HOG pathway controls the synthesis of compatible solutes such as glycerol, erythritol and mannitol, and for mannitol biosynthesis a salt-inducible mannitol dehydrogenase has been isolated that acts besides a non-inducible mannitol-1-phosphate dehydrogenase.

Biosensors for detection of biologically active substances. In the biosensor laboratory of the "Yeast Genetics" group, sensors have been developed and validated for

tes“) wie Glycerol, Erythritol und Mannitol notwendig sind. Hierbei wird Mannitol sowohl über eine salz-induzierbare Mannitol-Dehydrogenase als auch über eine nicht-induzierbare Mannitol-1-phosphat-Dehydrogenase synthetisiert.

Biosensoren für den Nachweis biologisch aktiver Substanzen. Im Biosensorlabor der Arbeitsgruppe „Hefegenetik“ wurden Sensoren entwickelt und validiert, mit denen sich arbuskuläre Mykorrhizapilze und phytopathogene Viren an Pflanzen einerseits sowie Hormonaktivitäten in Umweltproben und Tieren andererseits schnell, eindeutig und reproduzierbar nachweisen lassen. So ist der auf einer DNA-Hybridisierung basierende Mikrotiterplattenassay zur qualitativen und quantitativen Bestimmung von arbuskulären Mykorrhizapilzen an Wurzeln im Hochdurchsatzverfahren ausgelegt. Die auf Basis der Hefe *A. adeninivorans* arbeitenden mikrobiellen Hormonbiosensoren sind zur Detektion von östrogenen und androgenen Aktivitäten in Abwasser und Urin geeignet. Mit Nachweisgrenzen von 2 ng l^{-1} für 17 ß-Estradiol (E2) und 82 ng l^{-1} für 5a-Dihydrotestosteron (DHT) bei Messzeiten von ≤ 6 h zählen sie zu den derzeit sensitivsten Hormonsensoren.

Etablierung von Methoden zur Analyse von Stoffwechselflüssen. In der Arbeitsgruppe „Systembiologie“ wurde eine Methode aufgesetzt zur Bestimmung von intrazellulären Reaktionsraten im zentralen Stoffwechsel von Leguminosen- und Getreide-Samen. 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, Januar 2010

the fast and reproducible detection of arbuscular mycorrhizal fungi (AMF) and for phytopathogenic viruses on plants as well as for hormonal activities in environmental samples and animals. Based on DNA hybridisations a high-throughput microtiter plate assay has been established for the qualitative and quantitative detection of AMF on plant roots. The microbial biosensors based on the yeast *A. adeninivorans* detect estrogenic and androgenic activities in wastewater and urine. With detection limits of 2 ng l^{-1} for 17 ß-estradiol (E2) and 82 ng l^{-1} for 5α-dihydrotestosterone (DHT) at analysis times of ≤ 6 h these sensors are currently the most sensitive hormone sensors.

Establishment of methods for metabolic flux analysis in plant seeds. In the “Systems Biology” research group, a method for determining intracellular reaction rates in central metabolism has been implemented and adapted to legume and cereal seeds. 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 stable isotope feeding experiments, which are then compared to respective laboratory experiments. By adjusting the parameters of the model, simulation and experiment are brought close together in an iterative manner. Setting up the method required expertise in biochemistry, mathematics, and computer science. MFA is currently being applied in several BMBF-funded projects.

Nicolaus von Wirén, January 2010

Research Group: Molecular Plant Nutrition

(since 1st April 2009)

Head: Dr. Mohammad R. Hajirezaei

(provisional, till 31.03.2009)

Prof. Nicolaus von Wirén

(since 01.04.2009)

Scientists

IPK financed
Ahkami, Amirhossein (0,5 Pakt für Forschung und Innovation/Annex)
Bohner, Anne (0,5 P, since 01.10.2009)
Gruber, Benjamin D., Dr. (P, since 15.04.2009)
Hajirezaei, Mohammad Reza, Dr. (P)
Weishaar, Claudia (0,5 P, since 01.10.2009)

Grant Positions
Donath, Sebastian (0,5 DFG, since 01.05.2009)
Ghaffari, Mohammad Reza (0,5 BMBF, since 01.06.2009)
Jakob, Ines (0,5 DFG, till 14.02.2009)
Kim, Young-Min (0,5 DFG)
Schmid, Nicole (0,5 BMBF, since 01.08.2009)

Visiting Scientists/Scholars
Barunawati, Nunun (Indonesia Government, since 08.07.2009)
Bauer, Bernhard (DFG/University Hohenheim, 07.05.-31.12.2009)
Blanco, Ernesto Nicolás (IPK, 01.02.-30.06.2008; DAAD, 01.06.-30.11.2009)
Ceccoli, Romina (DAAD, since 02.09.2009)
Fedoseyenko, Dmitriy (EU/University Hohenheim, since 15.08.2009)
Hadavand Mirzaei, Hossein (Agricultural Biotechnology Research Institute of Iran, 22.01.-19.04.2009)
Mohammadi Bazargan, Mitra (Ministry of Science Research and Technology Iran, 15.06.-19.12.2008)
Monteoliva, Mariela (BMBF, 04.08.-04.11.2009)
Vazan, Saeed, Dr. (University of Karaj, 01.01.-30.04.2008)
Weishaar, Claudia (University Hohenheim, 17.09.-30.09.2009)
Zurbriggen, Matias Daniel (DFG, 30.06.-28.11.2008)

Goals

Characterisation of morphological and physiological responses of plants subjected to biotic and abiotic stress conditions, in particular nutrient deficiencies, and identification of rate-limiting steps in carbohydrate metabolism of stressed plants.

Research Report

The research group "Molecular Plant Nutrition" moved from Hohenheim University to the IPK in summer 2009. Since then, the new research topics are going to be established and are, as far as possible, merged or integrated with those projects that were previously running.

So far, it remains unclear why plants **sense** only some but not all **nutrients** by responding with enhanced lateral root growth into nutrient-rich soil patches. Therefore, a screening system is going to be established, in which most of the nutrients shall be investigated for their ability to stimulate lateral root growth under localised supply (B. Gruber). This is currently done in *Arabidopsis* wildtype plants growing on horizontally-split agar plates, where the nutrient in question is only supplied to the middle agar segment.

To explore **nitrogen signalling effects** in crop plants, field trials have been conducted, in which ten commercial wheat lines were fertilised either with urea, ammonium or nitrate in the starter dressing. A subsequent analysis of yield components showed that nitrate strongly stimulates tiller number while urea favors an increase in thousand kernel weight. Investigations on phytohormonal changes in the shoot are now underway (B. Bauer).

The aim of the EU project RHIBAC is to employ **beneficial rhizosphere bacteria** for reduced fertiliser input in cereal crops. Since our attempts failed so far to demonstrate reproducibly a beneficial effect of the wheat rhizosphere bacterium *Raoultella terrigena* on wheat or barley growth, *Arabidopsis* plants were cultivated in vertically oriented agar plates and inoculated. Interestingly, the presence of *Raoultella* at a certain density stimulated root growth by a factor of > 2, however, mainly on non-buffered medium with ammonium being the major nitrogen source. Current investigations focus on possible pH-modifying effects of *Raoultella* or phytohormonal changes in *Arabidopsis* roots as well as on finding appropriate substrates and growth systems in the greenhouse that allow transfering the growth stimulation of *Raoultella* to greenhouse trials with barley or wheat (C. Weishaar). In parallel, **root exudates** have been collected from commercial wheat lines for their metabolic profiling before and after inoculation with *Raoultella terrigena* (D. Fedoseyenko, M.R. Hajirezaei).

In an attempt to characterise metabolic triggers for **adventitious root formation in *Petunia* cuttings**, metabolic and transcript profiles were taken at early developmental stages of adventitious root formation. This analysis clear-

ly showed that the concentrations of certain hexoses and organic acids are subject to large variations during the re-establishment of adventitious roots. Besides the generation of transgenic *Petunia* with deregulated expression of some key enzymes in primary carbon metabolism, it is foreseen to include phytohormonal analyses and to link these with metabolic changes (A. Ahkami, M.R. Hajirezaei).

In our role as coordinator of a DFG research group on **nitrogen remobilization in senescing plants**, we focus on the role of ammonium and urea transport in senescing leaves, since in *Arabidopsis* the ammonium and urea transporter genes *AMT1;1* and *DUR3* are up-regulated during senescence, and DUR3 appears to contribute to urea loading of the phloem sap. After establishment of isotope ratio mass spectrometry, retranslocation studies with ^{15}N-labeled substrates will be undertaken in transgenic *Arabidopsis* and barley plants with deregulated expression of ammonium and urea transporter genes. Moreover, polyamine measurements are taken, since this class of 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 ear material for the analysis of N and metal micronutrients. Together with gene expression studies and the analysis of metal chelates in plant material, this approach shall provide information on how strongly **Fe, Zn, Mn, Cu and Ni retranslocation** from source leaves depends on N-regulated leaf senescence (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 a strategy I plants, or by the release of phytosiderophores and subsequent Fe(III)-phytosiderophore uptake, as in graminaceous (strategy II) plants. To screen for genes controlling Fe acquisition in *Arabidopsis*, a collection of 7,000 *Arabidopsis* T-DNA insertion lines is grown in batches of 200 on a self-made calcareous substrate for the identification of lines that show less or more severe Fe deficiency-induced chlorosis than wildtype plants. In a Plant-KBBE project this screen is accompanied by a yeast complementation approach for the identification of *Arabidopsis* genes conferring yeast growth on Fe-limited medium. To avoid the repeated isolation of known genes, such as IRT1, the screening conditions have been modified to allow counterselection against IRT1 and related transporters (N. Schmid).

To exploit the possibilities of substrate channelling in transgenic plants to enhance the concentration of an end product in carbohydrate metabolism, different isoforms of **tobacco hexokinases**, a key enzyme with sensing properties in glycolysis, have been isolated and characterised. Transgenic tobacco plants with up- and downregulated expression of three isoforms have been generated that are currently under investigation for metabolic responses (Y.-M. Kim, M.R. Hajirezaei).

In order to achieve a complete understanding of basic processes and regulation of **biomass accumulation** at the metabolic level as well as to find possibilities to increase

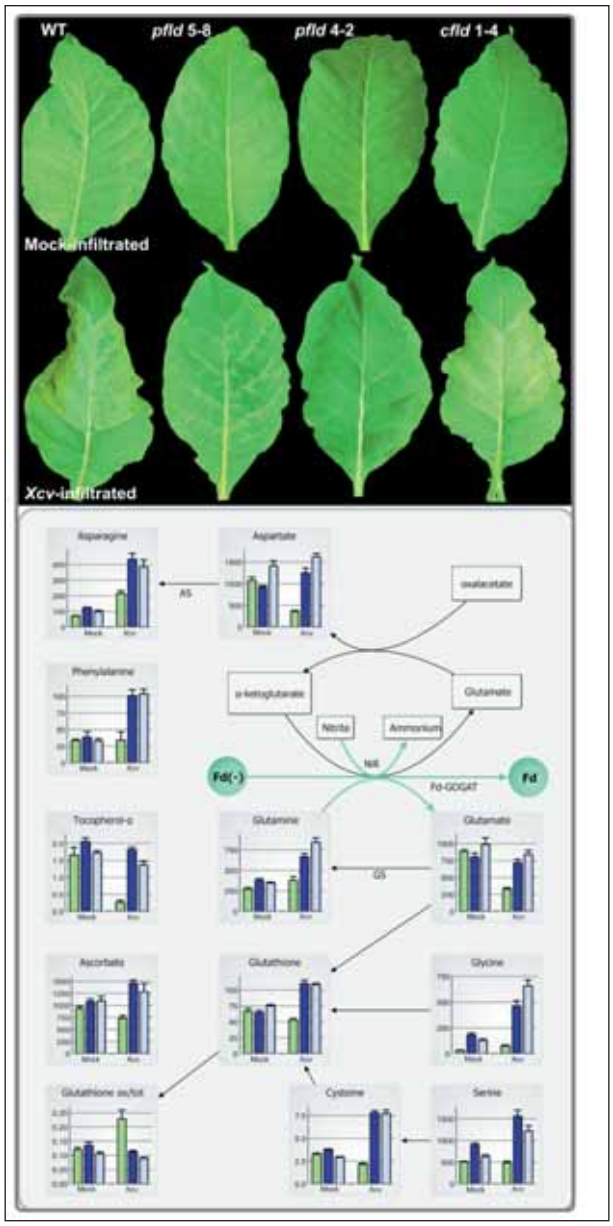

Fig. 41
Phenotypical alteration and metabolite changes in leaves infiltrated with *Xanthomonas campestris*. (A) The second fully expanded leaves of 5-6 week-old plants of WT, *pfld*5-8, *pfld*4-2 (plastidic) and *cfld*1-4 (cytosolic) lines were infiltrated with 10 mM $MgCl_2$ (mock, top), or the same solution containing ~10^8 CFU ml^{-1} *Xcv* (bottom). Photographs were taken at 24 hours post infiltration. (B) Extracts were prepared from mock- and *Xcv*-infiltrated leaf tissue of 6 week-old plants at 19 hpi, and the indicated metabolites were measured. Contents (± SE) are given for wild type (WT) (green bars), *pfld*5-8 (light blue bars) and *pfld*4-2 (blue bars) lines (n = 8-10 independent plants). Metabolite levels are expressed in µmol m^{-2}. AS: asparagine synthetase; GOGAT: glutamine-oxoglutarate amino transferase; GS: glutamine synthetase; NiR: nitrite reductase. The graph was created using the visualisation system VANTED (Junker et al. 2006) (M.R. Hajirezaei).

the biomass using methods of plant breeding and gene technology, a multiscale metabolic modeling project, Bioenergy 2021, has been started. This goal will be met by combining multiscale modeling with complementary biochemical analysis. Investigations are focusing on possibilities for the optimisation of C- and N-metabolism in barley (M.-R. Ghaffari, M.R. Hajirezaei).

The expression of a **bacterial flavodoxin** (Fld) in either the plastids or in the cytosol of tobacco aims at enhancing plant tolerance to biotic and abiotic stress factors. Transgenic tobacco plants have been generated that are tolerant against bacterial pathogens (M. Zurbriggen, M.R. Hajirezaei).
To avoid the complex phenotypes resulting from stress exposure that might affect other targets besides Ferredoxin (Fd), we generated transgenic tobacco lines in which Fd levels were knocked-down by RNA antisense or RNA interference technology. Transformants exhibited the typical symptoms of Fd deficiency, namely, arrested growth, diffuse or variable leaf chlorosis and inhibition of photosynthesis. Expression of Fld in these Fd-deficient plants after transformation of the chloroplast or nuclear genome with a cyanobacterial gene led to recovery of a WT phenotype and restoration of photosynthetic activities (see Fig. 41, p. 125). In addition, Fd-deficient lines expressing a chloroplast Fld were more tolerant than WT siblings to oxidative stress imposed by the redox-cycling herbicide methyl viologen (MV). The results confirm that Fld is able to functionally replace *in vivo* the essential activities of endogenous Fd (N. Blanco, R. Ceccoli, M.R. Hajirezaei, collaborator).

Collaborations (selection)

Within the Institute:
Dept. of Genebank, Research Group *In vitro* Storage and Cryopreservation; Dr. J. Keller;
Dept. of Cytogenetics and Genome Analysis, Research Group Transcriptome Analysis; Dr. P. Schweizer;
Dept. of Cytogenetics and Genome Analysis, Research Group Bioinformatics and Information Technology; Dr. U. Scholz;
Dept. of Molecular Genetics, Research Group Plant Bioinformatics; Prof. F. Schreiber;
Dept. of Physiology and Cell Biology, Research Group Applied Biochemistry; Dr. H.-P. Mock;
Dept. of Physiology and Cell Biology, Research Group Plant Reproductive Biology; Dr. J. Kumlehn;
Dept. of Physiology and Cell Biology, Research Group Yeast Genetics; Prof. G. Kunze.

Outside the Institute:
Friedrich Alexander University of Erlangen-Nuernberg, Department of Biochemistry, Erlangen; Prof. U. Sonnewald, Dr. R. Börnke;
University of Kaiserslautern, Department of Plant Physiology, Kaiserslautern; Prof. E. Neuhaus, Dr. T. Möhlmann, M. Flörchinger, Dr. T. Tjaden;
Institute of Vegetable and Ornamental Crops (IGZ), Department Plant Propagation, Erfurt; Dr. U. Drüge;
Agricultural Biotechnology Research Institute of Iran (ABRII), Department of Molecular and Cellular Biology, Karaj, Iran; Dr. G. Hosseini Salekdeh;
Instituto de Biología Molecular y Celular de Rosario (IBR), CONICET, División Biología Molecular, Facultad de Ciencias Bioquímicas y Farmacéuticas, Universidad Nacional de Rosario, Rosario, Argentina; Prof. N. Carrillo;
RIKEN Plant Science Center, Yokohama, Japan; Dr. H. Takahashi.

Publications

(All publications with a "*" are based on work that has been carried out when Nicolaus von Wirén was at the Institute of Plant Nutrition at the University of Hohenheim, Stuttgart, Germany)

Peer Reviewed Papers

2008

Chen, S., M.R. Hajirezaei, M.I. Zanor, C. Hornyik, S. Debast, C. Lacomme, A.R. Fernie, U. Sonnewald & F. Börnke: RNA interference-mediated repression of sucrose-phosphatase in transgenic potato tubers (*Solanum tuberosum*) strongly affects the hexose-to-sucrose ratio upon cold storage with only minor effects on total soluble carbohydrate accumulation. Plant Cell Environ. 31 (2008) 165-176.

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2009

Abbasi, A.R., A. Saur, P. Hennig, H. Tschiersch, M. Hajirezaei, D. Hofius, U. Sonnewald & L.M. Voll: Tocopherol deficiency in transgenic tobacco (*Nicotiana tabacum* L.) plants leads to accelerated senescence. Plant Cell Environ. 32 (2009) 144-157.

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ventitious root formation in *Petunia hybrida* cuttings: involvement of wound response and primary metabolism. New Phytol. 181 (2009) 613-625.

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Torabi, S., M. Wissuwa, M. Heidari, M.R. Naghavi, K. Gilany, M.R. Hajirezaei, M. Omidi, B. Yazdi-Samadi, A.M. Ismail & G.H. Salekdeh: A comparative proteome approach to decipher the mechanism of rice adaptation to phosphorous deficiency. Proteomics 9 (2009) 159-170.

Voll, L.M., M.R. Hajirezaei, C. Czogalla-Peter, W. Lein, M. Stitt, U. Sonnewald & F. Börnke: Antisense inhibition of enolase strongly limits the metabolism of aromatic amino acids, but has only minor effects on respiration in leaves of transgenic tobacco plants. New Phytol. 184 (2009) 607-618.

*von Blankenburg, F., N. von Wirén, M. Gülke, D. Weiss & T. Bullen: Fractionation of metal stable isotopes by higher plants. Elements 5 (2009) 375-380.

Yan, S.L., A.T. Lehrer, M.R. Hajirezaei, A. Springer & E. Komor: Modulation of carbohydrate metabolism and chloroplast structure in sugarcane leaves which were infected by Sugarcane Yellow Leaf Virus (SCYLV). Physiol. Mol. Plant Pathol. 73 (2009) 78-87.

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Books and Book Chapters

2009

Zurbriggen, M.D., N. Carrillo & M.R. Hajirezaei: Use of cyanobacterial proteins to engineer new crops. In: Kirakosyan, A. & P.B. Kaufmann (Eds.): Recent advances in Plant Biotechnology. Springer-Verlag, Berlin-Heidelberg (2009) 65-88.

Research Group: Applied Biochemistry

Head: Dr. Hans-Peter Mock

Scientists

IPK financed
Döll, Stefanie (0,5 Annex, till 31.08.2008)
Hennig, Anne (0,25 Annex, till 29.02.2008)
Kutz, Christiane (0,25 Annex, 01.01.-30.06.2009)
Matros, Andrea, Dr. (P)

Grant Positions
Dittbrenner, Anke (0,5/1,0 Industry, since 15.09.2008)
Döll, Stefanie (0,5 EU, 01.09.2008-31.05.2009; 0,5 Industry, since 01.06.2009)
Hedtmann, Christiane (0,5/0,25 Industry; scholarship Saxony-Anhalt, since 01.04.2009)
Hennig, Anne (0,5 BMBF, 01.03.-31.03.2008)
Kaspar, Stephanie (0,5 BMBF, 01.07.-30.09.2009; 0,5 Overhead, 01.10.-31.12.2009)
Lippmann, Rico (0,5 BMBF)
Merx, Kathleen (0,5 BMBF, since 01.04.2008)
Peterek, Silke, Dr. (EU, till 15.06.2008)
Peukert, Manuela (0,25 Overhead, 01.09.-30.11.2009; 0,5 DFG, since 01.12.2009)
Stiebitz, Beate, Dr. (Industry, 15.05.-31.08.2008)
Tandron, Yudelsy Antonia, Dr. (BMBF)
Vaas, Lea (0,5 Industry, 01.10.-31.12.2008)
Witzel, Katja, Dr. (BMBF, till 30.11.2009)

Visiting Scientists/Scholars
Capdesuner Ruiz, Yanelis Karina (DAAD scholarship, since 04.08.2009)
Janiak, Agnieszka (EU-COST, 21.09.-30.10.2009)
Janmohammadi, Mohsen (Research Scholar Islamic Republic of Iran, since 22.10.2009)
Moller, Anders, Dr. (EU COST, 09.06.-31.08.2008)
Witzel, Katja, Dr. (self-financed, 01.12.-31.12.2009)

Goals

The group works on the biosynthesis and regulation of secondary metabolism in plants. Protective functions of secondary metabolites against abiotic and biotic stresses as well as potential health effects as a part of the human diet are aspects of the studies. An ultimate goal is to gain further insights into regulatory programmes and mechanism of resource allocation into different branches of secondary metabolism. For this purpose, metabolomics together with genetic approaches are utilised. Moreover, proteomics techniques are used to study the integration of secondary metabolism into overall cellular defence mechanisms.

Research Report

Within the EU FLORA project the group was responsible for the phytochemical characterisation of plant material. Plant tissues were profiled for **flavonoids and related phenylpropanoids with potentially beneficial health effects** by using HPLC-UV-MS techniques. Plant materials studied comprised transgenic tomato fruits with ectopic expression of transcription factors regulating anthocyanin biosynthesis, maize as well as blood orange accessions. The structure of the main anthocyanins was elucidated by ESI-MS/MS and NMR (external cooperation, N. Hertkorn, GSF, Munich). Feeding studies demonstrated a protective effect of anthocyanin rich diet in an animal test system (S. Peterek, A. Matros; collaboration with FLORA partners). A follow-up EU project will be started at the beginning of 2010 with the emphasis to study the molecular significance of individual secondary compounds in the animal test systems in more detail.
The biochemical and molecular analysis of **glandular trichomes** of tobacco varieties has been extended to study the composition of leaf surface exudates. Methods for profiling of **diterpenoids** and **sucrose esters** have been introduced for standard HPLC as well as for UPLC with UV/ELS and MS detection. Exudates showed distinct composition for specific diterpenoids whereas the sucrose ester fractions were more similar between different accessions. Large quantitative differences between tobacco varieties were found for the accumulation of **coumarins in isolated trichomes** (Y. Capdesuner, Y. Tandron, R. Lippmann, A. Matros).
By screening a collection of activation-tagged *Arabidopsis* lines, a **putative regulatory factor of coumarin biosynthesis** was identified. The significance of the candidate gene is currently investigated using a knock-out mutant and over-expression lines and by growing of plants under different environmental conditions. The preferential localisation of the coumarin scopolin in the endodermis and the cortex of roots was shown by fluorescence microscope analysis of wild-type and of a knock-out mutant blocked in an step of the biosynthetic pathway (see Fig. 42, p. 129; S. Döll).

The functional characterisation of the **stress-induced protein STINT**, initially identified as a trichome-enriched protein of tobacco, has been continued. The recombinant protein was shown to be a dimer, both by gel filtration experiments and by native gel electrophoresis. Within protein extracts from various plant tissues, the dimeric form is dominating. In addition, presence in higher molecular weight fractions indicates protein-protein interaction of STINT in larger complexes. A major focus of the

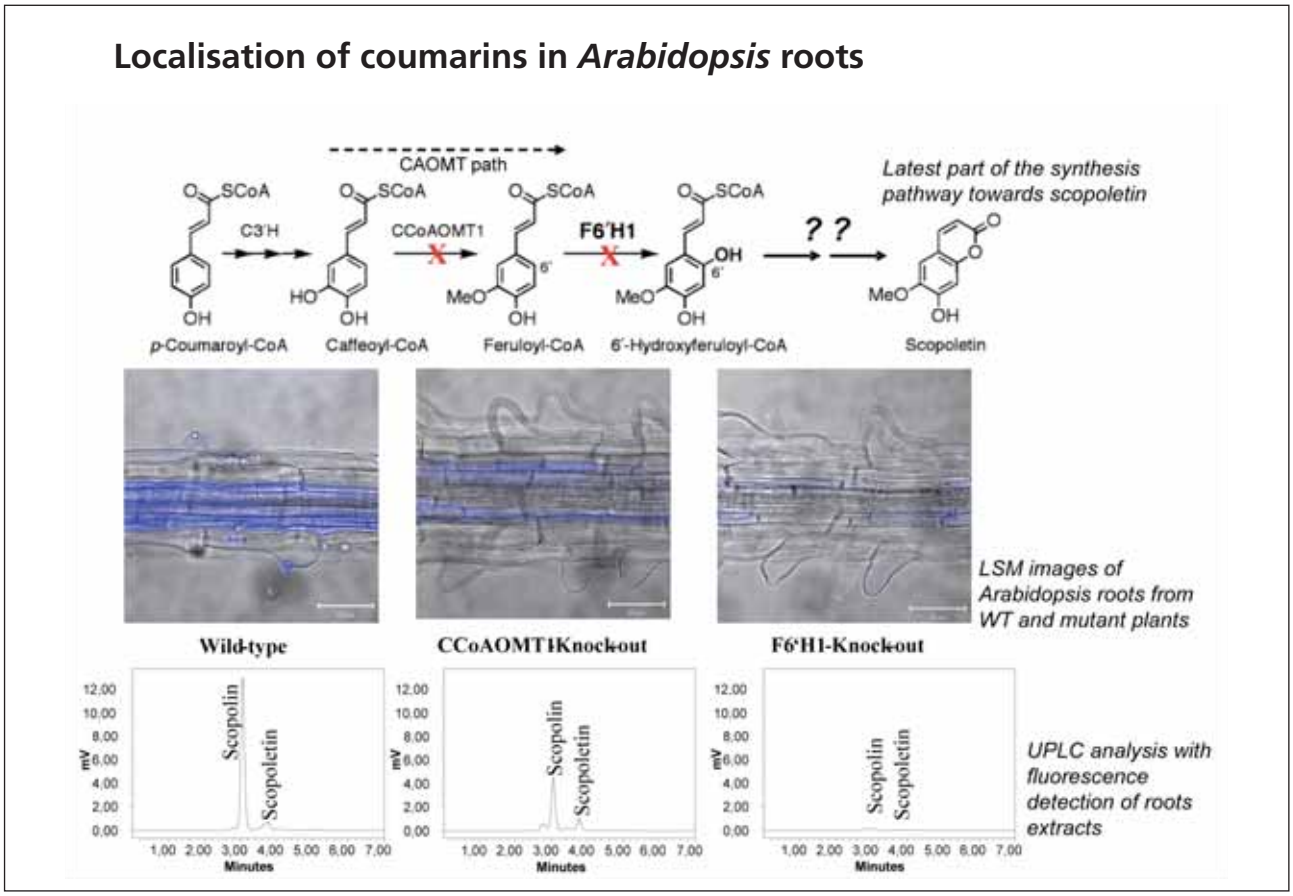

Fig. 42
Scopoletin and its storage form scopolin strongly accumulate in the endodermis of roots as shown by fluorescence microscopy in combination with HPLC analysis of wild-type and knock-out mutants of late stages in the biosynthetic synthesis (Mutants described by Kai et al. 2008). With the exception of coumarins, the phenylpropanoid profile of the F6'H1 mutant was found to be unaltered (S. Döll; collaboration with T. Rutten and M. Melzer).

on-going work is therefore the identification of putative interaction partners. Using **TAP (tandem affinity purification)** technique for STINT, HSP90 and HSP70 proteins were identified in an *Arabidopsis* cell culture system (cooperation with G. de Jaeger, VIB Ghent). TAP technology was also applied to identify the corresponding HSP interaction partners in the yeast system. Current work aims at the identification of the HSP form interacting with the three related STIAT proteins in *Arabidopsis*, as well as the elucidation of putative target proteins. The distinct function of the closely related STIAT proteins is studied in mutant and over-expression lines (C. Hedtmann, A. Matros).

Barley **seed proteome analysis** was continued in the Quant-Pro project (S. Kaspar, A. Matros; collaboration with U. Seiffert and W. Weschke). The seed proteome from **five developmental stages** has been analysed by LC-MS/MS; the complex sets of MS data were exported and processed to reveal classes of **kinetic patterns for protein abundance**. The sensitive **LC-MS/MS technique** also allowed the analysis of minute protein amounts in extracts obtained with laser-microdissection of barley seed sections; the approach is applied to study the proteome of transfer cells and other seed tissues. Moreover, the elaborated workflows have also been used for the characterisation of barley epidermal leaf tissue with respect to abiotic stress responses (S. Kaspar). Within the GABI-SysSeed consortium, a **platform for the determination of a wide range of enzymes in barley** was established (K. Merx; collaboration with Y. Gibon, Max Planck Institute of Molecular Plant Physiology, Golm). The introduced methodology has already been used to estimate enzyme activity data for a number of samples from collaborators.

The **proteome project** on **salt stress responses in barley mapping populations** has been continued (K. Witzel, A. Matros; collaboration with A. Börner (Resources Genetics and Reproduction group) and all groups of the Physiology and Cell Biology Department; see Fig. 40, p. 119). A range of potential novel candidates associated with the higher salt tolerance of the Morex variety have been identified by comparative 2-D gel electrophoresis of seed or root extracts and subsequent protein identification by MALDI-TOF as well as ESI-MS/MS. In addition, a cDNA library prepared from root tissue of the tolerant Morex variety was used to transform a **salt-sensitive yeast** strain. Screening of **transformants with increased tolerance under salinity conditions** led to a range of additional candidates, which are verified by studying their expression *in planta* using RT-PCR, and, when available,

by analysis of knock-out mutants in *Arabidopsis.* Plasma membrane fractions were prepared by the two-phase partitioning from the roots of the parental lines of the Steptoe-Morex population and proteins monitored by label free quantitative LC-MS. To enable the analysis of candidate proteins in the offspring lines, recombinant proteins for several of the candidates were expressed in *E. coli* and used to obtain antisera for Western blotting. Novel projects deal with the proteome analysis of sugar-beet taproot to elucidate mechanisms relevant for high sucrose accumulation (GABI-Betanet; K. Witzel), and the analysis of metabolite and protein factors controlling pollen embryogenesis (GABI-POEM; R. Lippmann). In addition spatial distribution patterns of metabolites and proteins will be evaluated by MALDI-*Imaging* technology (DFG, M. Peukert).

Collaborations (selection)

Within the Institute:

Dept. of Cytogenetics and Genome Analysis, Research Group Transcriptome Analysis; Dr. P. Schweizer;
Dept. of Molecular Genetics, Research Group Seed Development; Dr. W. Weschke;
Dept. of Physiology and Cell Biology, Research Group Yeast Genetics; Prof. G. Kunze;
Dept. of Physiology and Cell Biology, Research Group Plant Reproductive Biology; Dr. J. Kumlehn;
Dept. of Physiology and Cell Biology, Research Group Structural Cell Biology; Dr. M. Melzer;
Dept. of Genebank, Research Group Resources Genetics and Reproduction; Dr. A. Börner.

Outside the Institute:

Fraunhofer Institute for Factor Operation and Automation (IFF), Biosystems Engineering, Magdeburg; Prof. U. Seiffert;
Max Planck Institute of Molecular Plant Physiology, Golm; Dr. Y. Gibon, Prof. M. Stitt;
Christian-Albrechts-University at Kiel; Institute of Botany, Kiel; Prof. K. Krupinska;
Sperimentale per l'Agrumicoltura, Catania, Italy; Dr. G. Reforgiato;
John Innes Centre, Norwich, UK; Dr. C. Martin;
Plant Research International, Wageningen, The Netherlands; Dr. R. Hall, Dr. J. Beekwilder;
Technical University of Denmark, Institute BioCentrum, Copenhagen, Denmark; Prof. B. Svensson;
VIB Department of Plant Systems Biology, University of Ghent, Belgium; Dr. G. de Jaeger.

Publications

Peer Reviewed Papers

2008

Böttcher, C., D. Centeno, J. Freitag, R. Höfgen, K. Köhl, J. Kopka, J. Kroymann, A. Matros, H.P. Mock, S. Neumann, M. Pfalz, E. von Roepenack-Lahaye, N. Schauer, S. Trenkamp, M. Zubriggen & A.R. Fernie: Teaching (and learning from) metabolomics: the 2006 PlantMetaNet ETNA Metabolomics Research School. Physiol. Plant. 132 (2008) 136-149.

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Books and Book Chapters

2008

Mock, H.-P. & A. Matros: Proteome analysis of cellular responses to abiotic stresses in plants. In: Agrawal, G.K. & R. Rakwal (Eds.): Plant proteomics. Technologies, strategies and applications. John Wiley & Sons, Hoboken, NJ/USA (2008) 605-628.

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Research Group: Structural Cell Biology

Head: Dr. Michael Melzer

Scientists

IPK financed
Rutten, Twan, Dr. (P)

Grant Positions
Daghma, Diaa El-Din (0,50 BMBF)

Visiting Scientists/Scholars
Agarwal, Rachna (BMBF/DLR, 24.04.-23.06.2009)
Al-Rihani, Khaled (Scholarship Islamic Development Bank-Merit, 01.04.-30.04.2009)
Chittela, Rajani Kant (BMBF/DLR, 24.04.-23.06.2009)
Petterle, Anna (self-financed, 17.11.-27.11.2009)
Prokhorenko, Isabella, Prof. (DFG, 03.04.-01.07.2008; 22.06.-19.09.2009)
Sainis, Jayashree, Prof. (BMBF, 09.11.-04.12.2009)

Goals

As a **central service group for light and electron microscopy** at the institute we provide practical services and theoretical advice to solve cell biological problems. Our main focus is **ultrastructural characterisation**, **monitoring cell dynamic processes** and **spatial distribution of macromolecules** in plants cells and tissues. The facility is equipped with the following state-of-the-art microscopy imaging systems and instruments: **Transmission electron microscope** FEI Tecnai G2-Sphera 200 KV, **field emission scanning electron microscope** Hitachi S 4100, **confocal laser scanning microscope** Zeiss LSM 510 META, fluorescence microscopes Zeiss Axioskop and Axiovert 135 each with an AxioCam HRc camera system.

Research Report

Within the project "Comparative structural cell biological studies of gametophytic pollen development vs. initiation of POEM", as part of the consortium **Initial Mechanisms of Pollen Embryogenesis** (GABI-POEM), the morphological and ultrastructural aspects of **pollen differentiation** in wild-type plants were studied by light microscopy and transmission electron microscopy (TEM), employing conventional and **cryo-preparation methods** (D. Daghma). Semi-thin sections of isolated immature pollen 0 to 12 days after initiation of POEM and comparable pollen of the gametophytic developmental pathway have been used for histological analysis and 3-D reconstructions (see Fig. 43 A-B, p. 133). The analysis points out that significant structural changes related to the initiation of POEM occur within the first 4 days. For an optimal ultrastrutural analysis, it was decided to abandon chemical fixation in favour of a method less prone to causing artefacts. To obtain the immediate immobilisation of all molecules and cell dynamic processes under physiological conditions, we have established a protocol for **high pressure freezing** (HPF). The cyrofixation within a few milliseconds results in an excellent structural preservation and therefore enables us to examine the "real" condition of the isolated pollen (see Fig. 43 C-D). Another important goal is the **visualisation of the initial mechanism of POEM** by **life cell imaging** and time lapse using confocal laser scanning microscopy. For this purpose, the distribution of various GFP-fused gene products, including nucleus and actin linked proteins, will be followed during POEM (see Fig. 43 E-F).
The Indo-German collaborative project "Investigations of the Molecular Architecture of the Apparatus of Photosynthesis and DNA Recombination" with the Bhabha Atomic Research Centre was continued (R. Agarwal, R. Chittela and J. Sainis). **Immunogold localisation of Calvin cycle enzymes** in isolated thylakoids and in high pressure fixed cells of *Synechocystis* 6803 as well as proteomic analysis of thylakoid membranes confirmed their presence in the neighbourhood of thylakoids. In the project on rice recombinases, **structural analysis of DNA binding properties of OsDmc1 and OsRad51** using TEM showed that both proteins formed ring-like structures in presence of Ca^{2+} or Mg^{2+}. The preponderance of compact rings on binding to ssDNA or dsDNA was stronger in presence of Ca^{2+}. TEM analysis of joint molecules formed between open circular dsDNA and closed circular ssDNA in presence of Ca^{2+} or Mg^{2+} after the strand exchange reaction showed a complex network of DNA molecules.

The DAAD financed project with the Department of Forest Genetics and Plant Physiology of the Swedish University of Agricultural Science in Umeå (G. Wingsle and V. Srivastava) was continued with an engagement on alternative splicing studies of the **ROS gene network** in Poplar dismutase. The transcript analysis showed that the splice variant hipI-SODC1b was differentially expressed, being clearly expressed in cambial and xylem, but not phloem regions. Immunolocalisation and mass spectrometric data confirmed the presence of **hipI-SOD proteins** in the vascular tissue.
In the past two years we were involved in several internal and external co-operations that have been engaged with morphological, ultrastructural and cell biological problems.
The phenolic compounds scopoletin and its glucosylated form scopolin belong to the coumarins. Formation of these secondary metobolites is induced in response to

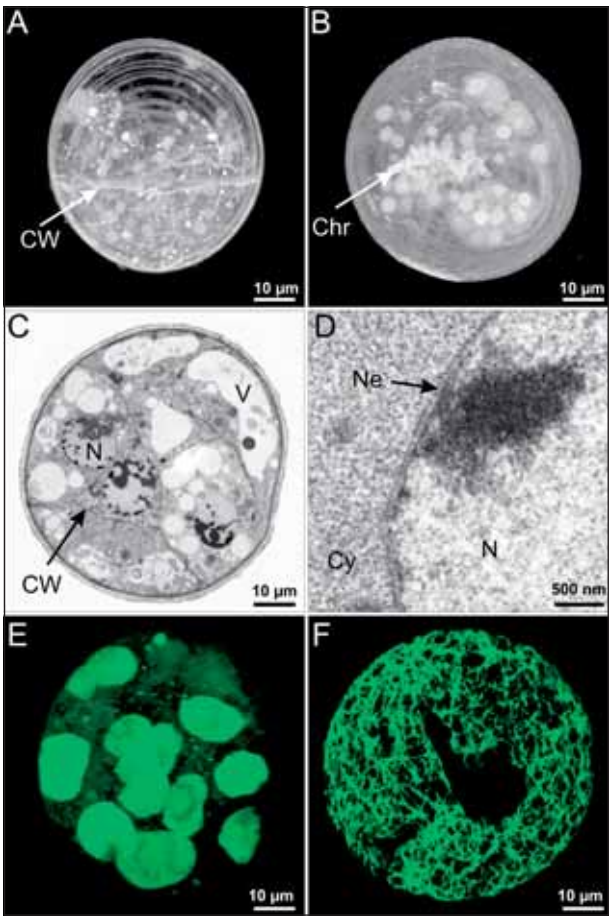

Fig. 43
Morphological, ultrastructural and fluorescence microscopical studies of immature pollen of *Hordeum vulgare*. 3D reconstruction of chemically fixed isolated immature pollen four (A) and ten days (B) after initiation of pollen embryogenesis (POEM). (C, D) Ultrastructure of high pressure frozen immature pollen six days after POEM. (E) Life cellimaging of immature pollen after six days of POEM with GFP targeted into the nucleus. (F) Microwave proceeded fluorescence labelling of actin filaments in immature pollen after ten days of POEM using Alexa 488 Phalloidin. Cy - cytoplasm, CW - cell wall; N - nucleus; Ne - nuclear envelope (D. Daghma, M. Melzer).

abiotic stress and to attack by pathogenic fungi. In cooperation with the Research Group Applied Biochemistry (S. Döll) the distribution of these coumarins was studied *in vivo* in *Arabidopsis* roots in dependence of environmental conditions, using the strong autofluorescence of scopolin and scopoletin under UV illumination. In close cooperation 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 the morphological and ultrastructural analysis of the **complementation of ferredoxin deficiency** in knocked-down transgenic tobacco plants by expressing a cyanobacterial flavodoxin (Fld). Chloroplast ultrastructure, as determined by transmission electron microscopy, was largely disrupted in both asFd1 and siFd1 plants, with loss of granal stacking and profusion of plastoglobules, indicative of ongoing thylakoid disassembly. **Fld expression** from either the nuclear or chloroplast genomes **led to substantial recovery of chloroplast morphology** and thylakoid stacking, resembling those of the WT controls.
In the ongoing collaborations with the department of Cytogenetics histon H3 as the most extensively modified histone protein and its kinases have been the focus of attention. In cooperation with the research group Chromosome Structure and Function (A. Houben, F. Agueci) the **cellular distribution of GFP-tagged NIMA**, which is involved in the control of the initiation of mitosis by induction of chromatin condensation, was analysed using CLSM. The results in interphase cells of *Nicotiana tabacum* revealed a distribution pattern along cytoskeletal elements. Life cell imaging showed that organelles did not move along these strands which could be disrupted by incubation with oryzalin. These observations thus identified the underlying cytoskeletal components as microtubules. A second cooperation focuses on aurora kinases that play a crucial role in cellular division by controlling chromatid segregation (D. Demidov). Using **split-YFP constructs** enabled us to visualise the *in vivo* interactions between AtAurora1 and **centromeric histon CENH3**. Spatially these interactions were confined to the nucleus. In cooperation with the research group Karyotype Evolution (I. Lermontova), we are presently investigating the dynamics of **YFP-tagged CENH3** during the plant cell cycle using life-cell imaging confocal microscopy. In the centromeric chromatin, the normal histone H3 is replaced with a centromere-specific variant, CENH3 which is believed to be important for the assembly of the kinetochore on the centromere. Measuring of fluorescence and **fluorescence recovery after photobleaching (FRAP)** has provided evidence that the CENH3 dynamics in plant differ considerably from those in animal cells.

In cooperation with of the research group Gene Regulation (A. Vorwieger), we continued our studies on the ectropic expression of LEC1 on plant development (see Fig. 44, p.134). Using the artifical **auxin inducible DR5:GFP** construct, auxin distribution in the root apical meristem (RAM) was found to remain under ectropic expression of LEC1. Under the same conditions **auxin accumulated also at the root-hypocotyl junction** the site of future callus formation. Since auxin is necessary for maintenance of the apical dominance and the accumulation is proceeding callus formation, we hypothesise that **LEC1** is somehow **stimulating auxin synthesis**. The LEC1 induced transformation of non-differentiated tissues into storage compartments may then be caused by a misdifferentiation of meristem initials.

Collaborations (selection)

Within the Institute:
Dept. of Genebank, Research Group Resources Genetics and Reproduction; Dr. A. Börner;
Dept. of Cytogenetics and Genome Analysis, Research Group Karyotype Evolution; Prof. I. Schubert;

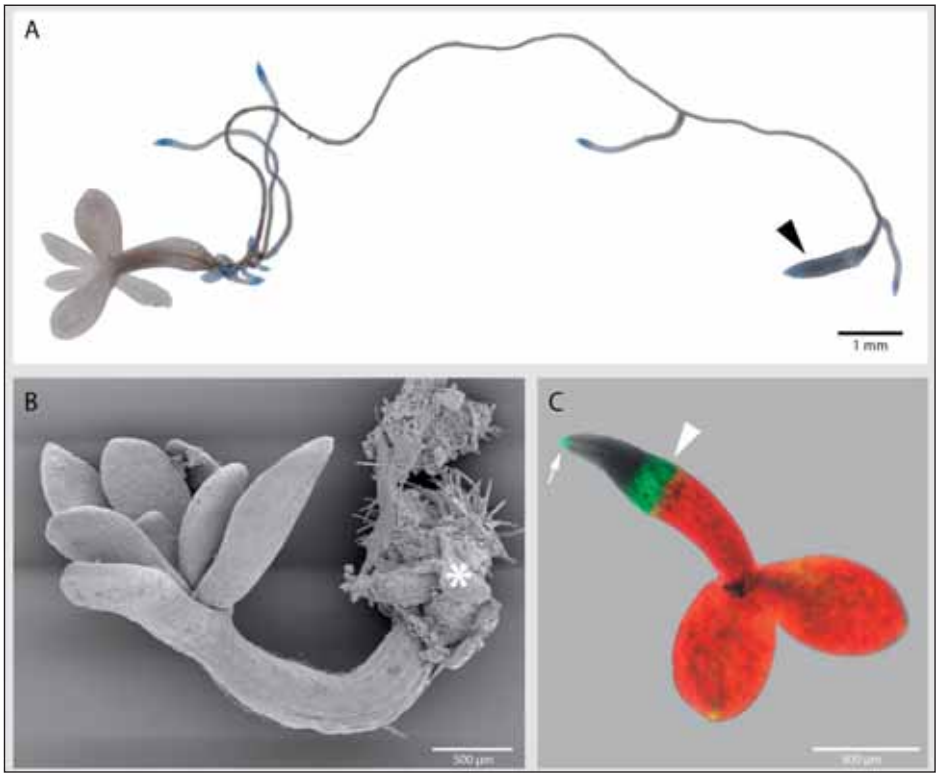

Fig. 44
Effect of constitutive LEC1 expression on seedling growth. Shoot growth is halted early on though root growth may continue until the tip develops a characteristic pickle-root phenotype (arrowhead in A). Prolonged incubation of *Arabidopsis thaliana* LEC1::GR seedlings on induction medium eventually leads to callus formation especially at the transition zone between hypocotyl and root (asterix in B). Using the auxin inducible promoter DR5 linked to GFP, auxin gradients, necessary for maintenance of apical meristems, were visualised. Despite an arrested growth auxin still concentrates in the root apex (arrow in C). Quite unexpected was the second clear auxin accumulation at the transition zone between root and hypcotyl (arrowhead in C) indicating that LEC1 influences auxin synthesis (A. Vorwieger, T. Rutten).

Dept. of Cytogenetics and Genome Analysis, Research Group Chromosome Structure and Function; Dr. A. Houben;
Dept. of Molecular Genetics, Research Group Heterosis; Prof. T. Altmann;
Dept. of Physiology and Cell Biology, Research Group Molecular Plant Nutrition; Prof. N. von Wirén;
Dept. of Physiology and Cell Biology, Research Group Applied Biochemistry; Dr. H.-P. Mock;
Dept. of Physiology and Cell Biology, Research Group Plant Reproductive Biology; Dr. J. Kumlehn.

Outside the Institute:
Friedrich Alexander University Erlangen-Nuernberg, Dept. of Molecular Plant Physiology, Erlangen; V. Huss, Dr. R. Stadler, Prof. N. Sauer;
Friedrich Alexander University Erlangen-Nuernberg, Dept. of Biochemistry, Erlangen; Dr. F. Börnke, Prof. U. Sonnewald;
University of Kaiserslautern, Dept. of Plant Physiology, Kaiserslautern; Prof. E. Neuhaus;
Swedish University of Agricultural Science, Dept. of Forest Genetics and Plant Physiology, Umeå, Sweden; Prof. G. Wingsle;
John Innes Centre, Dept. of Metabolic Biology, Norwich, UK; Dr. S. Kopriva;
University of Copenhagen, Dept. of Biology, Copenhagen, Denmark; Dr. D. Hofius;
University of Aalborg, Dept. of Life Sciences, Aalborg, Denmark; Prof. K. Grasser;
Russian Academy of Sciences, Institute of Basic Biological Problems, Pushino, Russia; Prof. I. Prokhorenko;
Bhabha Atomic Research Centre (BARC), Molecular Biology and Agriculture Division, Bombay, India; Prof. J. Sainis.

Publications

Peer Reviewed Papers

2008

Ivanov, R., J. Tiedemann, A. Czihal, A. Schallau, L. Diep, H.-P. Mock, B. Claus, A. Tewes & H. Bäumlein: EFFECTOR OF TRANSCRIPTION2 is involved in xylem differentiation and includes a functional DNA single strand cutting domain. Dev. Biol. 313 (2008) 93-106.

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Lippmann, R., S. Kaspar, T. Rutten, M. Melzer, J. Kumlehn, A. Matros & H.P. Mock: Protein and metabolite analysis reveals permanent induction of stress defense and cell regeneration processes in a tobacco cell suspension culture. Int. J. Mol. Sci. 10 (2009) 3012-3032.

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Srivastava, V., M.K. Srivastava, K. Chibani, R. Nilsson, N. Rouhier, M. Melzer & G. Wingsle: Alternative splicing studies of the reactive oxygen species gene network in *Populus* reveal two isoforms of high-isoelectric-point superoxide dismutase. Plant Physiol. 149 (2009) 1848-1859.

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Weigelt, K., H. Küster, T. Rutten, A. Fait, A.R. Fernie, O. Miersch, C. Wasternack, R.J. Emery, C. Desel, F. Hosein, M. Müller, I. Saalbach & H. Weber: ADP-glucose pyrophosphorylase-deficient pea embryos reveal specific transcriptional and metabolic changes of carbon-nitrogen metabolism and stress responses. Plant Physiol. 149 (2009) 395-411.

Zurbriggen, M.D., N. Carrillo, V.B. Tognetti, M. Melzer, M. Peisker, B. Hause & M.R. Hajirezaei: Chloroplast-generated reactive oxygen species play a major role in localised cell death during the non-host interaction between tobacco and *Xanthomonas campestris* pv. *vesicatoria*. Plant J. 60 (2009) 962-973.

Research Group: Plant Reproductive Biology

Head: Dr. Jochen Kumlehn

Scientists

IPK financed
Bruchmüller, Astrid (0,5 Annex, till 30.04.2009)
Goedeke, Stefanie (0,5 Annex, 01.03.-31.07.2008; 01.10.2008-31.12.2008; 0,5 Pakt für Forschung und Innovation, since 01.04.2009)
Guse, Tilo (0,5 Pakt für Forschung und Innovation, 01.01.-30.06.2009)
Hensel, Götz, Dr. (0,5 P, till 31.07.2008)
Kapusi, Eszter (0,5/1,0 Pakt für Forschung und Innovation, since 01.07.2009)
Rizzo, Paride (0,5 Pakt für Forschung und Innovation, till 31.12.2009)
Saalbach, Isolde, Dr. (0,5 P)
Zimmermann, Grit (0,5 Annex, till 30.09.2008)

Grant Positions
Bakos, Ferenc (Industry, 01.01.-31.03.2008)
Berger, Carolin, Dr. (BMBF, since 18.02.2008)
Bruchmüller, Astrid (0,5 BMBF, 01.05.-31.07.2009; 0,5 Overhead, since 01.08.2009)
Goedeke, Stefanie (0,5 BMBF, 01.08.-30.09.2008; 0,5 Overhead, 01.01.-31.03.2009)
Guse, Tilo (0,5 Overhead, 01.10.-31.12.2008; 0,5 Industry, since 01.07.2009)
Hensel, Götz, Dr. (0,5/1,0 BMBF)
Kapusi, Eszter (0,5 BMBF, till 30.09.2008)
Kastner, Christine (0,5 DFG, till 17.04.2009; 0,5 BMBF, since 18.04.2009)
Kugelmann, Eszter (0,5 BMBF)
Plasun, Katarzyna (0,5 BMBF)
Riechen, Jan (0,5 EU, till 30.04.2009; 0,5 Overhead, 01.05.-31.07.2009; 0,5 BMBF, since 01.08.2009)
Zierold, Uwe, Dr. (DFG, till 31.03.2009)
Zimmermann, Grit (0,5 Overhead, 01.10.-31.12.2008)

Visiting Scientists/Scholars
Kapusi, Eszter (self-financed, 08.10.2008-30.06.2009)
Khatib, Fateh, Dr. (ICARDA Syria, 22.06.-31.08.2009)
Tien, Vu Van (Vietnam Government, 15.04.-15.07.2009)
Zimmermann, Grit (self-financed, 01.01.-28.02.2009)

Goals

The research focus of the Plant Reproductive Biology group is to establish and implement genetic transformation, haploid and microdissection technologies in plants. Current research projects include application-oriented investigations on sexual and asexual plant reproduction, plant-pathogen interactions concerning various fungal and viral pathogens, mechanisms of plant tolerance towards abiotic stress, nutrient allocation and storage, domestication traits, as well as the plant-based production of valuable recombinant proteins.

Research Report

As the coordinating partner of the GABI POEM consortium we are interested to understand **initial mechanisms of pollen embryogenesis**. The knowledge gained from this project may eventually contribute to the improvement of methods of doubled haploid production both for research approaches and crop breeding. For the cellular analyses envisaged, we generated transgenic barley lines that express a *gfp* gene sequence translationally coupled to the nucleus localisation signal of Simian Virus 40 (SV40) with the expression being driven by the maize *Ubi*1 promoter. The greatly improved visibility of nuclei in live cells is exemplified in Fig. 45A which shows an immature pollen grain that undergoes early cell divisions of the pollen embryogenesis pathway. The ***in vivo* visualisation of nuclei** will facilitate a detailed structural analysis of the cellular behaviour during normal pollen development as compared to pollen embryogenesis. In the GABI POEM project we further aim to manipulate the **expression of candidate genes putatively triggering pollen embryogenesis**. Due to the lack of a microspore-specific promoter for grasses, tobacco has been chosen as a further experimental system. To confirm the functionality of the *Ntm19* promoter in the context of the GATEWAY-compatible IPKb binary vector system, the *Gus* gene was recombined into the destination cassette downstream of the *Ntm19* promoter and transgenic tobacco plants were generated. **Immature pollen-specific expression** was then confirmed by histochemical detection of *Gus* expression as shown in Fig. 45B (G. Hensel, C. Marthe, A. Müller, I. Otto).

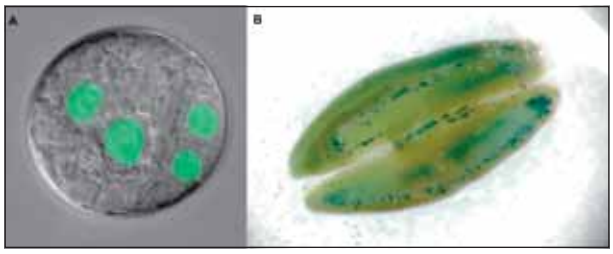

Fig. 45
Development of transgenic lines generated to facilitate the analysis and manipulation of pollen embryogenesis. A: Live embryogenic pollen grain stably expressing a *ZmUbi1*-promoter::*NLS:sgfp* construct shown by confocal laser scanning microscopy. The specific intracellular targeting of GFP (green) greatly improves the visibility of the nuclei *in vivo* (D. Dhagma, research group Structural Cell Biology. B: Immature anther of a transgenic tobacco plant harbouring an *Ntm19*-promoter::*Gus* construct. The specificity of the *Ntm19*-promoter is shown by histochemical detection of GUS activity (blue) which is confined to the immature pollen grains (J. Kumlehn).

To provide a technological prerequisite for the investigation of interactions of maize and fungal microbes, a reliable method of ***Agrobacterium*-mediated gene transfer to immature zygotic maize embryos** was developed. In Hi II hybrids, an average transformation efficiency of ca. 10 % was achieved, i.e. 10 independent primary transgenic lines are obtained per 100 inoculated embryos, with the maximum efficiency being over 40 %. This protocol proved also applicable to the maize donor lines DH141, A-18 and 'Early Golden Bantam', albeit with lower efficiency (Ch. Kastner, H. Büchner, S. Wolf).

A novel strategy has been pursued to generate selectable marker-free transgenic barley lines instantly homozygous for the transgene. Primary co-transgenic plants (T_0) containing both the selectable marker gene and a model gene-of-interest were produced via *Agrobacterium*-mediated gene transfer to immature embryos using two independent T-DNAs, with a total of 14 different inoculation variants being applied. A comparison of these treatments revealed that if the two binary vectors used together in one *Agrobacterium* clone the **generation of selectable marker-free, homozygous transgenic lines** was the most efficient. In two thirds of the co-transgenic lines generated by this method, the gene-of-interest segregated uncoupled from the selectable marker in the doubled haploid T_1 generation which was obtained via embryogenic pollen culture. Compared to conventional (i.e. sexual) segregation procedures, the **implementation of haploid technology in a co-transformation approach** was shown to be considerably less time-consuming and more efficient in producing true-breeding, selectable marker-free transgenic barley (E. Kapusi, G. Hensel, C. Marthe, I. Otto, S. Wolf).

Germins and Germin-like proteins (GERs) are involved in plant development and defense. In collaboration with the Transcriptome Analysis group (P. Schweizer, A. Himmelbach) and the MPI for Terrestrial Microbiology in Marburg (G. Döhlemann), the **pathogen-inducible, epidermis-specific barley *GER4c* promoter**, which had first been functionally characterised in barley, was analyzed in maize. At the end, 194 independent transgenic maize lines carrying the *Gus* gene under control of the *HvGER4c* promoter were produced. Most of the 42 lines tested so far showed promoter activity confined to epidermis cells penetrated by the fungal pathogen *Ustilago maydis* or upon contact with conidia of the host-incompatible fungus *Blumeria graminis hordei* (Ch. Kastner, H. Büchner, S. Wolf).

In a further cooperation with the Transcriptome Analysis group we are aiming to create transgenic wheat plants with increased resistance towards powdery mildew (*Blumeria graminis* f. sp. *tritici*). Under consideration of the allohexaploid genome of wheat which carries three homoeologues of the susceptibility factor gene *Mlo* (*TaMloA1*, *TaMloB1*, *TaMloD1*), we have embarked on an RNA interference-based knock-down approach. Transgenic plants stably expressing the ***Ta*Mlo-RNAi** cassette were created out of which three lines were selected to generate doubled haploid (DH) lines. The genetically homogeneous nature of each DH line's progeny enabled us to greatly reduce the phenotypic variability of the transgenic material in *Blumeria* infection experiments, thereby eventually identifying some DH-lines showing significantly reduced susceptibility (J. Riechen, H. Büchner, S. Wolf, E. Grützemann, C. Marthe, I. Otto, A. Müller).

Homozygous transgenic, **selectable marker-free winter wheat lines expressing the barley sucrose transporter *SUT1* gene** were generated in cooperation with the Seed Development group. Experiments based on several hundred T_3-plants under field-like conditions revealed a consistent and significant **increase in the thousand grain weight**, while one of the lines also showed a significantly improved nitrogen yield as compared to wild type plants (I. Saalbach, P. Hoffmeister, S. Knüpffer).

Collaborations (selection)

Within the Institute:

Dept. of Cytogenetics and Genome Analysis, Research Group Karyotype Evolution; Prof. I. Schubert;
Dept. of Molecular Genetics, Research Group Seed Development; Dr. W. Weschke, Dr. H. Weber, Dr. N. Sreenivasulu;
Dept. of Molecular Genetics, Research Group Gene Regulation; Dr. H. Bäumlein, D. Koszegi;
Dept. of Molecular Genetics, Research Group Phytoantibodies; Dr. U. Conrad, D. Floß;
Dept. of Physiology and Cell Biology, Research Group Applied Biochemistry; Dr. H.-P. Mock;
Dept. of Physiology and Cell Biology, Research Group Structural Cell Biology; Dr. M. Melzer.

Outside the Institute:

BASF Plant Science, Ludwigshafen; Dr. T. Wetjen, Dr. S. Bieri;
KWS and Planta GmbH, Einbeck; C. Springmann, Dr. K. Schmidt;
Technical University Munich, Institute of Phytopathology, Munich; Prof. R. Hückelhoven;
Max Planck Institute for Terrestrial Microbiology, Marburg; Dr. G. Döhlemann;
National Institute of Agrobiological Sciences, Plant Genome Research Unit, Tsukuba, Japan; Dr. T. Komatsuda.

Publications

Peer Reviewed Papers

2008

Abera, B., L. Negash & J. Kumlehn: Reproductive biology in the medicinal plant, *Plumbago zeylanica* L. Afr. J. Biotechnol. 7 (2008) 3447-3454.

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Pathuri, I.P., N. Zellerhoff, U. Schaffrath, G. Hensel, J. Kumlehn, K.H. Kogel, R. Eichmann & R. Hückelhoven: Constitutively activated barley ROPs modulate epidermal cell size, defense reactions and interactions with fungal leaf pathogens. Plant Cell Rep. 27 (2008) 1877-1887.

Weigelt, K., H. Küster, R. Radchuk, M. Müller, H. Weichert, A. Fait, A.R. Fernie, I. Saalbach & H. Weber: Increasing amino acid supply in pea embryos reveals specific interactions of N and C metabolism and highlights the importance of mitochondrial metabolism. Plant J. 55 (2008) 909-926.

2009

Floss, D.M., J. Kumlehn, U. Conrad & I. Saalbach: Haploid technology allows for the efficient and rapid generation of homozygous antibody-accumulating transgenic tobacco plants. Plant Biotechnol. J. 7 (2009) 593-601.

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Kumlehn, J. & G. Hensel: Genetic transformation technology in the Triticeae. Breed. Sci. 59 (2009) 553-560.

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Saker, M., H. Ghareeb & J. Kumlehn: Factors Influencing transient *Agrobacterium*-mediated GUS expression in embryogenic callus of date palm. Adv. Horticult. Sci. 23 (2009) 150-157.

Sharbel, T.F., M.L. Voigt, J.M. Corral, T. Thiel, A. Varshney, J. Kumlehn, H. Vogel & B. Rotter: Molecular signatures of apomictic and sexual ovules in the *Boechera holboellii* complex. Plant J. 58 (2009) 870-882.

Weigelt, K., H. Küster, T. Rutten, A. Fait, A.R. Fernie, O. Miersch, C. Wasternack, R.J. Emery, C. Desel, F. Hosein, M. Müller, I. Saalbach & H. Weber: ADP-glucose pyrophosphorylase-deficient Pea embryos reveal specific transcriptional and metabolic changes of carbon-nitrogen metabolism and stress responses. Plant Physiol. 149 (2009) 395-411.

Zimmermann, J., I. Saalbach, D. Jahn, M. Giersberg, S. Haehnel, J. Wedel, J. Macek, K. Zoufal, G. Glünder, D. Falkenburg & S.M. Kiprijanov: Antibody expressing pea seeds as fodder for prevention of gastrointestinal parasitic infections in chickens. BMC Biotechnol. 9 (2009) 79.

Books and Book Chapters

2009

Gugsa, L. & J. Kumlehn: Haploidy in Tef. In: Touraev, A., B.P. Forster & M.S. Jain (Eds.): Advances in haploid production in higher plants. Springer Netherlands, Dordrecht/The Netherlands (2009) 265-284.

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Kumlehn, J.: Embryogenic pollen culture: a promising target for genetic transformation. In: Touraev, A., B.P. Forster & M.S. Jain (Eds.): Advances in haploid production in higher plants. Springer Netherlands, Dordrecht, The Netherlands (2009) 295-305.

Weber, H., R. Radchuk, K. Weichert & I. Saalbach: Changing metabolic pathways to manipulate legume seed maturation and composition. In: Krishnan, H.B. (Ed.): Modification of seed composition to promote health and nutrition. American Society of Agronomy, Madison, WI/USA (2009) 55-78.

Patents

2009

Schweizer, P., G. Hensel, A. Gay & J. Kumlehn: Method for creating broad-spectrum resistance to fungi in transgenic plants. WO 2009/112270, Anmeldetag: 13.03.2008, Anmelder: IPK, Offenlegung: 17.09.2009, IPK Nr. 2008/01.

Research Group: Yeast Genetics

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Kaiser, Christian (0,25 Annex, since 01.12.2009)
Scholz, Anja (0,5 Annex, till 30.04.2008)
Sedzielewska, Kinga (0,5 Annex, 01.11.2008-31.01.2009)

Grant Positions
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Gerlach, Torsten (0,5 Overhead, 01.05.-31.05.2009; 0,5 BMBF, since 01.06.2009)
Giersberg, Martin, Dr. (IGF, since 01.08.2009)
Kaiser, Christian (0,5 Saxony-Anhalt, 15.08.2008-30.11.2009)
Körner, Martina, Dr. (IGF)
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Sedzielewska, Kinga (0,5 BMBF, 01.05.-31.10.2008)
Trautwein, Anke (0,25 Overhead, 01.04.-31.05.2009; 0,5 AIF, since 01.06.2009)
Wasiewicz, Dagmara (0,5 AIF, since 01.06.2009)

Visiting Scientists/Scholars
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Alvaro Benito, Miguel (CBMSO-Scholarship Madrid, 14.09.-18.12.2009)
Baronian, Keith, Dr. (Ministry New Zealand/DLR, 13.09.-25.09.2008)
Beri, Shanuja, Dr. (BMBF/DLR, 12.05.-07.07.2008)
Borrero, Juan (University Complutense Madrid, 15.04.-24.07.2009)
Krasovska, Olena (FEMS Research Fellowship, 18.09.-30.11.2009)
Kumar, Pardeep (DAAD, 03.04.-31.07.2008)
Pham, Thi Minh Ha (MOET Vietnam, since 03.02.2009)
Sedzielewska, Kinga (COMEAST scholarship, till 30.04.2008; AMykor GmbH, since 01.02.2009)
Vajpai, Shilpi (BMBF/DLR, 23.06.-15.09.2008)
Watzke, Katja (DBU-Scholarship, till 31.12.2008)

Goals

The major objective of the research group is the development of yeast as a model organism for the analysis of **osmo- and salt-tolerance**, as valuable tool for characterisation of **metabolic pathways** in eukaryotes, as microbial component for **biosensors** and as an expression platform for **heterologous gene expression**. The latter is being exploited for **functional gene analysis** in plants and microbes, as well as for the production of heterologous proteins. The yeast species used includes both *Saccharomyces cerevisiae* and **non-*Saccharomyces* yeasts** such as *Arxula adeninivorans* and *Hansenula polymorpha*. Yeast and filamentous fungi also constitute a source of genes which could be used for metabolic redesign of plants in order to engineer improved quality of end products, or to develop recombinant microbes for use as biosensors of environmental pollution.

Research Report

Yeast, such as *A. adeninivorans* which has extremely high levels of **osmo- and salt-tolerance,** are particularly suitable as model organisms for detailed analyses of this phenomenon in plants and yeasts. The programme which includes the intergroup project "Molecular analysis of salt-tolerance in barley" as well as the analysis of this tolerance in the osmo- and salt-tolerant yeast *A. adeninivorans* is focused on the analysis of the key pathways which underlie this tolerance and the identification of compatible solutes. cDNA sequences of barley and *A. adeninivorans* encoding for products improving osmo- and salt-tolerance are being identified after transformation of the osmo- and salt-sensitive yeast *S. cerevisiae*. The analysis of the selected *A. adeninivorans* genes including gene products demonstrates that in contrast to organisms with moderate osmo- and salt-resistance, which activate the **HOG pathway** by the phosphorylation of the relevant enzymes, highly osmo- and salt-resistant yeasts additionally induce the expression of all genes included in this pathway such as *ASLN1, AYPD1, ASSK1, ASTE20,* the MAPKK kinases *ASTE11* and *ASSK2*, the MAPK kinase *APBS2* as well as the MAP kinase *AHOG1.* Only the sensor-protein Asho1p is expressed by a constitutive gene. 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 osmolarity of medium. This effect, together with the combination of phosporylation and gene induction, seems to provide better adaptation during transition from low to high osmolarity conditions. In addition biochemical analysis has shown that *A. adeninivorans* is able to synthesise mannitol by two pathways; (1) fructose can be converted to mannitol by using a NaCl inducible mannitol dehydrogenase and (2) fructose-6-phosphate is converted via mannitol-1-phosphate to mannitol with the enzymes mannitol-1-phosphate-dehydrogenase (not NaCl inducible) and an unspecific phosphatase. Since

both enzymes are encoded by different genes and use different coenzymes, we could demonstrate that the function of these two pathways resulted in the conversion of NADH & NADPH and the use of mannitol as carbon source and a compatible solute. Analysis of gene expression levels including the construction of the respective gene disruption mutants should clarify this phenomenon in more detail (E. Böer, A. Trautwein, M.R. Hajirezaei, research group Molecular Plant Nutrition).

In addition *A. adeninivorans* is able to assimilate and ferment many compounds as its sole source of energy and carbon. This includes tannic acid, gallic acid, pyrogallol, protocatechuic acid, purine and uric acid. The metabolism of these compounds is based on pathways that are either completely unknown or only partially characterised (e.g., tannic acid and purine biodegradation). Based on the complete genome data which are available at the IPK, the first steps in **tannic acid metabolism** were identified and characterised by means of the isolation and characterisation of the genes involved and their respective gene products. Tannic acid is hydrolysed to gallic acid by the enzyme tannase, and subsequently converted to pyrogallol by gallate decarboxylase. The third step is the conversion of pyrogallol to 2-hydroxy mucoic acid by catechol-1.2 dioxygenase. All of the tannic acid and gallic acid inducible genes, which are of biotechnological interest, were isolated and over-expressed by strong inducible promoters in the homologous *Arxula* system. Based on the gene encoding tannase, a production strain was constructed by the newly established Xplor2 yeast expression system which allows the construction of resistance-marker free, mitotic stable transformants with very high expression levels of the *tannase* gene. The recombinant tannase is currently being tested for its suitability as supplement in animal feedstock to reduce the amount of tannic acid and as additive to improve biogas production based on plant materials (E. Böer, D. Wasiewicz, M. Benito Alvaro, J.B. del Pino, O. Krasovska, H.-P. Mock, research group Applied Biochemistry, see Fig. 46).

As second pathway the **purine degradation pathway** was characterised. All genes involved in this pathway are purine inducible genes. They express the enzymes which hydrolyse the purine nucleosides adenosine, inosine, xanthosine, guanosine to adenine, hypoxanthine, xanthine and guanine via uric acid to allantoin. After construction of super-transformants which produces and accumulates the respective recombinant enzymes in high levels, they are currently being tested for their suitability to reduce the purine content, especially the uric acid, in food (A. Trautwein, D. Wasiewicz, J. Radzikowski).

Another established direction in the research group covers the development of yeast biosensors (mainly *A. adeninivorans*) for the detection of hormone activities in environmental samples, urine, blood and milk. Sensors are based on recombinant *A. adeninivorans* cells which include the human estrogen receptor α (hERα), the human androgen receptor (hAR) and are designed as estrogen/

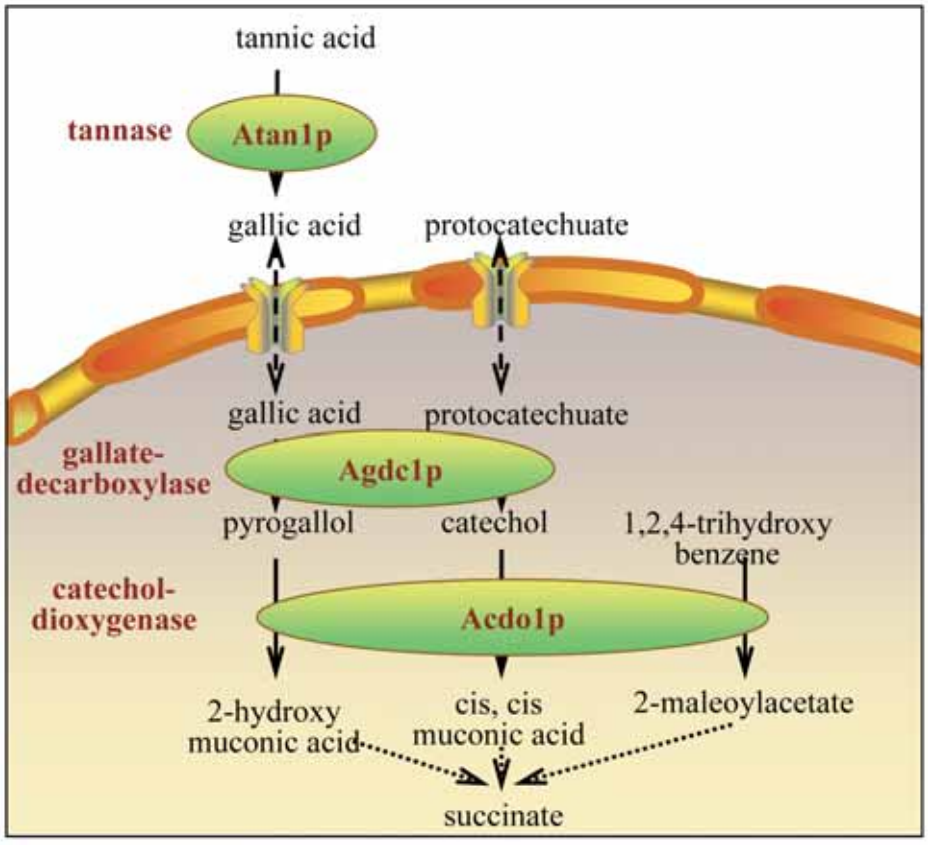

Fig. 46
Tannic acid degradation pathway of the yeast *Arxula adeninivorans* LS3. The secreted tannase Atan1p hydrolyse tannic acid extracellular into gallic acid and glucose. The gallic acid is transported into the cell where it is transformed into pyrogallol by the gallate decarboxylase Agdc1p. Subsequently the catechol dioxygenase Acdo1p transforms pyrogallol by ring cleavage into 2-hydroxy-muconic acid which is degradated to succinate. Both enzymes gallate decarboxylase and catechol dioxygenase exhibit a wide substrate spectrum, that means they are additionally involved in the degradation of protocatechuate and 1,2,4 trihydroxybenzene (E. Böer, R. Bode – University Greifswald).

androgen screen assays with biochemical measurement as well as microbial biosensors with an amperometric detection method. The **estrogen screen assay (A-YES assay)** has been validated for its suitability to measure estrogens and estrogen-like substances in samples of tap water, mineral water and different wastewater treatment plants which have high matrix effects. With a detection limit of approx. 2 ng l^{-1} for 17 ß-estradiol (E2), an in-house reproducibility lower than 5 ng l^{-1} the assay is applicable for a range of 2 to 80 ng l^{-1} effective E2 concentration. In combination with the **androgen screen assay (A-YAS assay)** the suitability of both sensors to analyse urine samples from female swine, calves and cattle was tested. For this purpose, the GS-MS analysis was used as a reference method. Calculation of the androgen/estrogen correlation gave a parameter which allows direct comparison between the urine samples (C. Kaiser, T. Gerlach, M. Giersberg, D. Strub, K. Florschütz).

DNA biosensors for the taxonomic analysis of fungi (arbuscular mycorrhiza) for the identification and classification of mycorrhiza residing on plant roots and the detection of phytopathogenic viruses on barley and potato have been developed and adapted. Based on DNA hybridisation, a **molecular beacon** microtiter plate assay and a microchip based on the **surface plasmon resonance technique,** is 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 *Vetiveria zizanioides,* and in a wood population growing under extreme conditions (K. Florschütz, A. Schröter, M. Körner, K. Sedzielewska, G. Oswald, see Fig. 47).

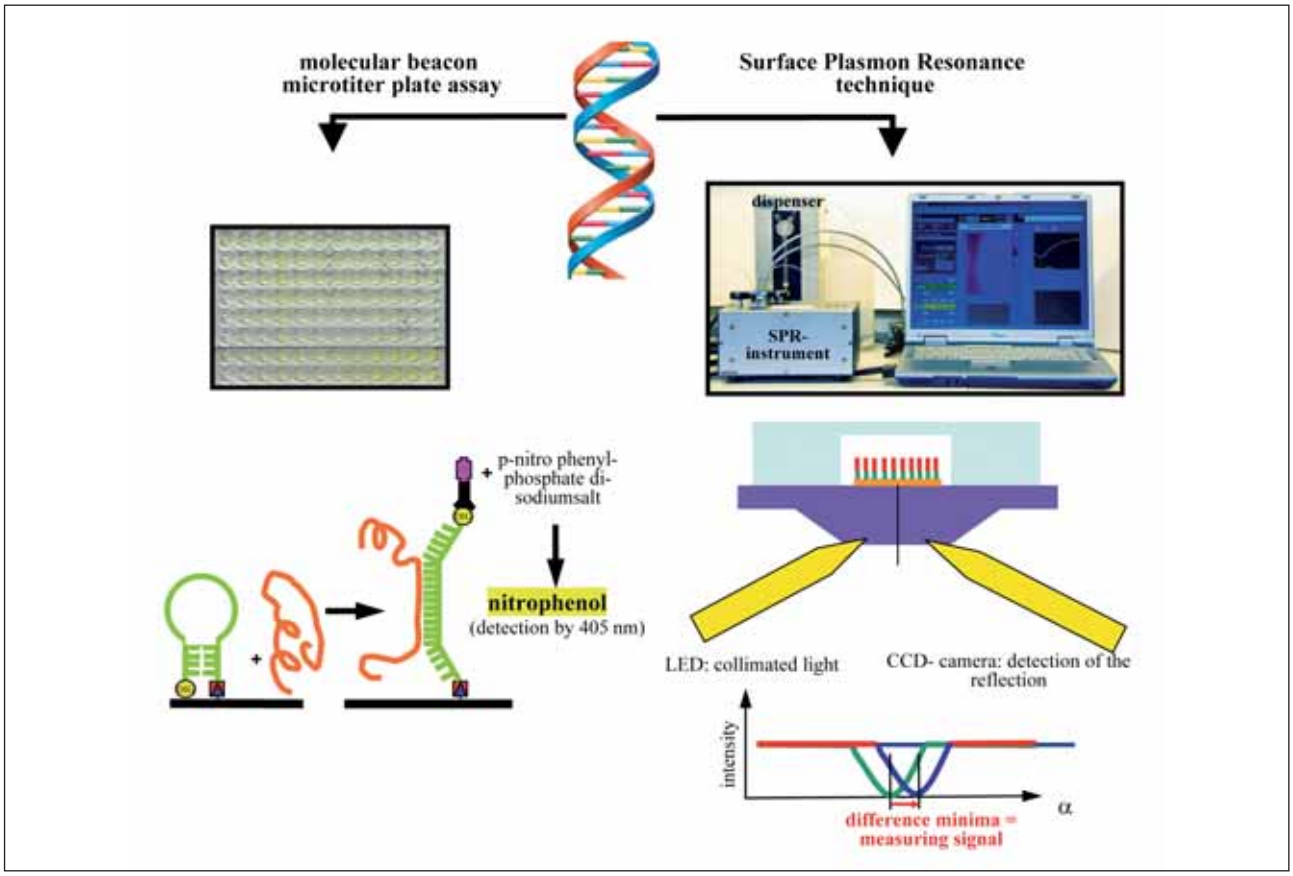

Fig. 47
DNA biosensors are used for the detection of arbuscular mycorrhiza on plant roots and phytopathogenic plant viruses based on a molecular beacon microtiter plate assay and the surface plasmon resonance technique.
For the molecular beacon microtiter plate assay arbuscular mycorrhiza or virus primers with digoxigenin (DIG) labelled 5´-end and biotin labelled 3´-end were bound on a streptavidin coated microtiter plate. Since both primer ends contain complementary nucleotide sequences, a loop structure is formed with the respective arbuscular mycorrhizal fungi or virus sequences internally. If the sample contains arbuscular mycorrhizal fungi or virus DNA they hybridised to the complementary loop sequences, at which the loop-structure is leaved and the DIG labelled 5´-end of the primers is able to bind anti-digoxigenin antibody, conjugated with alkaline phosphatase (AP). The hybridisation reaction can be detected by the phosphatase reaction.
The DNA sensor is based on a surface plasmon resonance technique which is composed of a SPR-chip with a gold surface and integrated optical elements. This focalises collimated light of a LED onto the gold surface. The refractive index of specific media with a specific angle of incidence, characterises the stimulation of surface plasmons on a specific region of the gold surface. At this location the reflection decreases, which is detected by the camera. The immobilisation of primers and the hybridisation reaction on the gold surface cause changes of thickness on top of the surface and therefore a change of the refractive index. Thus the angle of incidence towards stimulating the surface plasmons and decreasing reflection are changed. The reflected light leaves the SPR-chip as collimated light and is registered by a CCD camera. The minima are detected, differences and shifts of the minima are calculated by specific software and are documented on hard disk (K. Florschütz, R. Watzke – AMykor GmbH; A. Schröter, M. Körner, F. Sonntag – Fraunhofer-Institut für Werkstoff- und Strahltechnik).

Collaborations (selection)

Within the Institute:
Dept. of Cytogenetics and Genome Analysis, Research Group Transcriptome Analysis; Dr. P. Schweizer;
Dept. of Molecular Genetics, Research Group Phytoantibodies; Dr. U. Conrad;
Dept. of Physiology and Cell Biology, Research Group Molecular Plant Nutrition; Dr. M. Hajirezaei;
Dept. of Physiology and Cell Biology, Research Group Applied Biochemistry; Dr. H.-P. Mock;
Dept. of Physiology and Cell Biology, Research Group Structural Cell Biology; Dr. M. Melzer;
Dept. of Physiology and Cell Biology, Research Group Plant Reproductive Biology; Dr. J. Kumlehn.

Outside the Institute:
AMykor GmbH, Wolfen; Dr. R. Watzke;
Anhalt University of Applied Sciences, Köthen; Prof. G. Mägert, Prof. R. Pätz;
Arand Unternehmensberatungsgesellschaft mbH, Mühlhausen; Prof. E. Arand;
ARTES Biotechnology GmbH, Düsseldorf; Dr. M. Piontek;
ASA Spezialenzyme GmbH, Braunschweig; Dr. A. Cordes;
Baumschulen Oberdorla GmbH, Oberdorla; Dr. H. Dembny;
Bitop AG, Witten; Dr. G. Lentzen;
Bundesamt für Verbraucherschutz und Lebensmittelsicherheit, Referat 108 – EU- und Nationales Referenzlabor für Rückstände, Berlin; Dr. P. Gowik;
Christchurch Polytechnic Institute, Christchurch, New Zealand; Dr. K. Baronian;
Energy and Resources Institute (teri), Delhi, India; Dr. A. Adholeya;
Forschungszentrum Dresden-Rossendorf (FDZ), Dresden; Dr. L. Rebohle;
Gesellschaft für Silizium und Mikrosysteme mbH (GeSiM), Dresden; Dr. S. Howitz;
Institut für Energie- und Umwelttechnik e.V. (iuta), Duisburg; Dr. V. Plegge, Dr. J. Türk;
Institut für Werkstoff- und Strahltechnik (IWS), Dresden; Dr. F. Sonntag;
Kali-Umwelttechnik GmbH, Sondershausen; Dr. M. Schönau;
Lincoln Ventures Limited, Christchurch, New Zealand; Dr. N. Pasco;
Orgentis GmbH, Gatersleben; Dr. H.M. Vorbrodt;
PROLATEC GmbH, Dresden; Dr. G. Hanke;
Quo data GmbH, Dresden; Dr. S. Uhlig, K. Simon;
Technische Universität Dresden, Faculty Mechanical Engineering, Institute Food Technology & Bioprocess Engineering, Dresden; Prof. T. Bley;
UFL Umweltanalytik- & Forschungs GmbH, St. Egidien, Liechtenstein; Dr. D. Dornig;
University of Delhi, Department of Microbiology, New Delhi, India; Prof. T. Satyanarayana;
University of Greifswald, Institute of Genetics and Biochemistry, Greifswald; Prof. R. Bode, Prof. R. Schauer.

Publications

Peer Reviewed Papers

2008

Melmer, G., G. Kunze & G. Gellissen: Recombinant vaccine production in yeast. Biopharm Int. 1 (2008) 8-13.

2009

Böer, E., R. Bode, H.P. Mock, M. Piontek & G. Kunze: Atan1p - an extracellular tannase from the dimorphic yeast *Arxula adeninivorans*: molecular cloning of the *ATAN1* gene and characterization of the recombinant enzyme. Yeast 26 (2009) 323-337.

Böer, E., G. El Metabteb, A. El Fiki, P. Brückner, T. Wartmann, M. Piontek & G. Kunze: The MAPk *ASTE11* is involved in the maintenance of cell wall integrity and in filamentation in *Arxula adeninivorans*, but not in adaptation to hypertonic stress. FEMS Yeast Res. 9 (2009) 468-477.

Böer, E., M. Piontek & G. Kunze: Xplor® 2 - an optimised transformation/expression system for recombinant protein production in the yeast *Arxula adeninivorans*. Appl. Microbiol. Biotechnol. 84 (2009) 583-594.

Böer, E., A. Schröter, R. Bode, M. Piontek & G. Kunze: Characterization and expression analysis of a gene cluster for nitrate assimilation from the yeast *Arxula adeninivorans*. Yeast 26 (2009) 83-93.

Books and Book Chapters

2009

Böer, E., G. Steinborn, K. Florschütz, M. Körner, G. Gellissen & G. Kunze: *Arxula adeninivorans* (*Blastobotrys adeninivorans*) – a dimorphic yeast of great biotechnological potential. In: Satyanarayana, T. & G. Kunze (Eds.): Yeast Biotechnology: Diversity and Applications. Springer Science + Business Media B.V. (2009) 615-634.

Körner, M., S. Uhlig, K. Heide, K. Simon, C. Kaiser, K. Kunath, K. Florschütz, K. Suckau, E. Fischer & G. Kunze: Detection of estrogenic activities in environmental samples, urine and milk by a novel yeast biosensor. In: Kozlowski, R., G. Zaikov & F. Pudel (Eds.): Renewable resources - obtaining, processing and applying. Nova Science Publishers, New York (2009) 79-86.

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Kunze, G., A.H. Hang & G. Gellissen: *Hansenula polymorpha* (*Pichia angusta*): Biology and application. In: Satyanarayana, T. & G. Kunze (Eds.): Yeast Biotechnology: Diversity and Applications. Springer Science + Business Media B.V. (2009) 47-64.

Satyanarayana, T. & G. Kunze (Eds.): Yeast Biotechnology: Diversity and Applications. Springer Science + Business Media B.V. (2009) 547 pp.

Steinborn, G., G. Kunze & G. Gellissen: A wide range integrative expression vector (CoMed™) system for yeasts. In: Satyanarayana, T. & G. Kunze (Eds.): Yeast Biotechnology: Diversity and Applications. Springer Science + Business Media B.V. (2009) 357-368.

Patents

2008

Kunze, G., C. Tag, G. Steinborn, M. Koerner, K. Simon & G. Hanke: "Biosensor". WO 2008/152124, Anmeldetag: 12.06.2007, Anmelder: IPK, Offenlegung: 18.12.2008, IPK Nr. 2007/01.

Kunze, G. & G. Steinborn: Expression vectors for multiple gene interaction and overexpression of homologous and heterologous proteins in yeasts of the genus *Arxula*. WO2008/052797, Anmeldetag: 03.11.2006, Anmelder: IPK, Offenlegung: 08.05.2008, IPK Nr. 2006/07.

2009

Böer, E. & G. Kunze: Eukaryotic promoters for gene expression. WO2009/021853, Anmeldetag: 10.08.2007, Anmelder: IPK, Offenlegung: 19.02.2009, IPK Nr. 2007/03.

Research Group: Systems Biology

(since 1st July 2008)

Head: Dr. Björn H. Junker

Scientists

Grant Positions
Baker, Syed Murtuza (0,5 BMBF, since 01.01.2009)
Franke, Mathias (0,5 BMBF, since 01.05.2009)
Krach, Christian, Dr. (0,5 BMBF, since 01.10.2009)
Liiving, Tiina (0,5 BMBF, since 01.02.2009)
Schallau, Kai (BMBF, since 01.07.2008)

Goals

Investigating plant metabolic pathways, especially in developing seeds, with 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 are 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 was established on a 5-year **BMBF** grant as a **FORSYS-Partner Junior Research Group** in July 2008. Personnel had to be recruited and the laboratory had to be set up. Furthermore, the establishment of some major methods, which should become later the work of the group, was initiated. These are **kinetic modelling** on the dry lab side and steady state **metabolic flux analysis** on the wet lab side. In the FORSYS-Partner project, these methods will be applied to investigate metabolic processes taking place at the filling stage in **legume seeds**, especially pea (*Pisum sativum*) and barrel medic (*Medicago truncatula*, see Fig. 48). Various transgenic model systems are available for investigation via intra-institutional collaborations (H. Weber) and external ones (M. Udvardi). In the reported period, several kinetic models have been set up for these plants (K. Schallau, S. Weber, K. Lotz, S.M. Baker), covering central metabolism of the seeds. These models are constantly filled by experimental data, which are coming from metabolite and enzyme measurements (M. Müller, N. Schäfer, L. Fichtmüller), in material that in part has been fractionated into compartments earlier by a non-aqueous technique (T. Liiving). Parameters that could not be measured may be estimated by improved parameter estimation algorithm tailored for biochemical data (S.M. Baker). For steady-state metabolic flux analysis, several experimental and computational parts of the method had to be established in the group: embryo cultures, stable

Fig. 48
4-week old plantlets of the barrel medic, *Medicago truncatula* (N. Schäfer).

isotope feeding experiments and sample preparation (N. Schäfer), analysis by GC-MS, automatic data extraction and correction for natural isotope abundance (M. Müller, M. Franke), as well as model creation for pea and *Medicago* central metabolism (C. Krach). First detailed flux maps are expected for 2010.

In the early 2009, another BMBF project ("Multiscale Metabolic Modeling of barley") was initiated within the "**Bioenergy 2021**" framework as a collaboration with IPK-internal (F. Schreiber, M. Hajirezaei) and external partners (B. Usadel, J. Müller, R. Lemke). In this project, the flux analysis pipeline established for legumes is transferred to **barley seeds** (*Hordeum vulgare*). Therefore, a culture system had to be established, in this case spike cultures, which permitted to grow seeds over several days to about 20-fold initial biomass (F. Kellner, L. Fichtmüller). The analysis of ten introgression lines and ten diverse cultivars from the genebank barley core collection is currently under way. The flux data will then be compared with the other biochemical data, which is altogether integrated into **stoichiometric and kinetic pathway models**.

Collaborations (selection)

Within the Institute:

Dept. of Molecular Genetics, Research Group Seed Development; Dr. M. Müller, Dr. V. Radchuk, Dr. N. Sreenivasulu, Dr. H. Weber, Dr. W. Weschke;

Dept. of Molecular Genetics, Research Group Plant Bioinformatics; E. Grafahrend-Belau, A. Junker, Prof. F. Schreiber;

Dept. of Physiology and Cell Biology, Research Group Molecular Plant Nutrition; Dr. M.-R. Hajirezaei, Prof. N. von Wirén;

Dept. of Physiology and Cell Biology, Research Group Applied Biochemistry; Dr. H.-P. Mock;

Dept. of Physiology and Cell Biology, Research Group Plant Reproductive Biology; Dr. J. Kumlehn.

Outside the Institute:

Max Planck Institute of Molecular Plant Physiology, Dept. of Metabolic Networks, Potsdam-Golm; Prof. M. Stitt, Dr. B. Usadel;

Humboldt University Berlin, Institute for Theoretical Biology, Berlin; Dr. R. Steuer;

The Samuel Roberts Noble Foundation, Ardmore, USA; Dr. M. Udvardi;

Michigan State University, Dept. of Biology, East Lansing, USA; Prof. Y. Shachar-Hill;

BASF Plant Science Companies: Dr. C. Biesgen, Dr. I. Kunze, Dr. R. Lemke, Dr. M. Leps, K. Lotz (*SunGene*, Gatersleben); Dr. R. Fuchs, Dr. A. Krotzky (Metanomics, Berlin); Dr. V. Frankard (CropDesign, Ghent/Belgium).

Publications

Peer Reviewed Papers

2008

Grafahrend-Belau, E., F. Schreiber, M. Heiner, A. Sackmann, B.H. Junker, S. Grunwald, A. Speer, K. Winder & I. Koch: Modularization of biochemical networks based on classification of Petri net t-invariants. BMC Bioinformatics 9 (2008) 90.

Grafahrend-Belau, E., S. Weise, D. Koschützki, U. Scholz, B.H. Junker & F. Schreiber: MetaCrop: a detailed database of crop plant metabolism. Nucleic Acids Res. 36 (2008) D954-D958.

2009

Grafahrend-Belau, E., C. Klukas, B.H. Junker & F. Schreiber: FBA-SimVis: Interactive visualisation of constraint-based metabolic models. Bioinformatics 25 (2009) 2755-2757.

Grafahrend-Belau, E., F. Schreiber, D. Koschützki & B.H. Junker: Flux balance analysis of barley seeds: a computational approach to study systemic properties of central metabolism. Plant Physiol. 149 (2009) 585-598.

Steuer, R. & B.H. Junker: Computational models of metabolism: stability and regulation in metabolic networks. Adv. Chem. Phys. 142 (2009) 105-251.

Books and Book Chapters

2008

Junker, B.H.: Networks in biology. In: Junker, B.H. & F. Schreiber (Eds.): Analysis of biological networks. Wiley Book Series on Bioinformatics, John Wiley & Sons, Hoboken, NJ/USA (2008) 3-14.

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2009

Grafahrend-Belau, E., B.H. Junker, C. Klukas, D. Koschützki, F. Schreiber & H. Schwöbbemeyer: Topology of plant metabolic networks. In: Schwender, J. (Ed.): Plant Metabolic Networks. Springer New York (2009) 173-209.

Weise, S., C. Colmsee, E. Grafahrend-Belau, B. Junker, C. Klukas, M. Lange, U. Scholz & F. Schreiber: An integration and analysis pipeline for systems biology in crop plant metabolism. Proc. Int. Workshop "Data Integr. Life Sci." (DILS'09), Lect. Notes Bioinform. 5647 (2009) 196-203.

Weise, S., C. Colmsee, E. Grafahrend-Belau, B. Junker, C. Klukas, M. Lange, U. Scholz & F. Schreiber: Datenaustausch und Datenintegration zur Modellierung und Analyse metabolischer Netzwerke am Beispiel von Kulturpflanzen. In: Fischer, S., E. Maehle & R. Reischuk (Eds.): INFORMATIK 2009, Lect. Notes Inform. P-154 (2009) 693-697.

Pflanzengenom-Ressourcen-Centrum (PGRC)

Koordinator:
Dr. habil. Patrick Schweizer

Das Pflanzengenom-Ressourcen-Centrum (PGRC; http://pgrc.ipk-gatersleben.de/) des IPK erbrachte als Forschungs- und Dienstleistungsplattform in den Jahren 2008 und 2009 Serviceleistungen für interne Nutzer und externe Kooperationspartner, und koordinierte internationale Forschungsnetzwerke im Bereich Genomforschung des Getreides. An der Organisation des PGRC hat sich im Berichtszeitraum nichts geändert, abgesehen von einer Erweiterung der Serviceleistungen, die allerdings mit vorhandenem Personal erreicht wurde, wie untenstehend weiter ausgeführt werden soll.

Für den wissenschaftlichen Fortschritt der zum PGRC gehörenden Arbeitsgruppen wird auf die Jahresberichte der jeweiligen Gruppen verwiesen.

1. **PGRC-Service:**
   Neu wird ab 2008 ein „Genotyping"-Service auf MegaBACE 1000 angeboten, nachdem das Gerät für die Sanger-Sequenzierung vom System ABI 3730 abgelöst wurde. Dieser Service bietet den Nutzern DNA-Fragmentanalysen mit 96 Kapillaren an, wobei sich als optimale und flexible Lösung die Einarbeitung von ausgewählten Projektmitarbeitern der jeweiligen wissenschaftlichen Arbeitsgruppen durch PGRC-Personal als auch die Bereitstellung der benötigten Geräte-Verbrauchsmaterialien durch das PGRC herausgestellt hat.
   Neu wird ab 2009 ein „Next Generation Sequencing" (NGS) Service angeboten unter Verwendung des Roche/454 FLX Systems, das im BARLEX-Projekt (BMBF, Leiter Dr. N. Stein) zur „shotgun" als auch „BAC-by-BAC" Sequenzierung des Gerstengenoms angeschafft wurde. Für diese Serviceerweiterung wurde S. König, bis anhin zuständig für die Sanger-Sequenzierung des PGRC, in Kursen in die NGS-Methoden und Gerätebedienung eingearbeitet. Erste Aufträge aus dem IPK, wie die Sequenzierung des *Arxula adeninivorans* Genoms (Auftrag Ag Hefegenetik), sind erfolgreich durchgeführt worden.
   Die Unterstützung des TILLING-Projektes der Gerste (GABI-TILL, BMBF, Leiter Dr. N. Stein) im Haus wurde weitergeführt durch die Mitarbeit von B. Brückner, vorgängig mit zuständig für den Sanger-Sequenzierungs-Service. Im Verlauf von 2010 soll, im Zusammenhang mit der Beendigung des GABI-TILL-Projektes, eine gemeinsame Strategie des PGRC mit wissenschaftlichen Arbeitsgruppen gefunden werden, um

Plant Genome Resources Centre (PGRC)

Coordinator:
Dr. Patrick Schweizer

The Plant Genome Resources Centre (PGRC; http://pgrc.ipk-gatersleben.de/) of the IPK is a research and service platform and has provided service to users in-house as well as to collaborating partners in 2008 and 2009. In addition, PGRC has continued to coordinate international cooperations and networks in the field of crop plant genomics, especially barley genomics. Basically, the organisation of the PGRC has not changed during the reporting period although service offers have been extended as specified below. However, this was obtained by re-allocating responsibilities of current staff.

Scientific progress within working groups that belong to the PGRC is not presented here. Please refer to the annual reports of the corresponding groups.

1. **PGRC Service:**
   Since 2008 the new PGRC service "Genotyping" has been available on the MegaBACE 1000 instrument after it was replaced by the ABI 3730 instrument for Sanger sequencing. This service offers genotyping on 96 capillaries and consists of training of selected staff from scientific groups by PGRC staff that also provides consumables and technical support for the instrument.
   Since 2009 PGRC offers a Next Generation Sequencing (NGS) service on the Roche/454 FLX system, which was purchased within the project BARLEX (BMBF, head Dr. N. Stein) for shotgun as well as BAC-by-BAC sequencing of the barley genome. To run this new service, S. König, who had previously been responsible for the Sanger sequencing service, was trained in NGS methods as well as system operation. First NGS orders from within the IPK were performed successfully such as the sequencing of the *Arxula adeninivorans* genome (group Yeast Genetics).
   Support of the TILLING project of barley at the IPK (GABI-TILL, BMBF, head Dr. N. Stein) was continued by B. Brückner who formerly provided the Sanger-sequencing service together with S. König. During 2010, a strategy will be developed together with scientific groups at the institute in order to guarantee continuation of use of the TILLING platform after the GABI-TILL project will have ended.
   The remaining services of Arraying/Spotting (I. Walde) and of Libraries/Clones (S. Gentz) were contin-

die Nutzung der etablierten TILLING-Plattform zu verstetigen.
Die verbleibenden Dienstleistungen des „Arraying/Spotting“ (I. Walde) und des Banken/Klon-Service (S. Gentz) wurden weitergeführt. I. Walde hat zusätzlich die Durchführung des Sanger-Sequenzierungs-Service übernommen, zusammen mit S. König.

2. Netzwerke:
Zwei EU-Projektanträge zur Gerstengenom- und Diversitätsforschung wurden 2009 von BarleyGenomeNet, einem vom PGRC koordinierten Europäischen Netzwerk von Institutionen, eingereicht. Eine Entscheidung über Förderung der Projekte wird 2010 erwartet. Das BarleyGenomeNet-Jahrestreffen fand 2008 in Helsinki statt und 2009 in Mailand. Das nächste Treffen 2010 soll am IPK stattfinden. Ein weiteres, vom PGRC initiiertes bilaterales Deutsch-Ungarisches Netzwerk „PlantResource“, das vor allem die Verbesserung der abiotischen Stressresistenz von Getreide zum Ziel hat, wurde 2008 auf deutscher Seite abgeschlossen und läuft auf ungarischer Seite 2010 ebenfalls aus. Weitere für das PGRC bedeutsame Netzwerke wie das Internationale Gerstengenom-Sequenzierungs Konsortium (IBSC) und die COST-Aktivität „TritiGen“ wurden mit maßgeblicher Beteiligung von PGRC-Mitgliedern weitergeführt.
Die Schaffung thematischer „task forces“ wissenschaftlicher Arbeitsgruppen des IPK wurde Ende 2008 aus dem PGRC heraus vorgeschlagen. Ziel ist die Zusammenführung von Expertise in bestimmten Themenbereichen von arbeitsgruppenübergreifendem Interesse und ein effizienter Informationsfluss zwischen Wissenschaftlern im Hause. Perspektivisch könnten die „task forces“ auch eine Außenwirkung entfalten im Sinne eines geschärften Forschungsprofils des Instituts. Als erste wurde die „Association-Genetics Task Force“ ins Leben gerufen, koordiniert durch Dr. B. Kilian und Dr. I. Matthies. Eine Reihe von „task force“-Treffen fanden 2009 statt und förderten eine gemeinsame Wissensbasis für Methoden der Assoziationsgenetik. Darauf aufbauend sollen nun laufende assoziationsgenetische Projekte vertiefend diskutiert werden als auch Strategien für zukünftige (gemeinsame) Forschungsansätze entwickelt werden, nebst der Bereitstellung von *Know-how* für Einsteiger. Die Schaffung von vier weiteren PGRC „task forces“, nämlich „Phänotypisierung“ (Koordinator Prof. T. Altmann), „Abiotischer Stress“ (Koordinator Dr. P. Schweizer), „Metabolomics“ (Koordinator Dr. H.-P. Mock) und „Next Generation Sequencing“ (Koordinator Dr. N. Stein) sollen 2010 initiiert werden.

Patrick Schweizer, Januar 2010

ued. I. Walde is now sharing responsibility for the Sanger sequencing service with S. König.

2. Networks:
Two EU projects for barley functional genomics and diversity have been submitted in 2009 by BarleyGenomeNet, a European network of institutions that is coordinated by the PGRC. Funding decisions for these two proposals are expected in 2010. Annual meetings of the BarleyGenomeNet took place in Helsinki and Milano in December 2008 and 2009, respectively, and will take place at IPK in 2010. Funding for “PlantResource”, a bilateral German-Hungarian network initiated by the PGRC and aimed to enhance cereal yield security has ended in Germany in 2008 and will end in Hungary in 2010. Last but not least, further networks of high relevance to the PGRC such as the International Barley Sequencing Consortium (IBSC) and the COST action “TritiGen”were continued with strong commitment from PGRC members.
At the end of 2008 PGRC proposed the creation of task forces in order to combine scientific expertise in fields that are relevant to the interests of several research groups as well as to maximise the flow of information between IPK scientists. The task forces could in principle also reach out to further sharpen the research profile of the institute. First, the Association-Genetics Task Force coordinated by Dr. B. Kilian and Dr. I. Matthies came to life in 2009. A number of task-force meetings were organised and provided a common knowledge base of association-genetics approaches. This achievement will now be used to discuss in-depth current association-genetic projects and to develop strategies for future (common) projects, besides providing know-how for colleagues entering the field. The creation of four additional task forces was decided recently, namely “Phenotyping” (coordinator Prof. T. Altmann), “Abiotic Stress” (coordinator Dr. P. Schweizer), “Metabolomics” (coordinator H.-P. Mock) and “Next Generation Sequencing” (coordinator Dr. N. Stein).

Patrick Schweizer, January 2010

Die Entwicklung der Bioinformatik am IPK

Koordinator: Prof. Dr. Falk Schreiber

In den Jahren 2008/2009 hat sich die Bioinformatik kontinuierlich zu inzwischen fünf Arbeitsgruppen weiterentwickelt. 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.

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 der gemeinsam von allen Gruppen durchgeführte Intensivkurs Bioinformatik für die Christian-Albrechts-Universität zu Kiel (der in Zukunft im Rahmen der Kooperation IPK – Universität zu Kiel verstetigt wird); die internationalen Tagungen *International Symposium on Integrative Bioinformatics* vom 20. bis 22. August 2008 in der Leucorea Wittenberg, *International Workshop on Computational and Integrative Biology* vom 18. bis 20. September 2009 in Hangzhou (China), und *German Conference on Bioinformatics* vom 28. bis 30. September 2009 an der Martin-Luther-Universität Halle-Wittenberg (die von der Bioinformatik des IPK gemeinsam mit externen Kollegen organisiert wurden); sowie das neue Webportal http://bioinformatics.ipk-gatersleben.de (welches Informationen zu den Gruppen, zu am IPK entwickelten Datenressourcen und Software-Werkzeugen sowie aktuellen Veranstaltungen und Publikationen bietet). Zur Verbesserung der Zusammenarbeit hat sicher auch der Umzug von vier der fünf Gruppen ins Konrad-Zuse-Haus beigetragen.

Auch in den nächsten Jahren soll der erfolgreiche Kurs fortgeführt und die Bioinformatik am IPK im Kontext der biologischen Forschung am Institut weiterentwickelt werden. So ist die Stärkung von Bereichen geplant, die durch die Bioinformatik bisher nicht abgedeckt sind. Ein Beispiel ist die aktuell ausgeschriebene Arbeitsgruppe *Bildverarbeitung und automatische nicht-invasive Pflanzenphänotypisierung*.

Falk Schreiber, Januar 2010

The Development of Bioinformatics at IPK

Coordinator: Prof. Falk Schreiber

In 2008/2009 bioinformatics has continuously developed, encompassing now five bioinformatics 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.

To strengthen bioinformatics as a unit and increase its visibility beyond the IPK, in addition to their individual efforts, the bioinformatics groups have carried out a large number of joint activities. Worth mentioning here are: the bioinformatics course for the Christian-Albrechts-University at Kiel (which will be continued in the future as part of the cooperation between IPK and the University at Kiel); the international conferences *International Symposium on Integrative Bioinformatics* from 20th to 22nd August 2008 in the Leucorea Wittenberg, *International Workshop on Computational and Integrative Biology* from 18th to 20th September 2009 in Hangzhou (China), and *German Conference on Bioinformatics* from 28th to 30th September 2009 at the Martin Luther University of Halle-Wittenberg (which were organised by IPK bioinformatics groups along with external colleagues); as well as the new web portal http://bioinformatics.ipk-gatersleben.de (which offers information about the groups, to data resources and software tools developed at IPK as well as current seminars and publications). The relocation of four of the five groups to the Konrad-Zuse-Haus has certainly also contributed to the strengthening of collaboration between the groups.

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. Expansion of bioinformatics at IPK into new areas not yet covered is planned, for example, note the current opening for the research group *Image Analysis and Automated non-invasive Plant Phenotyping*.

Falk Schreiber, January 2010

Das Doktorandenprogramm

Sprecher: Nicolai M. Nürk

Bereits seit fünf Jahren besteht das *PhD Student Board* (PSB) als selbstorganisierte Doktoranden-Vertretung am IPK Gatersleben und ist seit 2008 mit einem eigenen Budget ausgestattet. Im selben Jahr haben sich die Mitglieder des PSB in einzelne Aufgabenbereiche organisiert und eine überarbeitete Internetpräsenz online gestellt: (www.ipk-gatersleben.de/Internet/Forschung/Doktorandenprogramm/StudentBoard).
Die verschiedenen PSB-Arbeitsgruppen organisieren neben gemeinschaftlich orientierten Veranstaltungen vor allem den Ausbau des Doktorandenprogramms und damit die Verbesserung der Ausbildung von Nachwuchswissenschaftlern am IPK. So wurden in den vergangenen zwei Jahren 16 bedeutende Wissenschaftler/-innen zu Vorträgen eingeladen (darunter die Nobelpreisträgerin Prof. Christiane Nüsslein-Volhard). Damit leistet das PSB einen Beitrag zum Seminarprogramm des IPK und fördert den Kontakt zwischen Doktoranden und der wissenschaftlichen Gemeinschaft über das IPK hinaus.
Als zweite Aktivität des PSB werden die mittlerweile fest in das Doktorandenprogramm integrierten Arbeitsseminare gesehen, in denen vor allem Sozial- und Schlüsselkompetenzen vermittelt werden. Insgesamt fanden seit Beginn des Seminar-Programms vor zwei Jahren 17 meist zweitägige Seminare statt, an denen mehr als 60 % der Doktoranden teilgenommen haben. Zu Beginn des Jahres 2009 wurde in Kooperation mit Dr. Tim Sharbel der wissenschaftliche Workshop „Methods in Population Genomics" organisiert.
Nach Evaluierung der verschiedenen Seminare durch die Teilnehmer und durch Nachfrage unter den Doktoranden hat das PSB mittlerweile ein Seminar-Angebot aufgebaut, das in Zukunft in einem ca. dreijährigen Turnus angeboten wird. Das wissenschaftlich orientierte Seminar-Angebot auszubauen, bleibt eine Zukunftsaufgabe im Rahmen des Doktorandenprogramms am IPK.
Als dritte, wichtige Aktivität des PSB hat sich die *Plant Science Student Conference* (PSSC) entwickelt, die von Doktoranden für Doktoranden jährlich im Wechsel mit dem IPB Halle ausgerichtet wird. Das letzte Mal 2008 am IPK mit fast 70 Teilnehmern und 2009 am IPB in Halle mit über 80 Teilnehmern ist die „Doktoranden-Konferenz" ein erfolgreiches und ständig wachsendes Treffen junger Wissenschaftler von Instituten der Leibniz-Gemeinschaft und der Max-Planck-Gesellschaft sowie der Julius Kühn-Institute.
Die vorerst letzte neu geplante, gemeinschaftlich und wissenschaftlich ausgerichtete Aktivität des PSB, ist die Etablierung eines Exzellenz-Wettbewerbes für das laufende Jahr innerhalb des IPK: der *Beagle Award*. Der Wettbewerb wird offen sein für alle Doktoranden des IPK und soll das Forschungsprojekt der Bewerber, als auch das

The PhD Programme

Speaker: Nicolai M. Nürk

The *PhD Student Board* (PSB), being the self-organised platform of graduate students at IPK Gatersleben for the last five years, manages its own budget starting in 2008. In the same year, the members of the PSB organised them selves into individual task forces and relaunched their own website (www.ipk-gatersleben.de/Internet/Forschung/ Doktorandenprogramm/StudentBoard).
The different PSB working groups are mainly engaged in the development of the graduate student programme and thus the improvement of education for young scientists at IPK. Contributing to the overall seminar programme of IPK and promoting discussion between graduate students and scientific community beyond IPK, 16 renowned scientists were invited by PSB to give lectures (amongst these the Nobel laureate Christiane Nüsslein-Volhard).
A workshop series teaching social and key competences became integral part of the graduate student programme. More than 60 % of graduate students participated in these 17 two-day seminars over the last two years.
After evaluation of the different seminars by participants and by interviewing graduate students, the PSB has developed a seminar programme that will be offered in a three-year-interval. Developing scientifically-oriented seminars remains a future task in the frame of the graduate student programme at IPK. However, in the early 2009, the scientific workshop "Methods in Population Genomics" has been co-organised already together with Dr. Tim Sharbel.
The *Plant Science Student Conference* (PSSC) was organised by PhD students for PhD students alternating with IPB Halle. PSSC 2008 at IPK attracted about 70 participants and PSSC 2009 at IPB Halle over 80 participants, reflecting that „The Student Conference" is a well received and constantly growing meeting of young scientists from institutes of the Leibniz Association, the Max Planck Society, and Julius Kühn-Institutes.
For 2010, the PSB plans an excellence competition: the *Beagle Award*. The competition will be open to all graduate students of IPK and will consider the research project of applicants as well as their commitment in organising community life at IPK. Applications will be evaluated by a jury of IPK scientists representing all career levels.

The further development of the graduate student programme has been discussed intensively by PSB members over the last two years. The *status quo* of training of PhD students at IPK is illustrated in Fig. 49, p. 150.
Evidently, the graduate student programme is mainly borne by the Board of Directors (and scientific administration) and is organised by the PSB. To

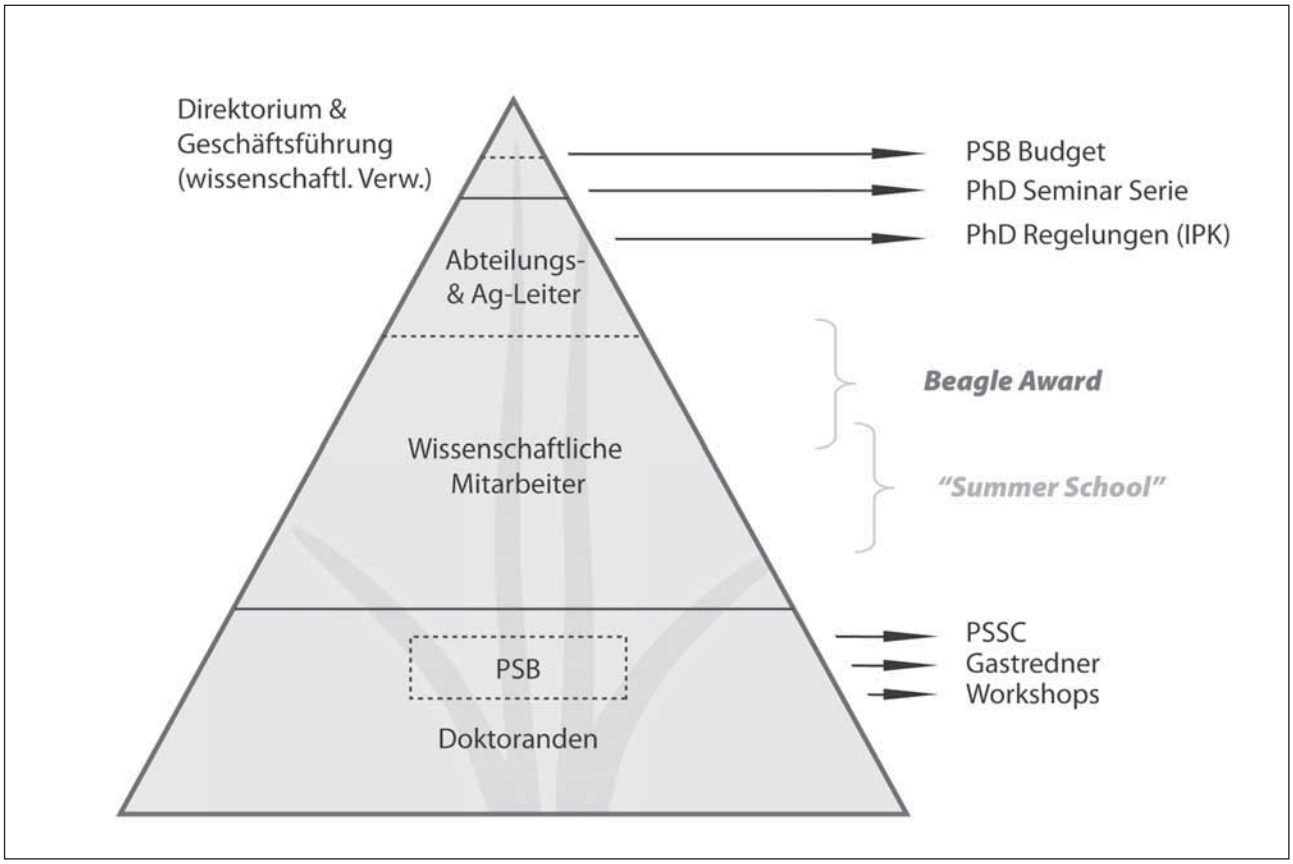

Fig. 49
Das IPK als Pyramide mit seinen verschiedenen wissenschaftlichen Stufen und deren Beitrag zum Doktorandenprogramm (rechts). In Grau dargestellt sind angestrebte Ergänzungen zu den bereits bestehenden Regelungen und Aktivitäten./ Pyramid with different scientific levels and their contribution (right) to the graduate student programme at IPK. Future activities of the already existing regulations and activities are highlighted grey (N. Nürk).

Engagement in Organisation und Gemeinschaftsleben des IPK berücksichtigen. Die Beurteilung der Kandidaten wird durch Vertreter verschiedener wissenschaftlicher Stufen des IPK erfolgen.

Der weitere Ausbau des Doktorandenprogramms wurde innerhalb des PSB in den vergangenen zwei Jahren intensiv diskutiert. Der *status quo* der Ausbildung von Doktoranden am IPK lässt sich wie in Fig. 49 darstellen.

Wie ersichtlich, wird das Doktorandenprogramm vor allem durch das Direktorium (und die wissenschaftliche Verwaltung) getragen und (bisher) durch das PSB organisiert. Als Ergänzung zum Bestehenden ist der *Beagle Award* geplant (als Auszeichnung persönlicher Leistungen), sowie die Einrichtung einer IPK-internen, wissenschaftlichen Seminarreihe (in Form einer „Summer School") erwogen worden. Dadurch sollen zu angekündigten Terminen die bekannten Disziplinen des IPK von IPK-Wissenschaftlern an die Doktoranden vermittelt werden.

Nicolai M. Nürk, Januar 2010

complement the existing programme, the *Beagle Award* (to honour personal engagement), and an IPK internal scientific seminar series (as a "summer school") are planned. For the latter, special disciplines at IPK will be taught to interested graduate students by IPK scientists.

Nicolai M. Nürk, January 2010

Vom Institut organisierte Tagungen und Veranstaltungen/ Conferences and Meetings Organised by IPK

2008

Mini-Workshop zum EU-Antrag „Marie Curie Initial Training Networks (ITN)"
14. März 2008, Gatersleben
7 Teilnehmer

IMPRS -Workshop „Methods in Plant Population Genetics"
14. - 18. April 2008, Gatersleben
18 Teilnehmer

Tag der offenen Tür der Genbank Teilsammlungen Nord „Junges Gemüse aus alten Zeiten – von Ackerbohne bis Zuckerwurz"
17. Mai 2008, Malchow/Poel
ca. 200 Teilnehmer

Tag der offenen Tür
4. Fest der Begegnung
7. Juni 2008, Gatersleben
ca. 2.000 Teilnehmer

Fig. 50
Besucher bereiten am Tag der offenen Tür 2008 in der Arbeitsgruppe *In vitro*-Erhaltung und Cryo-Lagerung Pflanzenmaterial für die Lagerung vor (Foto: B. Schäfer)./ Guests of the Open House Day 2008 preparing plant material for long term storage in the *In vitro* Storage and Cryopreservation lab (Photo: B. Schäfer).

„An Anthology of Molecular Biology"
Festsymposium zur Würdigung der Arbeiten von Prof. Dr. Ulrich Wobus
27. Juni 2008, Gatersleben
58 Teilnehmer

Fig. 51
Prof. Ulrich Wobus (r.) mit Forscherkollegen im Gespräch, die anlässlich des Abschieds-Symposiums nach Gatersleben kamen: Prof. Robert Goldberg (verdeckt), Prof. Lars Wieslander und Prof. Brain Larkins (v.l.) (Foto: H. Ernst)./ Exchange of thoughts with co-researchers on the occasion of the symposium held in honour of Prof. Ulrich Wobus (r.): Prof. Robert Goldberg (hidden), Prof. Lars Wieslander and Prof. Brain Larkins (from left) (Photo: H. Ernst).

Tag der offenen Tür zum „Internationalen Jahr der Kartoffel"
28. Juni 2008, Groß Lüsewitz
ca. 200 Teilnehmer

4th Plant Science Student Conference (PSSC)
1. - 4. Juli 2008, Gatersleben
70 Teilnehmer

Minisymposium „Plant Genomics"
9. Juli 2008, Gatersleben
85 Teilnehmer

2. Gaterslebener Gespräch 2008 „Programmierung und Reprogrammierung - Potentialität auf zellulärer und organismischer Ebene"
11. - 12. September 2008, Gatersleben
110 Teilnehmer

Verbundtreffen GABI-SysSeed
12. September 2008, Berlin
20 Teilnehmer

Institutstag 2008
Vortragsveranstaltung, Posterpräsentation aller wissenschaftlichen Arbeitsgruppen
29. - 30. September 2008, Gatersleben
ca. 200 Teilnehmer

Collaboration meeting apomixis *„Boechera – Hypericum"*
3. November 2008, Gatersleben
30 Teilnehmer

PGRC Meeting 2008
12. Dezember 2008, Gatersleben
30 Teilnehmer

2009

„Methods in Population Genomics" course (invited lectures and practical course)
2. - 5. Februar 2009, Gatersleben
20 Teilnehmer

Joint COST Action „TritiGen" (FA0604) und TriticeaeGenome Workshop „Triticeae Physical Maps – Development and Applications"
22. - 24. April 2009, Gatersleben
100 Teilnehmer

GABI-TILLING-Workshop
5. - 6. Mai 2009, Gatersleben
19 Teilnehmer

XI. Gaterslebener Begegnung „Der Begriff der Natur – Wandlungen unseres Naturverständnisses und seine Folgen"
7. - 10. Mai 2009, Gatersleben
ca. 140 Teilnehmer

Tag der offenen Tür am Standort Malchow/Poel „Genzentren – Kinderstuben unserer Kulturpflanzen"
16. Mai 2009, Malchow/Poel
ca. 250 Teilnehmer

Tag der offenen Tür am Standort Gatersleben
6. Juni 2009, Gatersleben
ca. 500 Besucher

Minisymposium „Taxonomy and Systematics of Wild and Cultivated Plants"
23. - 24. Juni 2009, Gatersleben
25 Teilnehmer

Fig. 52
Die Teilnehmer des gemeinsamen Workshops der COST Action FA0604 „Tritigen" und dem FP 7-Projekt „TriticeaeGenomics" (Foto: H. Ernst)./ The participants of the joint workshop of COST Action FA0604 „TritiGen" and FP 7 project „TriticeaeGenomics" gathered in front of the communication centre (Photo: H. Ernst).

Integration of Cryopreservation in Genebank Strategies
Meeting of Work Group 2 of the COST Action 871
„Cryopreservation of Crops Species in Europe“
9. - 11. September 2009, Gatersleben
39 Teilnehmer

23. Jahresmitgliederversammlung des Arbeitskreises Deutsche *In vitro*-Kulturen ADIVK
24. - 25. September 2009, Gatersleben
70 Teilnehmer

Institutstag 2009
12. - 14. Oktober 2009, Gatersleben
ca. 200 Teilnehmer

2nd Annual Hypericum Meeting
24. November 2009, Gatersleben
26 Teilnehmer

Fig. 53
Besucher des Tages der offenen Tür am Standort Malchow/Poel bestaunen die Pflanzenvielfalt (Foto: S. Hünmörder)./Visitors of the Open House Day at the Satellite Station Malchow/Poel (Baltic Sea) gazing at plant diverstity (Photo: S. Hünmörder).

Gatersleben Lectures

2008

10. Januar 2008
Prof. G. Jürgens, Lehrstuhl Entwicklungsgenetik, ZMBP, Eberhard-Karls-Universität, Tübingen, Germany: Axis formation in early embryogenesis.

15. Januar 2008
Prof. W. Gruissem, Institute of Plant Science, ETH Zurich, Switzerland: Systems analysis of integrated proteome and gene expression data.

12. März 2008
Prof. H. Puchta, Lehrstuhl Botanik II, Molekularbiologie und Biochemie der Pflanzen, Universität Karlsruhe (TH), Germany: My scientific life after Gatersleben: Genome instabilities and breast cancer.

13. März 2008
Dr. M. Van Lijsebettens, Chromatin and growth control group, Department of Plant Systems Biology, Ghent University, Ghent, Belgium: Impact of chromatin modifying complexes on plant growth.

27. März 2008
Prof. D. Schomburg, Abteilung für Bioinformatik und Biochemie, Institut für Biochemie und Biotechnologie, Technische Universität Braunschweig, Germany: From bioinformatics and metabolomics to systems biology.

15. April 2008
Prof. Y. Gleba, Managing Director, Icon Genetics GmbH, Halle/Saale, Germany: Novel expression technologies for making recombinant proteins in plants.

8. Mai 2008
Prof. W. Earnshaw, The University of Edinburgh, Scotland, UK: Heterochromatin kills kinetochores.

14. Mai 2008
Prof. E. Peiter, Institut für Agrar- und Ernährungswissenschaften, Pflanzenernährung, Martin-Luther-Universität Halle-Wittenberg, Halle/Saale, Germany: Cations on the move – The identification of novel cation channels and transporters.

19. Mai 2008
Dr. P. Zimmermann, Genevestigator/Bioinformatics, ETH Zurich, Switzerland: Modeling the spatio-temporal-response architecture of plant and animal transcriptomes.

3. Juni 2008
Dr. N. Stein, Abteilung Genbank, IPK, Gatersleben, Germany: The barley genome project – current state and future prospects.

10. Juni 2008
Prof. P. Hayes, Department of Crop and Soil Science, Oregon State University, Corvallis, Oregon, USA: Return to the wild: prospects for molecular breeding of malting and food barley.

17. Juni 2008
Dr. F. Engelmann, Research Institute for Development, Montpellier, France: Plant biodiversity conservation worldwide improved by *in vitro* culture and cryopreservation.

20. Juni 2008
Prof. A. Jerzmanowski, Laboratory of Plant Molecular Biology, University of Warsaw/IBB Polish Academy of Sciences, Poland: Chromatin remodeling and linker histones in plant development and in stress responses.

25. Juni 2008
Prof. K. Bachmann, Gatersleben: The evolution of genetic information.

30. Juni 2008
Prof. I. Broer, Institut für Bodenkunde und Pflanzenernährung, Universität Rostock, Germany: Biopolymers in plants: Cyanophycin as a suitable source for arginine and polyaspartat.

1. Juli 2008 (PSSC 2008)
Prof. M. Zabeau, Department of Molecular Genetics, Ghent University, Belgium: The food, feel and fuel challenge of plant science.

2. Juli 2008 (PSSC 2008)
PD Dr. F. Kirchhoff, Max-Planck-Institut für Experimentelle Medizin, Göttingen, Germany: Plastic structures in the brain – two-photon imaging uncovers dynamic cell-cell interactions.

4. Juli 2008 (PSSC 2008)
Prof. A. Brennicke, Molekulare Botanik, Universität Ulm, Germany: Can we still do science at the university?

9. Juli 2008 (Minisymposium „Plant Genomics")
Prof. T. J. Close, Department of Botany and Plant Sciences, University of California, Riverside, USA: Coupling expressed sequences and a BAC library to access the barley genome.

Prof. R. Waugh, Scottish Crop Research Institute, Invergowrie, Dundee, Scotland, UK: Steps towards the genomic dissection of barley morphology and development.

Prof. M. Morgante, Department of Crop Science and Agricultural Engineering, University of Udine, Italy: The structural and transcriptional landscape of the grape genome.

29. Juli 2008
Prof. A. Shutov, Laboratory of Protein Chemistry, State University of Moldova, Kishinev, Republic Moldova: Cupins: a protein superfamily.

18. August 2008
Prof. L. T. Binh, Institute of Biotechnology (IBT), Hanoi, Vietnam: Biotechnology approaches for control of Papaya Ringspot Virus (PSRV) and other virus diseases in Vietnam.

11. September 2008
Prof. A. Brennicke, Molekulare Botanik, Universität Ulm, Germany: RNA editing in plant mitochondria: Identification of a specific trans-factor.

16. September 2008
Dr. A. Koltunow, CSIRO Adelaide, Australia: Analysis of the locus responsible for the initiation of apomixis in the daisy-like plant *Hieracium*.

25. September 2008
Dr. A. J. Johnston, Institute of Plant Science, Plant Biotechnology, ETH Zurich, Switzerland: A cross-talk between retinoblastoma und polycomb controls cellular differentiation and genome integrity in *Arabidopsis.*

25. September 2008
Prof. H. Özkan, Department of Field Crops, Faculty of Agriculture, University of Cukurova, Adana, Turkey: Swimming in diversity: wild cereals in Turkey and their use for plant breeding.

24. November 2008
Prof. M. Udvardi, The Samuel Roberts Noble Foundation, Ardmore, OK, USA: Medicago functional and translational genomics.

3. Dezember 2008
Prof. C. Nüsslein-Volhard (Nobel laureate), Max-Planck-Institut für Entwicklungsbiologie, Tübingen, Germany: On flies and fishes and the origin of vertebrates.

15. Dezember 2008
Prof. S. Diekmann, Leibniz-Institut für Altersforschung, Fritz Lipmann-Institut, Jena, Germany: The human kinetochore and the mitotic checkpoint.

2009

19. März 2009
Prof. D. Geelen, VIB Ghent, Ghent, Belgium: *Arabidopsis thaliana* mutants producing unreduced microspores.

18. Juni 2009
Prof. G. Fincher, Australian Centre for Plant Functional Genomics, Adelaide, Australia: Evolutionary advances in cell wall biosynthesis in the grasses.

17. September 2009
Prof. M. Stitt, Max-Planck-Institut für Molekulare Pflanzenphysiologie, Golm, Germany: Systems analysis of diurnal regulation in *Arabidopsis*: How plants avoid a credit crunch in a fluctuating environment.

15. Oktober 2009
Prof. J. Loidl, University of Vienna, Center for Molecular Biology, Department of Chromosome Biology, Vienna, Austria: Meiotic chromosome pairing: How to find the right partner?

1. Dezember 2009
Prof. R. Wing, University of Arizona, Arizona Genomics Institute, Tucson, USA: Comparative genomics across the cereals: *Oryza* and Maize as model systems.

Eingeladene Vorträge auf internationalen Tagungen (Auswahl)/ Invited Lectures at International Conferences (Selection)

2008

V1. Blattner, F.R.: Hybridization and polyploidization – evolutionary accidents or driving forces of biodiversity? – Systematics 2008, 10. Jahrestagung der Gesellschaft für Biologische Systematik, 18. Internationales Symposium "Biodiversität und Evolutionsbiologie" der Deutschen Botanischen Gesellschaft, Göttingen, 07.-11.04.2008.

V2. Böer, E., A. Degelmann, S.G., M. Piontek & G. Kunze (vorgetragen von Kunze, G.): Wide Range Yeast Expression System Xplor – new results in *A. adeninivorans*. – 12th International Congress on Yeasts, Kiev/Ukraine, 11.-15.08.2008.

V3. Börner, A.: Plant genetic resources – maintenance and utilisation. – Congr. Int. Soc. Biol. Environ. Resposit. "No Resources, No Future", Seoul/Republic of Korea, 04.09.2008.

V4. Börner, A.: Plant genetic resources for future breeding. – 18th EUCARPIA General Congress "Modern Variety Breeding for Present and Future Needs", Valencia/Spain, 09.-12.09.2008.

V5. Börner, A., K. Neumann, U. Lohwasser, M.S. Röder, E.K. Khlestkina, O. Dobrovolskaya, T.A. Pshenichnikova, P. Martinek, M.R. Simon & B. Kobiljski (vorgetragen von Börner, A.): Germplasm collections as an important tool for breeding – examples on wheat. – Breeding 08, International Conference on Conventional and Molecular Breeding of Field and Vegetable Crops, Novi Sad/Serbia 24.-27.11.2008.

V6. Graner, A.: Overview on molecular mapping. – 10th International Barley Genetics Symposium (IBGS), Alexandria/Egypt, 05.-10.04.2008.

V7. Graner, A.: Exploiting biodiversity to breed barley, new trends in plant biology and biotechnology. – French Academy of Sciences, Paris/France, 15.-16.09.2008.

V8. Haseneyer, G., S. Stracke, H.-P. Piepho, A. Graner & H.H. Geiger (vorgetragen von Graner, A.): Association studies in a spring barley collection. – 10th International Barley Genetics Symposium (IBGS), Alexandria/Egypt, 05.-10.04.2008.

V9. Kaspar, S., A. Matros, F. Schreiber & H.-P. Mock (vorgetragen von Kaspar, S.): Characterization of the proteome of barley epidermis tissue and its responses to UV-B radiation. – PROTEOMLUX 2008, Luxembourg/Luxembourg 22.-25.10.2008.

V10. Kilian, B.: Einkorn wheat domestication. – Systematics 2008, 10. Jahrestagung der Gesellschaft für Biologische Systematik, 18. Internationales Symposium "Biodiversität und Evolutionsbiologie" der Deutschen Botanischen Gesellschaft, Göttingen, 07.-11.04.2008.

V11. Kilian, B.: Independent wheat B and G genome origins. – Systematics 2008, 10. Jahrestagung der Gesellschaft für Biologische Systematik, 18. Internationales Symposium "Biodiversität und Evolutionsbiologie" der Deutschen Botanischen Gesellschaft, Göttingen, 07.-11.04.2008.

V12. Kilian, B., H. Özkan, A. Walther, J. Kohl, T. Dagan, A. Graner, F. Salamini & W. Martin (vorgetragen von Kilian, B.): A dispersed-specific model of plant domestication. – 4th EPSO Conference 2008 "Plants for life", Toulon/France, 22.-26.06.2008.

V13. Knüpffer, H.: Plant genetic resources from Greece preserved in the German Genebank in Gatersleben, with emphasis on Hans Stubbe's Balkan Collections in 1941-1942. – 12th Panhellenic Conference of Hellenic Society of Plant Breeding, Naoussa/Greece, 08.-10.10.2008.

V14. Kumlehn, J.: Genetic engineering in barley: Current technologies and recent applications. – 10th International Barley Genetics Symposium (IBGS), Alexandria/Egypt, 05.-10.04.2008.

V15. Mock, H.-P.: Proteomics to evaluate genetic resources for stress defence responses. – International Symposium on Frontier in Plant Proteome Research, Tsukuba/Japan, 10.-11.03.2008.

V16. Schreiber, F.: Centrality analysis of biological networks and applications for gene regulation. – Systems Biology – From Molecules to Life, Melbourne/Australia, 19.-28.05.2008.

V17. Schreiber, F.: From pathways to systems – compiling, visualising and modelling of crop plant metabolism. – Systems Biology – From Molecules to Life, Melbourne/Australia, 19.-28.05.2008.

V18. Schreiber, F.: Integrative bioinformatics – from data to networks. – Humboldt Japanese-German Frontiers of Science Symposium, Mainz, 30.10.-02.11.2008.

V19. Lermontova, I., V. Schubert, J. Fuchs, J. Macas & I. Schubert (vorgetragen von Schubert, I.): The centromeric histone H3 variant in plants – what is different? – Cantoblanco Workshop on Biology "Chromatin at the nexus of cell division and differentiation", Madrid/Spain, 30.06.-02.07.2008.

V20. Stein, N., D. Schulte, T. Sretenovic Rajicic, B. Shi, P. Langridge & A. Graner (vorgetragen von Stein, N.): Towards a physical map of the barley genome. – Plant and Animal Genome XVI. Conference, San Diego/USA, 12.-16.01.2008.

V21. Stein, N.: Impact of next generation sequencing technology on barley genome sequencing? – 7th Plant Genomics European Meeting (Plant GEM 7), Albena/Bulgaria, 24.-27.09.2008.

V22. Wobus, A.M.: Embryonic stem cells: prospects for developmental biology and cell therapy – cardiac and pancreatic differentiation. – International Congress "Stem Cells in Tissue Homeostasis, Repair and Cell Therapy", Rome/Italy, 28.-30.05.2008.

V23. Wobus, A.M.: *In vitro* differentiation of murine embryonic stem cells into the pancreatic lineage. – 4th International Conference of the Collaborative Research Center SFB 575 "Experimental Hepatology", Düsseldorf, 07.-08.11. 2008.

2009

V1. Altmann, T.: Analysis of *Arabidopsis* natural variation in biomass accumulation and metabolism. – 25th Anniversary Symposium "Bioenergy: Harnessing Plant Metabolism", The Otto Warburg Minerva Center for Agricultural Biotechnology, Hebrew University of Jerusalem/Israel, 23.-25.02.2009.

V2. Altmann, T.: Analysis of *Arabidopsis* natural variation in biomass accumulation and metabolism. – 14th European Congress on Biotechnology, Barcelona/Spain, 13.-16.09.2009.

V3. Banaei, A., J. Fuchs, M. Seifert, M. Strickert, F. Roudier, T. Czauderna, V. Colot, A. Houben & M.F. Mette (vorgetragen von Mette, M.F.): Relationship between intraspecies hybridization and DNA/histone modification in *Arabidopsis thaliana* L. – International Conference on Heterosis in Plants, Stuttgart, 07.-09.09.2009.

V4. Blattner, F.R.: Phylogenetic and population level analyses to understand evolutionary processes in *Hordeum*. – 6th International Triticeae Symposium, Kyoto/Japan, 01.-05.06.2009.

V5. Börner, A., K. Neumann, B. Kobiljski, E. Khlestkina & U. Lohwasser (vorgetragen von Börner, A.): Genetic diversity in wheat – how to exploit? – EPSO Workshop on Plant Productivity for Food, Ghent/Belgium, 07.-08.09.2009.

V6. Douchkov, D., A. Johrde, A. Himmelbach, R. Aghnoum, R. Niks & P. Schweizer (vorgetragen von Schweizer, P.): Convergent evidence for genes underlying quantitative powdery mildew resistance in barley. – 12th International Cereal Rusts and Powdery Mildews Conference, Antalya/Turkey, 13.-16.10.2009.

V7. Graner, A.: LD mapping in barley: insights into the genetic architecture of agronomic traits. – Plant and Animal Genome XVII. Conference, San Diego/USA, 10.-14.01.2009.

V8. Hensel, G., D. Nowara, G. Zimmermann, A. Gay, J. Kumlehn & P. Schweizer (vorgetragen von Hensel, G.): Plant-expressed RNAi constructs to induce knock-down of fungal genes. – AgriGenomics World Congress, London/UK, 02.-03.07.2009.

V9. Houben, A.: Plant B chromosomes – what makes them different? – 17th International Chromosome Conference, Boone/USA, 23.-26.06.2009.

V10. Houben, A.: Histone H3 phosphorylation in plants – a dynamic affair. – Gordon Research Conference Epigenetics, The Holderness School, Plymouth, New Hampshire/USA, 09.-14.08.2009.

V11. Houben, A.: Plant B chromosomes – what makes them different? – 9th International Plant Molecular Biology (IPMB) Congress, St. Louis/USA, 25.-30.10.2009.

V12. Jakob, S.S., D. Rödder & F. R. Blattner (vorgetragen von Jakob, S.S.): Niche stability and niche shifts during speciation in *Hordeum*. – Niche Evolution Symposium, Zurich/Switzerland, 04.07.2009

V13. Keller, E.R.J., A. Senula & C. Zanke (vorgetragen von Keller, E.R.J.): Alliaceae in cryopreservation, achievements and constraints. – 1st International Symposium of ISHS Cryopreservation in Horticultural Species, Leuven/Belgium, 05.-08.04.2009.

V14. Kilian, B.: Genetic diversity, evolution and domestication of einkorn and emmer wheat in the Fertile Crescent. – Rank Prize Funds: Minisymposium on Domestication of Cereals and Exploitation of Genetic Diversity in Improvement. Grasmere/UK, 21.09.2009.

V15. Knüpffer, H.: Genetic resources of Triticeae - cultivated species and genebank collections. – 6th International Triticeae Symposium, Kyoto/Japan, 01.-05.06.2009.

V16. Kumlehn, J.: Genetic engineering in cereals: Current technologies for the elucidation of gene functions. – 6th International Triticeae Symposium, Kyoto/Japan, 01.-05.06.2009

V17. Kumlehn, J.: Generation of instantly true-breeding mutant barley lines through the use of embryogenic pollen cultures. – 1st FAO/IAEA Research Coordination Meeting (RCM) on Enhancing the Efficiency of Induced Mutagenesis through an Integrated Biotechnology Pipeline, Vienna/Austria, 25.-29.05.2009.

V18. Kunze, G.: Yeast - a valuable tool for characterization of metabolic pathways in eukaryotes, producer of recombinant proteins and microbial component for biosensors. – International Conference on Emerging Trends in Biotechnology & 6th Annual Convention of Biotech Research Society, Banaras Hindu University, Varanasi/India, 04.-06.12.2009.

V19. Mock, H.-P.: The plant aerial surface: analysis of trichomes and epidermal tissue. – 2nd Iranian Proteomics Conference, Royan Institute, Teheran/Iran, 23.-24.04.2009.

V20. Mock, H.-P.: Characterization of plant co-chaperones with homology to the human protein HOP (HSP-organizing protein). – 3rd Mexican Symposium on Mass Spectrometry, Molecular and Cellular Proteomics, San Luis Potosi/Mexico, 08.-12.11.2009.

V21. Schubert, I.: Interphase nuclear architecture in plants. – 17th International Chromosome Conference, Boone/USA, 23.-26.06.2009.

V22. Schubert, I.: Plant chromosome at interphase – Paired? Cohesed? Dynamic? – 34th FEBS Congress, Prague/Czech Republic, 04.-09.07.2009.

V23. Schubert, I.: The centromeric histone H3 variant in plants - still an enigma. – 9th International Plant Molecular Biology (IPMB) Congress, St. Louis/USA, 25.-30.10.2009.

V24. Schubert, V., A. Weissleder, J. Fuchs, I. Lermontova & I. Schubert (vorgetragen von Schubert, V.): Sister chromatid cohesion in higher plants. – Plant and Animal Genome XVII. Conference, San Diego/USA, 10.-14.01.2009.

V25. Sharbel, T.F.: Apomeiosis in *Boechera*: a wave of differential gene expression in megaspore mother cells. – 9th International Plant Molecular Biology (IPMB) Congress, St. Louis/USA, 25.-30.10.2009.

V26. Stein, N.: Barley genome sequencing: First steps. – Plant and Animal Genome XVII. Conference, San Diego/USA, 10.-14.01.2009.

V27. Stein, N.: Sequencing the barley genome accelerated by Next-Generation Sequencing Technology. – 19th ITMI and 3rd COST-Tritigen Joint Workshop, Clermont-Ferrand/France, 31.08.-04.09.2009.

V28. Stein, N.: Triticeae genome sequencing - burden or basis? – 9th International Plant Molecular Biology (IPMB) Congress, St. Louis/USA, 25.-30.10.2009.

V29. von Wirén, N.: A role of autophagocytosis in intracellular iron efficiency. – Phoenix Symposium "Protein complexes in signaling and development", Glasgow/UK, 25.-27.06.2009.

V30. Weber, H.: Molecular physiology and genetics of seed heterosis in the model "*Vicia faba*". – International Conference on Heterosis in Plants, Stuttgart, 07.-09.09.2009.

V31. Wobus, A.M.: Differentiation of embryonic stem cells into endoderm and pancreatic cells. – 21st Meeting of the European Society of Animal Cell Technology (ESACT), Dublin/Ireland, 07.-10.06.2009.

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/international)	Anzahl Teilnehmer
2008				
Plant and Animal Genomes Conference	12.-16.01.2008 San Diego USA	Scherago International Dr. E. Albertini, University of Perugia, Italy Dr. T.F. Sharbel	international	100
Cryopreservation of Crop Species in Europe	20.-23.02.2008 Oulu Finland	University Oulu Work Groups 1 and 2 of the COST Action Dr. J. Keller	international	50
Full Meeting of the ECPGR Cereals Network	21.-24.04.2008 Foça, Izmir Turkey	Aegean Agricultural Research Institute, Izmir, Turkey ECPGR, Rome Dr. H. Knüpffer	international	ca. 80
14. Mitteldeutscher Schweineworkshop	16.-17.05.2008 Bernburg	Mitteldeutscher Schweinezuchtverband Prof. G. Kunze K. Suckau	international	ca. 300
4th Swiss-Czech Symposium „Biopharmaceuticals – why use yeasts?“	22.-23.05.2008 Wädenswill Switzerland	Inst. Biotechnol. Zurich Univ. Appl. Sci. ZHAW E. Böer	international	ca. 200
NAROSSA 2008	09.-10.06.2008 Magdeburg	PPM Pilot Pflanzenöltechnologie Magdeburg e.V. Prof. G. Kunze	international	ca. 300
5th International Symposium on Adventitious Root Formation	20.06.2008 Madrid Spain	University of Alcala de Mendres Dr. M.R. Hajirezaei	international	ca. 150
XX. Internationaler Genetik-Kongress	12.-17.07.2008 Berlin	International Genetics Federation German Genetics Society Prof. I. Schubert	international	ca. 100
12th International Congress on Yeasts	11.-15.08.2008 Kiew Russia	Ukrainian Soc. Cell Biol. Prof. G. Kunze	international	ca. 400
5th International Symposium Integrative Bioinformatics	20.-22.08.2008 Lutherstadt Wittenberg	Leucorea R. Hofestädt, University Bielefeld, J. Köhler, Norway, P. Verrier, Rothamsted Research, UK Prof. F. Schreiber Dr. U. Scholz Dr. M. Lange	international	85
IWGSC-IBSC Workshop on Sequencing Technologies	11.-12.09.2008 Evry France	Genoscope National Sequencing Center Dr. N. Stein	international	100

Thema	Zeitpunkt der Veranstaltung Ort Land	Veranstalter/Mitorganisatoren (beteiligte Einrichtungen)	Art der Veranstaltung (national/international)	Anzahl Teilnehmer
European BioPerspectives	07.-09.10.2008 Hannover	DECHEMA Dr. B. Junker	international	50
Mini-Symposium "From basic science to biotechnological applications"	27.11.2008 Urla, Izmir Turkey	Izmir Institute of Technology Gulbahce Koyu Campus Dr. M.R. Hajirezaei	international	ca. 25
2. AMykor Symposium	03.12.2008 Greppin	AMykor GmbH Prof. G. Kunze Dr. K. Florschütz K. Sedzielewska	national	ca. 80
First Biology Conference for Iranian Scholars in Europe	06.-07.12.2008 Hamburg	Scientific Association of Iranian Biologists in Europe A. Amir-Hossein	international	ca. 100
2009				
Cryopreservation in Horticultural Species	05.-08.04.2009 Leuven Belgium	Catholic University Leuven COST Action 871 Dr. J. Keller	international	149
Cereal Diversity, Plant Domestication and Human History in the Fertile Crescent	10.-15.05.2009 Adana Turkey	University of Çukurova Dr. B. Kilian	international	25
6th International Triticeae Symposium	01.-06.06.2009 Kyoto Japan	Plant Germplasm Institute, Kyoto University, International Triticeae Consortium Dr. H. Knüpffer	international	128
Niche Evolution – A Unifying Concept for Systematics, Ecology, Paleontology and Conservation Biology	03.-05.07.2009 Zurich Switzerland	Institute of Botany University of Zurich Dr. F. Blattner	international	125
Annual Meeting and Scientific Conference Society of Low Temperature Biology	07.-09.09.2009 Hannover	Dr. J. Keller Dr. A. Senula	international	90
Workshop on Computational and Integrative Biology	18.-20.09.2009 Hangzhou China	Zhejiang University University of Bielefeld University of Essex Rothamsted Research Yamaguchi University Prof. F. Schreiber Dr. U. Scholz Dr. M. Lange	international	100
German Conference on Bioinformatics	28.-30.09.2009 Halle/Saale	MLU Halle-Wittenberg IPB Halle Prof. F. Schreiber Dr. U. Scholz	international	250
Biodiversity Information Standards (TDWG) "e-Knowledge about Biodiversity and Agriculture"	08.-13.11.2009 Montpellier France	TDWG Agropolis, Montpellier, Bioversity International Dr. H. Knüpffer	international	270

Ehrungen, Preise/ Honours, Awards

2008

Anlässlich des 8th GABI-Statusseminars erhielten **Dr. Katja Kempe**, **Dr. Myroslava Rubtsova** und **Dr. Mario Gils** für das Poster „Development of an innovative hybrid seed production system for wheat" den Posterpreis 2008. Das Seminar wurde vom 4. bis 6. März 2008 in Potsdam durchgeführt.

Während der 4th Plant Science Student Conference (PSSC), die vom 1. bis 4. Juli 2008 im IPK stattfand, wurden folgende Doktoranden des IPK ausgezeichnet:

Vorträge

2. Platz: **Anja Hanemann**, **R. Cossu**, **G. Schweizer** & **Dr. M. Röder**: Development of diagnostic markers for the Rrs2 scald resistance gene in barley.

3. Platz: **Annika Johrde** & **Dr. P. Schweizer**: Identification of candidate genes for durable powdery mildew resistance in barley by association genetics.

Publikumspreis: **Nicolai M. Nürk** & **Dr. F.R. Blattner**: Revealing evolution of apomixis in *Hypericum* L. – phylogeny and the apospory marker.

und jeweils zweite Preise für ***Poster*** gingen an:

Stephanie Kaspar, **A. Matros**, **Dr. W. Weschke**, **Dr. U. Seiffert** & **Dr. H.-P. Mock**: Comparative proteome analysis of barley grain development using a label-free LC-based approach.

Christine Kastner, **Dr. G. Hensel**, **Dr. M. Gahrtz** & **Dr. J. Kumlehn**: *Agrobacterium*-mediated transformation of maize.

Maryam Sanei, **Dr. A. Houben** & **Dr. R. Pickering**: Analysis of uniparental elimination of chromosome in wide crosses.

Im Rahmen der 4th International Bulgarian-Greek Scientific Conference „Computer Science'08" and International Workshop „BioComputing'2008", 17. bis 20.09.2008, Kavala/Greece, erhielt der Beitrag „DALIGRES: A graph query tool to unravel the life science database maze" von **Dr. Matthias Lange, Matthias Klapperstück, Karl Spies** und **Dr. Uwe Scholz** den Best Paper Award.

Ebenfalls im September 2008 erhielt **Enoch Gbenato Achigan-Dako** den Vavilov-Frankel Award von Bioversity International. Der Preis ist mit einem Stipendium verbunden, mit dem Herr Achigan-Dako seine Doktorarbeit am IPK vollenden konnte. In dieser widmete er sich der Untersuchung westafrikanischer Cucurbitaceen.

Die Arbeiten im QuantPro Projekt „3-D Mikrodissektion biologischer Objekte und Analyse schock-gefrorener molekularer Komponenten" wurden mit einem Posterpreis für **Stephanie Kaspar** und **Dr. Andrea Matros** als Teilnehmerinnen der Proteomlux-Konferenz gewürdigt. Die Veranstaltung fand vom 22. bis 25. Oktober 2008 in Luxemburg statt.

Im Rahmen der Zusammenarbeit mit der Masaryk-Universität in Brnó, Tschechische Republik, wurde **Dr. Andreas Houben** am 8. Dezember 2008 mit einer ‚Dozentur für Innovationen' gewürdigt.

2009

Auf dem 9th GABI Status Seminar erhielten Frau **Katarzyna Plasun** und **Dr. Jochen Kumlehn** für die Posterpräsentation „Pollen embryogenesis in anther and isolated pollen cultures of *Arabidopsis thaliana*" den Best Poster Award. Die Veranstaltung fand vom 3. bis 5. März 2009 in Potsdam statt.

Folgende Preise wurden auf der 5th Plant Science Student Conference (PSSC) „Plant your Ideas", die vom 23. bis 26. Juni 2009 stattfand, vergeben:

Vorträge

1. **Nicolai M. Nürk:** Cladistic analysis of morphological characters in the genus *Hypericum*.

2. **Manuela Nagel**, I. Kranner & A. Börner: Oxidative stress response as indicator for seed longevity in wheat.

3. **Hendrick Mehlhorn**: De novo motif detection using iterative algorithms and centroids.

Poster

1. **Diep Le Hong**, G. Mönke, A. Junker, A. Matros, H.-P. Mock, U. Conrad & H. Bäumlein: Molecular characterisation of EFFECTOR OF TRANSCRIPTION (ET) in *Arabidopsis.*

Hendrik Rohn erhielt auch den Auditoriumspreis für den besten Vortrag.

Auf der alljährlichen Botanikertagung am 7. September 2009 in Leipzig erhielt der ehemalige Mitarbeiter (2000–2004) der Arbeitsgruppe Karyotypevolution, **Dr. Martin Lysak**, den Horst-Wiehe-Preis 2009. Mit der Auszeichnung würdigte die Jury seine Arbeit „Mechanisms of chromosome number reduction in *Arabidopsis thaliana* and related Brassicaceae species". Zur Zeit der Verleihung weilte Dr. Lysak für einen mehrmonatigen Forschungsaufenthalt am IPK.

Auf dem XVIth International Plant Nutrition Colloquium in Sacramento, USA (8. September 2009), erhielt das Poster „Influence of associative bacteria on root morphology in *Arabidopsis* plants and dependence of the supplied nitrogen form" von **Claudia Weishaar** und **Prof. Dr. Nicolaus von Wirén** den Best Poster Award.

Lehrtätigkeit/Teaching

2008

Name der/des Lehrenden	Thema	Universität/ Hochschule	Fakultät/ Fachbereich (FB)	SWS
Priv.-Doz. Dr. A. Börner (GB) Dr. J. Keller (GB) Dr. U. Lohwasser (GB) Dr. A. Weidner (GB) Dr. A. Senula (GB)	Erhaltungsstrategien und Management pflanzengenetischer Ressourcen (Vorlesung und Praktikum)	Martin-Luther-Universität Halle-Wittenberg	Naturwissenschaftliche Fakultät III	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 (MZB)	Moderne Techniken der Mikroskopie und Cytogenetik (Studentenpraktikum)	Martin-Luther-Universität Halle-Wittenberg	Naturwissenschaftliche Fakultät III	1
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-/Funktions-beziehungen in Eukaryontengenomen (Seminar)	Universität Potsdam	Mathematisch-Naturwissenschaftliche Fakultät	2
Prof. Dr. A.M. Wobus (CYG)	Aktuelle Aspekte der Stammzellforschung (Vorlesung)	Martin-Luther-Universität Halle-Wittenberg	Medizinische Fakultät	0,5
Dr. habil. L. Altschmied (CYG)	Pflanzenphysiologisches Praktikum	Friedrich-Schiller-Universität Jena	Institut für Pflanzenphysiologie	4
Dr. U. Scholz (CYG) Dr. M. Lange (CYG)	Einführung in die Bioinformatik (Vorlesung und Übung)	Hochschule Anhalt Köthen	FB Biotechnologie, Lebensmitteltechnologie, Verfahrens- und Umwelttechnik	4
Prof. Dr. F. Schreiber (MOG)	Analyse biologischer Netzwerke (Vorlesung und Übung)	Martin-Luther-Universität Halle-Wittenberg	Naturwissenschaftliche Fakultät III Institut für Informatik	4
Priv.-Doz. Dr. H.-P. Mock (MZB)	Pflanzenphysiologie (Grundpraktikum)	Martin-Luther-Universität Halle-Wittenberg	FB Biologie	4
Prof. Dr. G. Kunze (MZB)	Molekulargenetik Teil I (Vorlesung)	Hochschule Anhalt Köthen	FB Biotechnologie, Lebensmitteltech-nologie, Verfahrens- und Umwelttechnik	3
Prof. Dr. G. Kunze (MZB)	Molekulargenetik Teil II (Vorlesung)	Hochschule Anhalt Köthen	FB Biotechnologie, Lebensmitteltech-nologie, Verfahrens- und Umwelttechnik	3
Prof. Dr. G. Kunze (MZB)	Biosensoren für die Umweltkontrolle (Vorlesung)	Hochschule Anhalt Köthen	FB Biotechnologie, Lebensmitteltech-nologie, Verfahrens- und Umwelttechnik	2
Prof. Dr. G. Kunze (MZB)	Hefegenetik (Praktikum)	Ernst-Moritz-Arndt-Universität Greifswald	Mathematisch-Naturwissenschaftliche Fakultät, FB Biologie	4
Semesterwochenstunden (SWS) insgesamt:				**53,5**

2009

Name der/des Lehrenden	Thema	Universität/ Hochschule	Fakultät/ Fachbereich (FB)	SWS
Prof. Dr. A. Graner (GB) Dr. N. Stein (GB) Dr. B. Kilian (GB)	Genetische Kartierung / Molekulare Diversität	Martin-Luther-Universität Halle-Wittenberg	Naturwissenschaftliche Fakultät III	2
Priv.-Doz. Dr. A. Börner (GB) Dr. J. Keller (GB) Dr. U. Lohwasser (GB) Dr. A. Weidner (GB) Dr. A. Senula (GB)	Erhaltungsstrategien und Management pflanzengenetischer Ressourcen (Vorlesung und Praktikum)	Martin-Luther-Universität Halle-Wittenberg	Naturwissenschaftliche Fakultät III Landwirtschaftliches Institut	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 (Studentenpraktikum)	Martin-Luther-Universität Halle-Wittenberg	Naturwissenschaftliche Fakultät III	1
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-/Funktions-beziehungen in Eukaryontengenomen (Seminar)	Universität Potsdam	Mathematisch-Naturwissenschaftliche Fakultät	2
Prof. Dr. A.M. Wobus (CYG)	Grundlagen der Zell- und Gewebekultur und aktuelle Aspekte der Stammzell-forschung (Vorlesung)	Martin-Luther-Universität Halle-Wittenberg	Medizinische Fakultät	1
Dr. habil. L. Altschmied (MOG)	Pflanzenphysiologisches Praktikum	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. M. Strickert (MOG) Dr. B. Junker (PZB) Dr. H. Knüpffer (GB)	Bioinformatik (Vorlesung und Übung)	Christian-Albrechts-Universität Kiel	Agrar- und Ernährungs-wissenschaftliche Fakultät	4
Dr. N. Sreenivasulu (MOG) Senior Lecturer	Vorlesung	University of Western Australia, Perth		1
Priv.-Doz. Dr. H.-P. Mock (PZB)	Pflanzenphysiologie (Grundpraktikum)	Martin-Luther-Universität Halle-Wittenberg	FB Biologie	4
Prof. Dr. G. Kunze (PZB)	Molekulargenetik Teil I (Vorlesung)	Hochschule Anhalt Köthen	FB Biotechnologie, Lebensmitteltech-nologie, Verfahrens- und Umwelttechnik	3
Prof. Dr. G. Kunze (PZB)	Molekulargenetik Teil II (Vorlesung)	Hochschule Anhalt Köthen	FB Biotechnologie, Lebensmitteltech-nologie, Verfahrens- und Umwelttechnik	3
Prof. Dr. G. Kunze (PZB)	Biosensoren für die Umweltkontrolle (Vorlesung)	Hochschule Anhalt Köthen	FB Biotechnologie, Lebensmitteltech-nologie, Verfahrens- und Umwelttechnik	2

Name der/des Lehrenden	Thema	Universität/ Hochschule	Fakultät/ Fachbereich (FB)	SWS
Prof. Dr. G. Kunze (PZB)	Hefegenetik (Praktikum)	Ernst-Moritz-Arndt-Universität Greifswald	Mathematisch-Naturwissenschaftliche Fakultät, FB Biologie	4
Semesterwochenstunden (SWS) insgesamt:				**53,0**

Mitarbeit an wissenschaftlichen Zeitschriften/ Editing Scientific Journals

Mitarbeiter des Leibniz-Instituts für Pflanzengenetik und Kulturpflanzenforschung sind Herausgeber bzw. Mitherausgeber folgender Zeitschriften:

BBA – Gene Regulatory Mechanism, Elsevier, Maryland Heights, USA (A. Houben, Board Member).

Botanical Journal of Iran, Rostaniha, Tehran, Iran (R. Fritsch, Editorial Board).

BMC Plant Biology, BioMed Central, London, UK (N. Stein, Associate Editor 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).

Cell Biology and Toxicology, Springer, Dordrecht, The Netherlands (A. M. Wobus, Consulting Editor).

Cells Tissues Organs, Karger AG, Basel, Switzerland (A. 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).

Cytogenetics & Genome Research (CGR), Karger AG, Basel, Switzerland (I. Schubert, Editorial Board).

Current Trends in Biotechnology and Pharmacy, USA (N. Sreenivasulu, Editorial Board).

Electronic Wheat Information Service, Shizuoka, Japan (A. Houben, Editorial Advisory Board).

Functional & Integrative Genomics, Springer, Berlin-Heidelberg (N. Stein, Editorial Board).

Genetic Resources and Crop Evolution (GRACE), Springer, Dordrecht, The Netherlands (K. Pistrick, Managing Editor; F.R. Blattner, 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).

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).

Journal of Plant Physiology, Elsevier, Amsterdam, The Netherlands (J. Kumlehn, Editorial Board).

Journal of Stem Cells, Nova Science Publishers, Inc., New York, USA (A. M. Wobus, Editorial Advisory Board Member).

Journal of Tissue Engineering and Regenerative Medicine, John Wiley & Sons, Ltd., UK (A. M. Wobus, Editorial Board Member).

Molecular Breeding, Springer, Dordrecht, The Netherlands (A. Graner, 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, Springer, Berlin-Heidelberg (R. Schmidt, 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 (A. M. Wobus, Editorial Board Member).

The International Journal of Developmental Biology, The University of the Basque Country Press, Bilbao, Spain (A. 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 (U. Wobus, Advisory Board; T. Altmann, Editor, Supporting Editorial Board Member of Comparative and Functional Genomics).

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/Saale;
- Leiter der Ag „Genomforschung" der Gesellschaft für Pflanzenzüchtung e.V. (GPZ);
- 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 Züchtungsforschung, Köln;
- Mitglied des „Beratungs- und Koordinierungsausschusses (BEKO) des Nationalen Fachprogramms zur Erhaltung und nachhaltigen Nutzung pflanzengenetischer Ressourcen landwirtschaftlicher und gartenbaulicher Kulturpflanzen", BMVEL, Bonn;
- Mitglied des wissenschaftlichen Beirates „Otto Warburg Center for Agricultural Biotechnology", Hebrew University, Jerusalem, Israel;
- Honorary Fellow, Scottish Crop Research Institute (SCRI), Dundee, UK;
- Mitglied des Steering Committee, International Barley Sequencing Consortium (IBSC);
- Stellvertretender Vorsitzender der Gemeinschaft zur Förderung der Kulturpflanzenforschung Gatersleben e.V.;
- Mitglied im Wissenschaftlichen Beirat, Julius Kühn-Institut (JKI), Quedlinburg;
- Mitglied des Direktoriums, Interdisziplinäres Forschungszentrum für Nutzpflanzen (IZN), Martin-Luther-Universität Halle/Saale;
- Executive Board, Generation Challenge Program (GCP), Consultative Group of International Agricultural Research;
- Review panel, Graduate School "Experimental Plant Sciences", Wageningen University, The Netherlands (2009).

Abteilung Genbank

Dr. N. Stein

- Chair des International Barley Genome Sequencing Consortium (IBSC, http://barleygenome.org);
- Koordinator der European Triticeae Genomics Initiative (ETGI, http://www.etgi.org);
- National Representative der COST Action Tritigen FA0604;
- Vorsitzender des GABI Scientific Coordinating Committee (SCC).

Priv.-Doz. Dr. A. Börner

- Koordinator der European Wheat Aneuploid Co-operative;
- Vorstandsmitglied und Schriftführer der Gemeinschaft zur Förderung der Kulturpflanzenforschung Gatersleben e.V.;
- Mitglied als deutscher Experte der Wheat Working Group des ECPGR.

Dr. J. Keller

- Mitglied der Koordinierungsgruppe des ECPGR Vegetables Network und Vice-Chairman der *Allium*-Arbeitsgruppe;
- Vorstandsmitglied der Gesellschaft für Pflanzenbiotechnologie e.V.;
- Vorstandsmitglied in der Internationalen Gesellschaft für Tieftemperaturbiologie (Society of Low Temperature Biology);
- Mitglied im Lenkungsausschuss der europäischen COST-Initiative 871 „Kryokonservierung in Europa".

Dr. H. Knüpffer

- Koordinator des Cereals Network sowie Chairman der Barley Working Group des European Co-operative 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).

Dr. K.J. Dehmer

– Mitglied in der ECPGR Working Group on Potatoes.

E. Willner

– Mitglied (Vice chairperson) in der ECPGR Working Group on Forages.

Dr. K. Pistrick

– Mitglied im Nomenclature Committee of the International Seed Testing Association (ISTA).

Abteilung Cytogenetik und Genomanalyse

Prof. Dr. I. Schubert

– Mitglied im Advisory Board of the Centre of Excellence in Plant Agrobiology and Molecular Genetics (PAGEN).

Dr. habil. P. Schweizer

– Koordinator des BarleyGenomeNet;

– Mitglied im Projekt Management Team BIOEXPLOIT (EU FP6);

– Mitglied der Zentralen Kommission für Biologische Sicherheit (ZKBS).

Priv.-Doz. Dr. R. Schmidt

– Gewähltes Mitglied des DFG-Fachkollegiums „Pflanzenwissenschaften".

Prof. Dr. A. M. Wobus

– Mitglied der Deutschen Akademie der Naturforscher LEOPOLDINA – Nationale Akademie der Wissenschaften, Halle/Saale;

– Ordentliches Mitglied der Berlin-Brandenburgischen Akademie der Wissenschaften (BBAW);

– Mitglied der Zentralen Ethik-Kommission für Stammzellenforschung (ZES) am Robert-Koch-Institut, Berlin;

– Mitglied des Novartis Ethics Advisory Board (NEAB) von NOVARTIS Pharma International, Basel, Schweiz;

– Mitglied der Arbeitsgruppe „Gentechnologie-bericht" der Berlin-Brandenburgischen Akademie der Wissenschaften (BBAW);

– Mitglied des Programmbeirats des Wissenschaftszentrums Sachsen-Anhalt (WZW).

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 Genome Program GABI;

– 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 „The Arabidopsis Functional Genomics Network (AFGN)";

– 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. U. Wobus

- Mitglied und Obmann der Sektion Genetik/ Molekularbiologie der Deutschen Akademie der Naturforscher LEOPOLDINA – Nationale Akademie der Wissenschaften, Halle/Saale;
- Ordentliches Mitglied der Berlin-Brandenburgischen Akademie der Wissenschaften (BBAW);
- Korrespondierendes Mitglied der Nordrhein-Westfälischen Akademie der Wissenschaften;
- Mitglied des Wissenschaftlichen Beirates der Gemeinschaft zur Förderung der privaten deutschen Pflanzenzüchtung (GFP), Bonn;
- Stellvertretender Vorsitzender der InnoPlanta e.V. Pflanzenbiotechnologie Nordharz/Börde;
- Mitglied der *WGL*-Jury Wissenschaftspreis des Stifterverbandes „Gesellschaft braucht Wissenschaft";
- Mitglied der Jury für die Forschungspreise für Angewandte Forschung und für Grundlagenforschung in Sachsen-Anhalt;
- Mitglied des Kuratoriums der Sparkassenstiftung Aschersleben-Staßfurt;
- Vorsitzender des Fördervereins des Schülerlabors „Grünes Labor Gatersleben".

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;
- Editor System Biology Graphical Notation Initiative.

Abteilung Physiologie und Zellbiologie

Prof. Dr. N. von Wirén

- Mitglied des „IPNC-Steering Committees" (International Plant Nutrition);
- Vize-Präsident der Deutschen Gesellschaft für Pflanzenernährung;
- Fachgutachter der Deutschen Forschungsgemeinschaft im Fachkollegium 207 „Agrar-, Forstwissenschaften, Gartenbau und Tiermedizin";
- Mitglied des Wissenschaftlichen Beirats des Leibniz-Instituts für Pflanzenbiochemie, Halle/Saale;
- Koordinator des EU-(STREP)-Projekts „RHIBAC – Rhizosphere bacteria for reduced fertilizer input in wheat";
- Koordinator der DFG-Forschergruppe 948 „Nitrogen uptake, metabolism and remobilization in leaves during plant senescence";
- Mitglied des Programmkomitees zur Einrichtung eines DFG-Schwerpunktprogramms mit dem Titel „Flowering time control: from natural variation to crop improvement";
- Mitglied des Programmkomitees zur Etablierung eines *WGL*-Wissenschaftscampus an der MLU Universität Halle-Wittenberg, Halle/Saale.

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.;
- Mitglied des Arbeitskreises Systembiologie und Synthetische Biologie der DECHEMA e.V.

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Prof. Dr. Christian Jung, Kiel, (Vorsitz Wissenschaftlicher Beirat) seit 01.12.2009,
Prof. Dr. Joachim Kadereit, Mainz, (stellv. Vorsitz Wissenschaftlicher Beirat) bis 30.11.2009,
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Bernd Eise, Administrativer Leiter und Leiter der Abteilung Verwaltung und Zentrale Dienste, bis 30.11.2009,
Juliane Becker, Kommissarische Leiterin der Abteilung Verwaltung und Zentrale Dienste, 01.12.2009 bis 31.12.2009,
Prof. Dr. Ingo Schubert, Leiter der Abteilung Cytogenetik und Genomanalyse,
Prof. Dr. Ulrich Wobus, Leiter der Abteilung Molekulare Genetik, bis 31.03.2008,
Prof. Dr. Thomas Altmann, Leiter der Abteilung Molekulare Genetik, seit 01.04.2008,
Prof. Dr. Gotthard Kunze, komm. Leiter der Abteilung Molekulare Zellbiologie, bis 31.03.2009,
Prof. Dr. Nicolaus von Wirén, Leiter der Abteilung Physiologie und Zellbiologie, seit 01.04.2009.

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.

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Prof. Dr. Eberhard Schäfer, Freiburg, (Vorsitz) bis 30.11.2009,
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Prof. Dr. Ralph Bock, Potsdam-Golm, (stellv. Vorsitz) seit 01.12.2009,
Prof. Dr. George Coupland, Köln,
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Prof. Dr. Ulf-Ingo Flügge, Köln, bis 30.11.2009,
PD Dr. Christiane Gebhardt, Köln, (Vorsitz Genbank-Beirat),
Prof. Dr. Ueli Großniklaus, Zürich, bis 30.11.2009,
a.o. Univ. Prof. Dr. Josef Loidl, Wien, seit 01.12.2008,
Prof. Dr. Marcus Koch, Heidelberg, seit 01.12.2009,
Prof. Dr. Jerzy Paszkowski, Genf, seit 01.12.2009,
Prof. Dr. Dierk Scheel, Halle, seit 01.12.2009,
Dr. Ralf-Michael Schmidt, Ludwigshafen,
Prof. Dr. Chris-Carolin Schön, München, seit 01.12.2009,
Prof. Dr. Dieter Schweizer, Wien, bis 30.11.2009.

Der Wissenschaftliche Beirat hat als Unterausschuss einen **Genbank-Beirat**, der den Stiftungsrat und das Direktorium in Abstimmung mit dem Wissenschaftlichen Beirat in allen Fragen der Genbankarbeit berät.

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Dr. Tankred Schuhmann (Beauftragter für Datenschutz),
Ellen Weiß (Gleichstellungsbeauftragte),
Wolfgang Schmidt (Beauftragter für Abfallbeseitigung und Schwerbehindertenbeauftragter), bis 31.12.2008,
Steffen König (Schwerbehindertenbeauftragter), seit 01.01.2009,
Peter Schreiber (Beauftragter für Havarie- und Katastrophenschutz),
Carmen Höpfner (Beauftragte für Lehrausbildung),
Hans-Jürgen Winkelmann (Fachkraft für Arbeitssicherheit – Mitarbeiter der Fa. WAKO Berlin).

Betreuer des IPK-Doktorandenprogramms

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