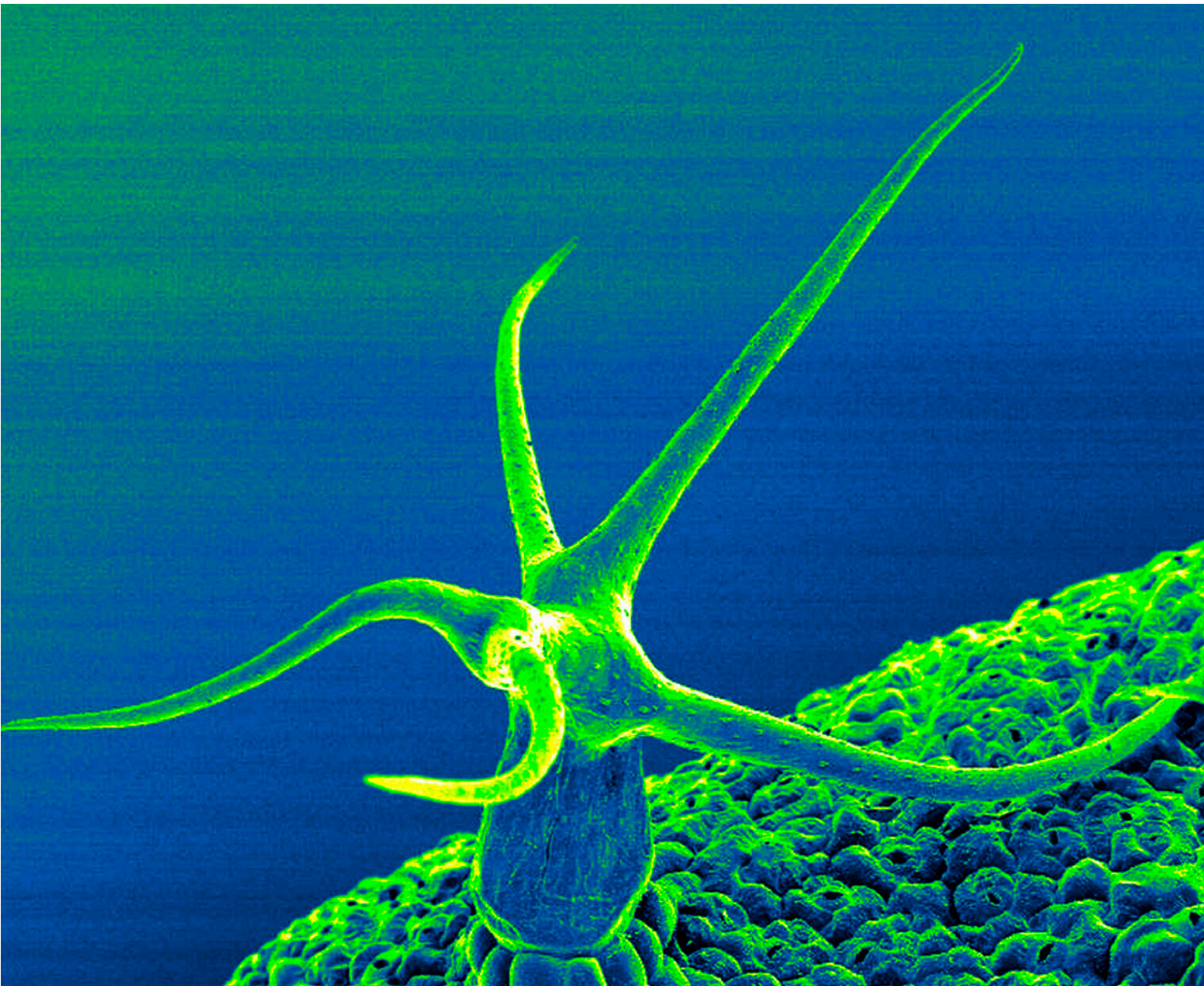
Leibniz-Institut für Pflanzengenetik und Kulturpflanzenforschung (IPK)
Leibniz Institute of Plant Genetics and Crop Plant Research (IPK)

FORSCHUNGSBERICHT 2016 | 2017
SCIENTIFIC REPORT 2016 | 2017



Leibniz Association

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As of 1 January 2016

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Umschlag Fotos: Trichom einer Arabidopsis *tex1 mos11* Doppelmutante mit sieben Verzweigungspunkten als gefärbtes Rasterelektronenmikroskopiebild ▪ Trichome of Arabidopsis *tex1 mos11* double-mutant plants with seven branch points as coloured SEM image (Foto: Michael Melzer)
Pflanzenkulturhalle ▪ Plant Cultivation Hall (Foto: Roxana Lange)

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Vorwort ▪ Introduction

Wir leben in der *besten aller möglichen Welten*. Diese Erkenntnis aus der Feder unseres Namengebers Gottfried Wilhelm Leibniz war das Motto des Themenjahrs der Leibniz-Gemeinschaft anlässlich des 370. Geburtstags und des 300. Todestags des Universalgelehrten im Jahr 2016.

Das genannte Zitat wurde im Laufe der Geschichte vielfach missinterpretiert. Es besagt nicht, dass alles so bleiben soll wie es ist, sondern war dynamisch gedacht: Nicht der derzeitige Zustand der Welt ist der bestmögliche, sondern die Welt mit ihrem Entwicklungspotential macht sie zur besten aller möglichen Welten. Seit dem Tod von Leibniz sind viele Jahre vergangen, in denen Akademien und Universitäten gegründet wurden, aus welchen wiederum große Forscher und Entdecker hervorgingen. Der Mensch drang in entlegenste Winkel der Erde vor und setzte seinen Fuß auf den Mond. Das Entwicklungspotential der Welt erschien über lange Zeit unendlich, bis Mitte der 1970er Jahre mit der vom *Club of Rome* veröffentlichten Studie zu den Grenzen des Wachstums eine Phase des Umdenkens begann. Die Natur und ihre Ressourcen stellten plötzlich kein unerschöpfliches Reservoir mehr dar. Der Mensch war dabei, Ressourcen, die über Zeiträume von vielen Millionen Jahren entstanden waren, binnen weniger Jahrzehnte zu erschöpfen. Technischer Fortschritt war vielfach zu Lasten von Umwelt und Natur erkauft worden. Innerhalb weniger Jahrzehnte hatte der Mensch unauslöschliche Spuren auf der Erde hinterlassen. Die Menschheit war im neuen Zeitalter des Anthropozäns zu einem erdgeschichtlichen Faktor geworden.

Der *Club of Rome* hat uns sensibilisiert. Er hat unsere Aufmerksamkeit darauf gelenkt, dass Fortschritt seinen Preis hat. Ein Beispiel hierfür ist die Grüne Revolution. Diese führte in der zweiten Hälfte des vergangenen Jahrhunderts durch die Züchtung verbesserter Sorten, den Einsatz von Mineraldünger und durch chemischen Pflanzenschutz zu einem weltweiten Anstieg der Ernteerträge. Milliarden Menschen konnten so vor dem Hungertod bewahrt werden. Der Preis ist allerdings eine gestiegene Umweltbelastung, der Rückgang der biologischen Vielfalt und der Verlust wertvoller Ackerflächen durch das stetige Wachstum der Städte. Hieraus jedoch abzuleiten, dass wir nur das Rad der Geschichte zurückdrehen müssen und wieder zu althergebrachten Formen der Landbewirtschaftung zurückkehren können, wäre ein Trugschluss. Die Weltbevölkerung wächst weiterhin um 60 – 70 Millionen Menschen pro Jahr. In drei Jahrzehnten werden mehr als 9 Milliarden Menschen auf der Erde leben. Deren Ernährung und Rohstoffversorgung unter Berücksichtigung des Prinzips der Nachhaltigkeit sicherzustellen, erfordert Innovationen, durch welche die Erträge und die Ertragssicherheit unserer Nutzpflanzen weiter gesteigert werden können.

Dieser großen Herausforderung stellt sich das IPK mit seinen Forschungsarbeiten. Das zentrale Thema *Biodiversität und Leistung* vereinigt die Arbeiten in den fünf großen Forschungsschwerpunkten des Instituts mit dem Ziel, wissensbasierte Lösungsansätze zu schaffen. *Biodiversität und Leistung* bedeutet auch die Aktivierung der in der Bundeszentralen *ex situ*-Genbank erhaltenen genetischen Vielfalt verbunden mit der Weiterentwicklung derselben in ein *Biologisch-Digitales Ressourcenzentrum.* Eine Schlüsselrolle auf dem Weg dahin nimmt die Entschlüsselung der Genome wichtiger Kulturpflanzen ein, wie die von Gerste, Weizen oder Roggen. Diese stellt die Grundlage für die Aufklärung der Zusammenhänge zwischen der allelischen Di-

We live in the best of all possible worlds. This insight from the pen of our eponym Gottfried Wilhelm Leibniz has been chosen as the slogan for the Leibniz Association's theme for 2016 to mark the polymath's 370th birthday and the 300th anniversary of his death. His words have been misinterpreted many times over the course of history. They were never intended to signify that things should remain as they are, but rather, they were intended to convey change: rather than the current state of things being optimal, it is the potential for development which makes it the best of all possible worlds. The passing of the many years since Leibniz's death has seen the foundation of academies and universities, which in turn have nurtured great researchers and discoverers. Mankind has explored the remotest corners of the earth and has set foot on the moon. For a long time, the potential for further development seemed boundless, but this began to be rethought in the mid-1970s, as signalled by the *Club of Rome*'s study of the limits to growth. Nature and natural resources were suddenly no longer considered as inexhaustible. Mankind was set, within a few decades, to irrevocably deplete the resources which had accumulated over a period of millions of years. Technical progress has typically been achieved only at the expense of the environment and of nature. Within just a few decades, mankind has left an indelible mark on the earth; it has been the agent of a new geological era, termed the Anthropocene.

The *Club of Rome* has sensitized us. It has drawn our attention to the fact that progress has a price. An example is represented by the Green Revolution, which succeeded in raising crop yields across the world in the second half of the previous century through the breeding of improved varieties, along with the widespread use of mineral fertilizer and chemical crop protectants. The Green Revolution has rescued billions of people from starvation, but at a price: environmental pollution has worsened, biodiversity has declined and valuable arable land has been lost to urban development. It would be naive to conclude that all we need to do is therefore to turn back the clock by resuming traditional forms of land management. The world's population is growing by 60-70 million people per year, and is expected to reach 9 billion within the next 30 years. Innovations able to boost crop yields and to improve the reliability of production are needed to ensure that the population is both adequately fed and supplied with raw materials, in a way which takes sustainability into consideration.

The IPK's research programme is focused on this great challenge. The core theme *Biodiversity and Performance* unifies the work of the Institute's five major research areas, which strive to create knowledge-based solutions. *Biodiversity and Performance* also involves the exploitation of the genetic diversity preserved in the Federal Central *ex situ* Gene Bank, accompanied by its development into a *Biological Digital Resource Centre*. Acquiring the genome sequences of important crop species such as barley, wheat and rye is a key component in this process, since it provides the basis to connect allelic diversity with differences in gene expression at various functional levels.

versität und der Merkmalsausprägung auf den verschiedenen biologischen Funktionsebenen dar.

Die vielfältigen wissenschaftlichen Verdienste von Gottfried Wilhelm Leibniz sind weithin bekannt. Weniger bekannt ist, dass er bei der technischen Umsetzung seiner Erfindungen auch Rückschläge hinnehmen musste, durch die er sich jedoch nicht entmutigen lies. Im übertragenen Sinne trifft das auf die Forschungsarbeiten zur Grünen Biotechnologie zu, deren gesellschaftliche Ablehnung nicht durch wissenschaftliche Fakten begründbar ist. Die *Grüne Gentechnik* und das *Genome Engineering* stehen in keinem Widerspruch zur Nutzbarmachung der genetischen Vielfalt der Genbanksammlungen. Erkenntnisse aus dem Zusammenhang von Merkmalsausprägung und genetischer Konstitution liefern wertvolle Ansatzpunkte, die Grüne Gentechnik oder das Genome Engineering für die Verbesserung von Nutzpflanzen einzusetzen. Wir sehen hierin, trotz der gesellschaftlichen Ablehnung dieser Verfahren, die wissenschaftlich nicht begründbar ist, neue Potentiale für die Nutzbarmachung natürlicher Diversität. Die vielversprechenden Ergebnisse der Forschungsarbeiten bekräftigen uns, die Arbeiten auf diesem Gebiet fortzusetzen, uns durch Rückschläge nicht entmutigen zu lassen, und weiterhin den sachlichen Dialog mit der Öffentlichkeit zu suchen.

Die Aktivierung der genetischen Vielfalt erfordert auch das Beschreiten neuer Wege in der phänotypischen Analyse. Hier wurde am IPK in den vergangenen Jahren eine umfangreiche technische Infrastruktur für die Erfassung und Analyse pflanzlicher Merkmale geschaffen. Mit Hilfe bildgebender Verfahren und durch den Einsatz unterschiedlichster Sensortechniken kann so der zeitliche Verlauf der Merkmalsentwicklung in Zellen, Organen, Einzelpflanzen oder im Feldbestand untersucht werden. Die entsprechenden Einrichtungen sind Teil des *Europäischen Strategieforums für Forschungsinfrastrukturen* (ESFRI). Als vorläufiger Höhepunkt wurde im August 2017 mit der *Pflanzenkulturhalle* eines der weltweit größten Phytotrons, in Anwesenheit der Ministerin Johanna Wanka und des Ministerpräsidenten Reiner Haseloff, eingeweiht. Die genannten Entwicklungen zur Phänotypisierung, Genomsequenzierung und Erfassung der allelischen Diversität von Genbanksammlungen sowie die Analyse der damit verbundenen Datenmengen erfordern eine leistungsfähige Bioinformatik. Durch personelle Verstärkungen und den technischen Ausbau der IT-Infrastruktur konnte das IPK in den vergangenen zwei Jahren seine Rolle als eines der führenden Zentren für Pflanzenbioinformatik weiter festigen.

Die Kombination aus wissenschaftlicher Exzellenz und gesellschaftlicher Relevanz spiegelte sich in den vergangenen zwei Jahren in über 300 begutachteten Veröffentlichungen, Fachvorträgen auf einer Vielzahl von Tagungsveranstaltungen in der ganzen Welt sowie in der Einwerbung von Projektmitteln im Wert von über 22 Mio. Euro wider. Wichtige Beiträge hierzu lieferten auch die unabhängigen Arbeitsgruppen, welche als Instrument zur Förderung junger Wissenschaftlerinnen und Wissenschaftler vor wenigen Jahren eingerichtet wurden und die weiterhin an Fahrt gewannen.

Gemeinsam mit den Zuwendungsgebern blicken wir auf zwei Jahre sehr erfolgreicher Arbeit zurück. Wir hoffen, dass unsere Forschungsergebnisse, ganz im Sinne von Leibniz, einen kleinen Beitrag zum Schutz und zur Zukunftssicherung der *besten aller möglichen Welten* liefern werden. Einzelheiten hierzu finden Sie in den nachfolgenden Kapiteln des Forschungsberichts.

Danke für Ihr Interesse und viel Freude beim Lesen.

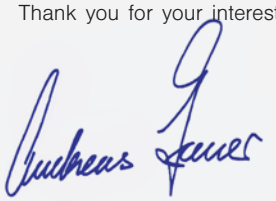
The diverse scientific achievements of Gottfried Wilhelm Leibniz are widely recognized. What is less well known is that he also experienced various setbacks in attempting to implement certain of his inventions, although these did not discourage him. In a figurative sense, this also applies today to green biotechnology, the societal rejection of which cannot be justified by scientific evidence. *Green genetic engineering* and *genome engineering* are not inimical to utilizing the genetic diversity represented in gene bank collections. Discoveries of the relationships between gene expression and genotype can provide a valuable starting point for using green genetic engineering or genome engineering methods to improve crops. Despite the societal scepticism of these procedures, we foresee new potential for the exploitation of natural diversity. The promising outcomes of this research are encouraging us to continue to work in this area, rather than feeling discouraged by setbacks; we must strive to connect with the public through objective dialogue.

The exploitation of genetic diversity also demands novel approaches to be taken to monitor phenotype. Over the past few years, IPK has created a wide-ranging set of technical platforms designed to facilitate the recording and analysis of plant traits. With the aid of imaging technology and the use of a variety of sensors, growth and development at the level of individual cells, organs, plants or plots in the field can now be ever more efficiently monitored. These platforms form part of the *European Strategy Forum for Research Infrastructures* (ESFRI). As an interim highlight, one of the world's largest phytotrons, the so-called *Plant Cultivation Hall*, was inaugurated in August 2017 in the presence of Minister Johanna Wanka and Prime Minister Reiner Haseloff. The aforementioned activities in phenotyping, genome sequencing and characterization of the allelic diversity represented in the gene bank collection, as well as the downstream analyses of the data sets acquired, require an efficient bioinformatics infrastructure. Over the past two years, IPK has further strengthened its position as one of the leading centres for plant bioinformatics by expanding its staff and enhancing its IT infrastructure.

The combination of scientific excellence and societal relevance has enabled, over the past two years, the publication of over 300 peer-reviewed scientific articles, the giving of a number of specialist lectures at numerous conferences around the world and the raising of project funding to the tune of more than 20M €. Important scientific contributions have been made by the Institute's independent working groups, which were set up a few years ago as a means to promote the careers of young scientists, and which continue to gain momentum.

Together with our sponsors, we now look back on two years of very successful work. We hope that our research results, in the spirit of Leibniz, will make a small contribution to protecting and securing the future of the *best of all possible worlds*. Details can be found in the chapters of IPK's research report which follow.

Thank you for your interest and enjoy what you read here.



Geschäftsführender Direktor ▪ Managing Director/IPK

Das Leibniz-Institut für Pflanzengenetik und Kulturpflanzenforschung ▪ The Leibniz Institute of Plant Genetics and Crop Plant Research

Aufgabenstellung

Als eine der international führenden Einrichtungen auf den Gebieten der Pflanzengenetik und Kulturpflanzenforschung trägt das Institut mit seinen Forschungsarbeiten und dem Betrieb der *Bundeszentralen ex situ-Genbank für landwirtschaftliche und gartenbauliche Kulturpflanzen* in großem Maße zum Erhalt der biologischen Vielfalt und zu ihrer Erforschung sowie Erschließung bei. Mit der Zusammenführung von wissenschaftlicher Exzellenz und gesellschaftlicher Relevanz sieht sich das IPK als wichtiger Wegbereiter für eine effiziente und nachhaltige Nahrungs-, Energie- und Rohstoffversorgung sowie, in direkter Verbindung damit, für die Bewältigung globaler Zukunftsaufgaben. Basierend auf der Aufklärung grundlegender Prinzipien der pflanzlichen Merkmalsausprägungen und der Erforschung evolutionärer Anpassungen erfolgt die Entwicklung innovativer Lösungsansätze zur züchterischen Verbesserung von Kulturpflanzen. Damit leistet das Institut Beiträge zum Erreichen der in der Nationalen Forschungsstrategie *BioÖkonomie 2030* sowie in der *Nationalen Strategie zur biologischen Vielfalt* aufgeführten Ziele.

Finanzierung

Das IPK wurde auf der Grundlage von Vorgängereinrichtungen 1992 als eine Stiftung des öffentlichen Rechts gegründet und ist seit 1997 Mitglied der Leibniz-Gemeinschaft.

Organe der Stiftung sind der Stiftungsrat, das Direktorium, die Geschäftsführung und der Wissenschaftliche Beirat (Fig. 1). Der Zuwendungsbedarf des Instituts 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 Minister für Wirtschaft, Wissenschaft und Digitalisierung. Ein erheblicher Anteil der Personal- und Forschungsmittelausstattung wird über Drittmittel eingeworben.

Struktur

Das IPK ist in die vier wissenschaftlichen Abteilungen *Genbank* (GB), *Züchtungsforschung* (BR), *Molekulare Genetik* (MOG), *Physiologie und Zellbiologie* (PZB) und die Abteilung *Verwaltung und Zentrale Dienste* (VZD) gegliedert. Die einzelnen Abteilungen untergliedern sich wiederum in Forschungsbereiche und Arbeitsgruppen (Ag, vgl. Organigramm, innere Umschlagseiten). Zur Erschließung neuer, innovativer Forschungsfelder etablierte das Institut vier unabhängige Arbeitsgruppen.

Mandate

As one of the world's leading international institutions in the field of plant genetics and crop science, the institute's research programme, along with its curation of the *Federal ex situ Gene Bank for Agricultural and Horticultural Crop Species*, makes a significant contribution to the conservation and utilisation of biological diversity. By combining scientific excellence with social relevance, the IPK sees itself as catalyst for increasing the efficiency and sustainability of the supply of food, energy and raw materials, thereby addressing global challenges related to the environment. Strategies are being developed relevant to the genetic improvement of crop plants via breeding, based on trait analysis and an understanding of naturally evolved adaptation. In this way, the institute seeks to make knowledge-based contributions to the wider goals specified by the *BioEconomy 2030* National Research Strategy and by the *National Strategy for Biological Diversity*.

Financial Arrangements

Representing the successor to several erstwhile institutions, the IPK was established in 1992 as a foundation under public law, and is a member of the Leibniz Association since 1997.

The institute is overseen by the Governing Board, the Board of Directors, the Management Office and the Scientific Advisory Board (Fig. 1). In accordance with Article 91b of the German Constitution, it receives matching funds from the Federal Republic of Germany and the local Federal State. The granting body is the State of Saxony-Anhalt, represented by its Minister for Economy, Science and Digitalization. A significant proportion of the staffing and research budget is covered by outside funding.

Organisational Structure

The IPK is organised into the four scientific departments *Genebank* (GB), *Breeding Research* (BR), *Molecular Genetics* (MOG) and *Physiology and Cell Biology* (PZB), all of which are supported by the department *Administration and Central Services* (VZD). Each department pursues a number of research areas and comprises several research groups (RG, see the organizational chart on the inside cover). Four independent research groups have been established, aiming to open up novel, innovative research topics. Through this extension in its research structure, the institute has created an

Fig. 1 Wissenschaftlicher Beirat ▪ Scientific Advisory Board (Foto: Lynne Main)

Mit dieser Erweiterung der Forschungsstruktur wurde auch eine wichtige Grundlage für die Förderung des wissenschaftlichen Nachwuchses gelegt. Am IPK sind regelmäßig über 450 Personen aus ca. 30 Nationen beschäftigt.

Forschungskonzept

Die strategische und inhaltliche Ausrichtung der Forschungsarbeiten am Institut wird in einer jährlich aktualisierten Programmplanung festgelegt. Die vier Programme sind abteilungszentriert und spiegeln in wesentlichen Zügen die sich komplementierenden zentralen Arbeitsfelder und Kompetenzen wider:

1. Management, Analyse und Evolution pflanzengenetischer Ressourcen
2. Cyto-molekulare Züchtungsforschung
3. Systemanalyse pflanzlicher Produktivität
4. Angewandte Physiologie und Zellbiologie.

Durch die Vernetzung, der über weite Strecken disziplinär ausgerichteten Programme, erfolgt die Bearbeitung von fünf abteilungs- und disziplinübergreifenden Forschungsschwerpunkten (Fig. 2). Diese liefern wissenschaftliche Erkenntnisse sowie biotechnische und züchterische Innovationen, welche Beiträge zur Bewältigung umweltbezogener Zukunftsaufgaben beitragen. Die entsprechenden Forschungsaktivitäten erstrecken sich dabei von der reinen Grundlagenforschung bis hin zu angewandten Fragestellungen im Vorfeld der Pflanzenzüchtung bzw. Biotechnologie und konzentrieren sich in erster Linie

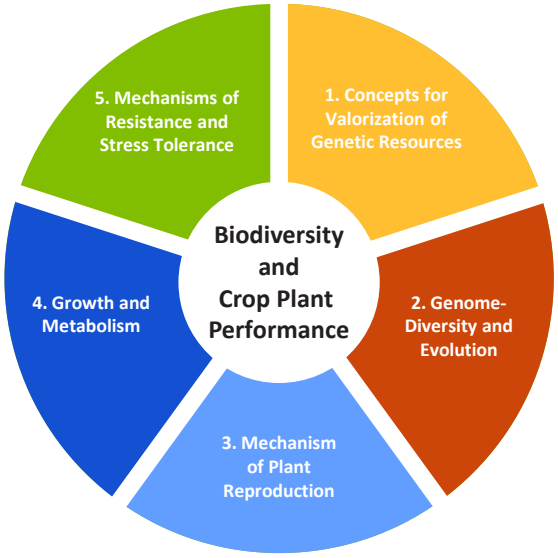


Fig. 2 Forschungsschwerpunkte ▪ Research Themes

important stepping stone to support the scientific careers of young researchers. The IPK consistently employs over 450 staff, originating from more than 30 countries.

Overall Research Concept

An annual planning exercise is conducted to determine and refine the institute's strategy and research programme. The four programmes map on to the departments, essentially mirroring each of the centre's research mandates and reflecting the departmental competencies:

1. Management, analysis and evolution of plant genetic resources
2. Cyto-molecular breeding research
3. Systems analysis of plant productivity
4. Applied physiology and cell biology

The largely discipline-oriented programs address current biological topics in the form of five overarching inter-departmental and inter-disciplinary research themes (Fig. 2). They have been generating novel scientific insights, and deliver innovations in biotechnology and plant breeding to contribute to overcoming global challenges related to the environment and to food security. The corresponding research activities address both basic and applied issues relevant to breeding and biotechnology. Given the Gene Bank's focus on crop plants research activities mainly focus on major agricultural plant species. However, increasing importance is also being given to

auf landwirtschaftlich bedeutsame Pflanzenarten. Deren genetische Vielfalt ist in der Genbank durch umfangreiche Sammlungen abgebildet. Ergänzend zu den Forschungsarbeiten an Pflanzen werden ausgewählte Forschungsthemen zur angewandten Biotechnologie an Hefe bearbeitet.

Integrative Strukturen und Netzwerke

Das IPK verfügt mit seiner Bioinformatik-Plattform über eine koordinative Struktur, in der alle in den verschiedenen Abteilungen angesiedelten Bioinformatik-Gruppen miteinander vernetzt sind. Sie dient zum einen als Plattform für die Bereitstellung bedarfsorientierter interner Dienstleistungen sowie dem Betrieb und der Pflege von Datenbanken, und zum anderen erfolgt die systematische Weiterentwicklung der technisch-wissenschaftlichen IT-Infrastruktur.

Daneben ist das Institut in, über die Projektförderung hinaus gehende, nationale und internationale Forschungskooperationen eingebunden. Diese dienen der Entwicklung und Förderung langfristiger Kooperationsprojekte, der Einwerbung von Projektmitteln und der Gewinnung von wissenschaftlichem Nachwuchs.

Darüber hinaus ist das IPK in eine Reihe von bilateralen Kooperationen mit Universitäten und Forschungseinrichtungen im In- und Ausland eingebunden. Einzelne Arbeitsgruppen sind an einer Vielzahl nationaler und internationaler Verbundprojekte beteiligt.

exploiting the genetic diversity present in wild forms and wild relatives. Selected research topics regarding applied biotechnology have taken advantage of yeast-based systems.

Integrated Structures and Networks

The IPK's Bioinformatics Platform consists of a distributed, co-ordinated network of bioinformatics staff housed within each of the scientific departments. It serves as a platform for the provision of services and support to experimental groups on a demand basis. It both operates and manages a number of databases and works to systematically improve the quality of the institute's scientific and technical IT infrastructure.

In addition, the institute is tied into a number of both national and international research collaborations, which help develop and promote long-term collaborative projects, win project funding and develop the careers of young researchers.

In addition to the platforms and associations listed above, the IPK is also involved in several bilateral collaborations with both national and international universities and research institutions. Individual research teams take part as partners in many national and international projects.

Das Institut in den Jahren 2016 und 2017 ▪ The Institute during 2016 and 2017

Die vergangenen zwei Jahre waren von einer Reihe von Entwicklungen und Ereignissen gekennzeichnet, welche die außerordentliche Dynamik der Kulturpflanzenforschung widerspiegeln. Hierbei wurde besonderes Augenmerk auf die Erschließung neuer Forschungsfelder gelegt. In diesem Zusammenhang wurden eine Reihe neuer Arbeitsgruppen (Ags) etabliert sowie vorhandene Ags im Rahmen von Neubesetzungen thematisch adjustiert. Dieser Weg der schrittweisen Weiterentwicklung war, wie in den vergangenen Jahren, durch herausragende Forschungsergebnisse, eine beachtliche Drittmitteleinwerbung, eine Vielzahl nationaler und internationaler Kooperationen sowie Rufe und Ernennungen an Universitäten geprägt. Nachfolgende Abschnitte sollen einen Überblick verschaffen. Weiterführende Informationen sind den Berichten zu den Abteilungen sowie den einzelnen Ags zu entnehmen.

Organisatorische und Personelle Veränderungen

In der Abteilung *Genbank* (GB) ging Ende 2015 der Leiter der Ag *In vitro-Erhaltung und Cryolagerung* (IVC) in den Ruhestand. Die Arbeiten zum weiteren Ausbau der Cryosammlungen wurden 2016 mit leicht veränderten Forschungsschwerpunkten in der neu gegründeten Ag *Cryo- und Stressbiologie* (CSB) fortgesetzt.

Im Zuge interner Umstrukturierungen in der Abteilung *Züchtungsforschung* (BR) erfolgten im Mai und Juli 2017 die Schließungen der Arbeitsgruppen *Apomixis* (APM) und *Genomplastizität* (GP).

In der Abteilung *Molekulare Genetik* (MOG) wurden die langjährigen Leiter der Ags *Samenentwicklung* (SE) und *Genregulation* (GR) Ende 2015 bzw. im Frühjahr 2017 in den Ruhestand verabschiedet. Die Arbeiten der Ag *SE* werden seit Oktober 2017 unter neuer Leitung fortgeführt. Im Rahmen der noch ausstehenden Nachbesetzung der Ag *GR* ist die Erschließung eines neuen Forschungsgebiets (Systemakklimierungsdynamik) vorgesehen. Als weitere neue Arbeitsgruppen der Abteilung wurden im Januar 2016 die Ag *Assimilatallokation und NMR* (AAN) sowie die Ag *Netzwerkanalyse und Modellierung* (NAM) eingerichtet. Im Oktober 2016 erfolgte die Fortführung der Arbeiten in der Ag *Bildanalyse* (BA) unter neuer Leitung.

Entsprechend der zeitlichen Befristung der unabhängigen Arbeitsgruppen ergaben sich auch hier eine Reihe von Veränderungen. Nach dem Auslaufen der Drittmittelförderung wurde die unabhängige Ag *Abiotische Stressgenomik* (SGN) geschlossen. Die mit DFG-Mitteln geförderte Emmy-Noether-Gruppe *Metalloid-Transport* (MT) arbeitet seit August 2016 als unab-

The last two years have been marked by a series of developments and events reflecting the extraordinary dynamism of crop research. Particular attention has been paid to opening up new fields of research. In this context, a number of new research groups (RGs) have been established and the themes of the existing RGs adjusted through new appointments. As in previous years, a strategy of incremental development has produced a number of outstanding research results, attracted considerable external funding, initiated numerous both national and international collaborations and promoted appointments at several universities. The following sections present an overview of this activity. More detailed information is given in the Departmental and individual RG reports.

Organizational and personnel changes

The head of the *in vitro Storage and Cryopreservation* (IVC) RG, within the *Genebank* (GB) Department, retired at the end of 2015. The further expansion of the cryocollection was continued in 2016, under slightly altered research priorities, by the newly founded RG *Cryo- and Stress Biology* (CSB).

As part of an internal restructuring exercise within the *Breeding Research* (BR) Department, the two RGs *Apomixis* (APM) and *Genome Plasticity* (GP) were terminated (the former in May 2017 and the latter in July 2017).

Within the *Molecular Genetics* (MOG) Department, the long-serving heads of the RGs *Seed Development* (SE) and *Gene Regulation* (GR) both retired (the former at the end of 2015 and the latter in the spring of 2017). The activity of the *Seed Development* (SE) RG was continued, under new management, from October 2017. As a successor to the *Gene Regulation* (GR) RG, a new research area - Systems Acclimation Dynamics - will shortly be initiated. In January 2016, the *Assimilate Allocation and NMR* (AAN) RG, along with the *Network Analysis and Modelling* (NAM) RG were established as additional RGs within the Department. From October 2016, the activity of the *Image Analysis* (BA) RG was continued under new management.

A number of changes have been instigated to maintain the time limits set for the non-Departmental RGs. The *Abiotic Stress Genomics* (SGN) RG was terminated as a result of the expiry of its external funding. The DFG-funded Emmy Noether *Metalloid Transport* (MT) group has been working as an independent RG since August 2016. The BMBF-funded independent *Meiosis* (ME) RG started up in October 2016. Negotiations are nearing completion to initiate an indepen-

hängige Ag. Im Oktober 2016 nahm die mit BMBF-Mitteln geförderte unabhängige Ag *Meiose* (ME) ihre Arbeit auf. Die Verhandlungen für eine weitere unabhängige Ag zur angewandten Chromosomenbiologie, deren Leitung im Rahmen einer gemeinsamen Berufung mit der *Martin-Luther-Universität Halle-Wittenberg* (MLU) erfolgt, stehen vor dem Abschluss.

Drittmitteleinwerbung

Die Einwerbung von Drittmitteln setzte sich in den Jahren 2016 und 2017 mit 11,4 Mio. Euro (143 Projekte) und 10,6 Mio. Euro (149 Projekte) auf hohem Niveau fort. Diese weiterhin sehr erfreuliche Entwicklung ist zum einen das Ergebnis einer guten Passfähigkeit der IPK Forschungsstrategie mit laufenden Ausschreibungen im BMBF. Sie zeigt auch, dass das Institut ein gesuchter Partner für die Zusammenarbeit mit dem privaten Sektor, insbesondere der Pflanzenzüchtung, ist. Die Grundlagenforschung wurde durch die Einwerbung umfangreicher DFG Mittel unterstützt. In diesem Zusammenhang ist die Vergabe eines ERC-Stipendiums an einen Wissenschaftler aus dem IPK als besonderer Exzellenznachweis hervorzuheben.

Ausbau der Forschungsinfrastruktur

Phänotypisierungsinfrastruktur: Am 28. August 2017 wurde die neu errichtete Pflanzenkulturhalle des IPK in Gatersleben feierlich mit Grußworten des Ministerpräsidenten des Landes Sachsen-Anhalt, Dr. Reiner Haseloff, der Bundesministerin für Bildung und Forschung, Prof. Dr. Johanna Wanka, und des Präsidenten der Leibniz-Gemeinschaft, Prof. Dr. Matthias Kleiner, eröffnet (Fig. 3). Die Pflanzenkulturhalle wird die Pflanzenanzucht unter hoch reproduzierbaren und präzise einstellbaren Umweltbedingungen ermöglichen. Damit wird am IPK eine wichtige Voraussetzung zur Etablierung neuester Untersuchungsverfahren und Konzepte in der grundlagen- und anwendungsorientierten Pflanzenforschung geschaffen. Mit Hilfe modernster Technologien, die im Rahmen des BMBF-geförderten *Deutschen Pflanzenphänotypisierungsnetzwerks* (DPPN) entwickelt und in der Pflanzenkulturhalle installiert werden, können Eigenschaften und Merkmale von Kulturpflanzen unter verschiedenen Umweltbedingungen erfasst und analysiert werden. Neben dem DPPN ist das IPK mit seiner Pflanzenphänotypisierungsinfrastruktur Teil der *European Strategy Forum for Research Infrastructures Roadmap* (ESFRI) und in nationale und internationale Netzwerke eingebunden.

Fig. 3 Prof. Dr. Thomas Altmann, Prof. Dr. Matthias Kleiner, Prof. Dr. Johanna Wanka und Dr. Reiner Haseloff bei der feierlichen Eröffnung der Pflanzenkulturhalle ▪ Official Opening of IPK Plant Cultivation Hall (Foto: Markus Scholz)

dent RG focusing on applied chromosome biology; this will be headed by a joint appointment with Halle *Martin Luther University* (MLU).

External funding

External funding continued at a high level during 2016 and 2017, amounting to, respectively, 11.4M Euro (143 projects) and 10.6M Euro (149 projects). This continued and positive development on the one hand reflects the good fit between IPK's research strategy and current calls for proposals from the BMBF, but it also demonstrates that the Institute is a much sought-after partner for collaboration with private sector plant breeding companies. The basic research portfolio has been supported by the winning of extensive funding from DFG. A particular demonstration of the Institute's excellence in this context is the award of an ERC fellowship to an IPK researcher.

Expansion of the research infrastructure

Phenotyping infrastructure: On 28 August 2017, the newly built IPK Plant Cultivation Hall in Gatersleben was officially opened with words of greeting given by Dr. Reiner Haseloff (the Prime Minister of Saxony-Anhalt), Prof. Dr. Johanna Wanka (Federal Minister of Education and Research) and Prof. Dr. Matthias Kleiner (President of the Leibniz Association). The Plant Cultivation Hall will enable plants to be raised under highly reproducible and precisely adjustable environmental conditions. This represents an important requirement for IPK to establish state-of-the-art research methods and concepts of relevance to both basic and applied plant research. With the help of cutting edge technologies developed within the framework of the *German Plant Phenotyping Network* (DPPN) and funded by the BMBF, crop traits can be monitored and analysed under various environmental conditions. In addition to the DPPN, IPK has associated its plant phenotyping infrastructure with the *European Strategy Forum for Research Infrastructures Roadmap* (ESFRI) and integrated it into national and international network (Fig. 3).

Infrastructure for field trials: Over the last two years, the Institute has made a substantial effort to expand its field trial area, increasing it by 12 hectares. This process has involved a strong level of coordination with our funding agencies. In

Infrastruktur für Feldversuche: Das Institut hat in den letzten zwei Jahren große Anstrengungen unternommen, die zur Verfügung stehenden Feldversuchsflächen um insgesamt 12 ha zu erweitern. Hierzu befindet sich das Institut in intensiver Abstimmung mit den Zuwendungsgebern. Darüber hinaus wurde das Feldversuchswesen technisch ausgebaut und um eine moderne Saatgutaufbereitungsanlage erweitert. Automatisierung und Digitalisierung erlauben nun die GPS-gestützte Durchführung von Forschungsarbeiten im Feld.

Publikationen und Vorträge

Die im Berichtszeitraum veröffentlichten wissenschaftlichen Artikel spiegeln sowohl das hohe Niveau der am IPK durchgeführten Forschungsarbeiten als auch die abteilungsübergreifende Zusammenarbeit der verschiedenen Arbeitsgruppen des Institutes untereinander und mit nationalen und internationalen Partnern wider. Insgesamt wurden in den Jahren 2016 und 2017 146 und 168 Artikel in referierten Fachzeitschriften, u. a. in *Nature* und *Science*, veröffentlicht (Fig. 4).

Um diesen positiven Trend weiter zu befördern und die Arbeitsgruppenleitungen bei der Entwicklung ihrer Publikationsstrategie zu unterstützen, wurde der Editor in Chief von *Nature Genetics*, Myles Axton, zu einem Vortrag ins IPK und zum Gespräch mit den Wissenschaftlerinnen und Wissenschaftlern eingeladen.

Die Wissenschaftlerinnen und Wissenschaftler des IPK hielten in den Jahren 2016 und 2017 insgesamt 81 und 75 eingeladene Vorträge auf nationalen und internationalen Tagungen, Seminarveranstaltungen und Workshops.

addition, the conduct of field trials has been technically enhanced and a modern seed processing plant has been established. Automation and digitization now allow GPS-aided operations to be carried out in the field.

Publications and lectures

The scientific publication record during the reporting period reflects both the high standard of the research carried out at IPK and the extent of interdepartmental cooperation, involving the various RGs, in conjunction both national and international partners. In 2016 and 2017, respectively 146 and 168 articles were published in peer-reviewed journals, including *Nature* and *Science* (Fig. 4).

In order to promote this positive trend and to support the RG leaders in developing their publication strategy, an invitation was extended to Myles Axton, the editor-in-chief of *Nature Genetics*, to give a lecture at IPK and to talk to a number of our scientists.

During 2016, IPK scientists gave 81 invited lectures at various national and international conferences, seminars and workshops; the equivalent figure for 2017 was 75.

Prizes, awards and university appointments

In March 2016. Prof. Dr. Andreas Graner was selected to serve as the president of the *German Society for Plant Breeding e.V.* (GPZ). A further eleven IPK researchers received various awards for their scientific work or their commitment to the scientific community (Fig. 5).

Three staff were offered posts in the university sector: in 2016, Dr. Nils Stein (head of the *Genomics of Genetic Re-*

Fig. 4 Mascher et al. 2017 auf dem Cover der Nature 544. ▪ Mascher et al. 2017 on the cover of Nature 544.

Fig. 5 Dr. Matthias Jost wurde im Oktober 2016 mit dem Gaterslebener Forschungspreises ausgezeichnet ▪ Dr. Matthias Jost received in October 2016 the Gaterslebener Research Award (Foto: Lynne Main/IPK).

Preise, Auszeichnungen, Rufe

Im März 2016 wurde Prof. Dr. Andreas Graner zum Präsidenten der *Gesellschaft für Pflanzenzüchtung e.V.* (GPZ) gewählt. Weitere elf wissenschaftliche Mitarbeitende des IPK erhielten im Berichtszeitraum Auszeichnungen verschiedener Art für ihre wissenschaftliche Arbeit oder ihr Engagement in der wissenschaftlichen Gemeinschaft (Fig. 5).

Folgende Wissenschaftlerinnen und Wissenschaftler erhielten Rufe an Hochschulen:

Dr. Nils Stein, Leiter der Ag *Genomik Genetischer Ressourcen* (GGR), wurde im Jahr 2016 an die *Georg-August-Universität Göttingen* (GAU) auf die Professur (W3) für Nutzpflanzengenetik berufen (abgelehnt).

Dr. Andrea Bräutigam, Leiterin der Ag *NAM*, wurde im Jahr 2017 an die *Universität Bielefeld* auf eine Professur (W2) berufen (angenommen).

Ebenfalls im Jahr 2017 wurde PD Dr. Andreas Houben an der *Martin-Luther-Universität Halle-Wittenberg* (MLU) zum außerplanmäßigen Professor ernannt.

Die Arbeit der Gremien

Die Aufgabe des *Wissenschaftlichen Beirats* besteht in der Beratung des *Direktoriums* und des *Stiftungsrates* zu wissenschaftlichen und technischen Fragestellungen. Die Mitglieder der Wissenschaftlichen Beirats treffen sich jährlich, anlässlich des *Institutstages*, zur Begutachtung der Arbeiten am IPK. Im Jahr 2016 (10.–12. Oktober) befasste sich der Wissenschaftliche Beirat mit den Abteilungen *Genbank* und *Züchtungsforschung* sowie mit den neu gegründeten unabhängigen Arbeitsgruppen. Im Jahr 2017 (9.–11. Oktober) wurden die Forschungsarbeiten in allen wissenschaftlichen Abteilungen sowie deren Zusammenarbeit im Rahmen der Forschungsstrategie begutachtet. Der Stiftungsrat tagte am 28. April und 16. November 2016, sowie am 20. März und 14. Dezember 2017.

Ein besonderer Schwerpunkt der Beratungen, sowohl mit dem Wissenschaftlichen Beirat als auch mit dem Stiftungsrat, war die strategische und infrastrukturelle Weiterentwicklung des Instituts seit der letzten Evaluierung durch die Leibniz-Gemeinschaft im Jahr 2012.

Zusammenarbeit mit Universitäten und Forschungseinrichtungen

Ein wichtiger Aspekt im Hinblick auf die Weiterentwicklung des Forschungsprogramms ist die Vernetzung mit anderen Forschungseinrichtungen. Ziel ist die Nutzung von Komplemen-

sources RG) was invited to become a professor (W3) of Crop Genetics at *Goettingen Georg August University*, but he declined to accept the post; in 2017, Dr. Andrea Bräutigam (head of the *Network Analysis and Modelling* RG) was pleased to accept a professorial post (W2) at *Bielefeld University*; finally, and also in 2017, PD Dr. Andreas Houben was appointed as an adjunct Professor at *Martin Luther University*.

Committee activities

The *Scientific Advisory Board* advises the *Board of Directors* and the *Governing Board* on both scientific and technical matters. The *Scientific Advisory Board* meet annually, coinciding with the *Institute Day*, to assess IPK's work. From 10-12 October 2016, the Scientific Advisory Board dealt with the *Genebank* and *Breeding Research* departments and the newly established independent RGs, while from 9-11 October 2017, the research activities in each of the scientific Departments and their cooperation within the framework of the global research strategy were reviewed. The *Governing Board* met during 2016 on April 28 and November 16, and during 2017 on March 20 and December 14; the specific focus of these meetings was to review the strategic and infrastructural development of the Institute since its most recent evaluation by the Leibniz Association in 2012.

Networking with universities and research institutions

Networking with other research institutions is considered to be an important aspect of the development of the research programme. The aim is to exploit complementarity in both know-how and infrastructure, and to attract young scientists.

The *Leibniz Association* promotes thematically focused collaborations between Leibniz Institutes and universities, using the concept of a *Science Campus* to drive equal, complementary and regional partnerships. The goal is to create networks able to develop particular research areas and to strengthen the relevant local scientific environment. The IPK works closely with MLU and other Leibniz Institutes at the *Leibniz Science Campus Halle - Plant-based Bioeconomics* (WCH) , which is currently enjoying its second funding phase. Together with Rostock University and four other Leibniz Institutes located in Rostock, Dummerstorf, Warnemünde and Greifswald, IPK participates in the *Leibniz ScienceCampus - Phosphorus Research Rostock* (WCR). In addition, IPK is a network partner in the *Science Outreach Campus* (KiSOC), founded on 16 July 2016, along with the *Leibniz Institute for Science and Mathematics Education* (IPN) and *Kiel Christian Albrechts University* (CAU) as lead partners.

täreffekten (Know-how, Infrastruktur) und die Gewinnung von Nachwuchswissenschaftlerinnen und -wissenschaftlern.

Die *Leibniz-Gemeinschaft* befördert die thematisch fokussierte Zusammenarbeit zwischen Leibniz-Instituten und Universitäten mit dem Instrument der WissenschaftsCampi im Sinne einer gleichberechtigten, komplementären und regionalen Partnerschaft. Ziel ist es, Netzwerke zu schaffen, um den jeweiligen Forschungsbereich weiter zu entwickeln und das wissenschaftliche Umfeld für diese Thematik zu stärken. Das IPK arbeitet eng mit der *MLU* und weiteren Leibniz-Instituten im *Leibniz-WissenschaftsCampus Halle – Pflanzenbasierte Bioökonomie* (WCH) zusammen, der sich in seiner zweiten Förderphase befindet. Mit der Universität Rostock und vier weiteren Leibniz-Instituten aus Rostock, Dummerstorf, Warnemünde und Greifswald beteiligt sich das IPK am *Leibniz-WissenschaftsCampus – Phosphorforschung Rostock* (WCR). Darüber hinaus ist das IPK Netzwerkpartner des am 16. Juli 2016 gegründeten *Science Outreach Campus* (KiSOC). Das *Leibniz-Institut für die Pädagogik der Naturwissenschaften und Mathematik* (IPN) und die *Christian-Albrechts-Universität zu Kiel* (CAU) sind Lead Partner dieses Zusammenschlusses.

Um aktuelle Themen von hoher wissenschaftlicher und gesellschaftlicher Relevanz zu bearbeiten und dabei Lösungen für komplexe gesellschaftliche Herausforderungen zu finden, schließen sich Leibniz-Einrichtungen in inter- und transdisziplinären *Leibniz-Forschungsverbünden* zusammen. Diese werden von zentralen Gremien der *Leibniz-Gemeinschaft* eingerichtet und von der Gemeinschaft finanziell unterstützt. Die *Leibniz-Forschungsverbünde* sind zentrale Ansprechpartner für Politik, Wirtschaft, Förderer, Medien sowie für die Zivilgesellschaft und offen für die Zusammenarbeit mit Universitäten, anderen außeruniversitären Forschungs- und Infrastruktureinrichtungen sowie internationalen Forschungsgruppen und Partnern aus der Wirtschaft. Bereits seit 2013 ist das IPK am *Leibniz-Forschungsverbund Biodiversität* und seit 2014 am *Leibniz-Forschungsverbund Nachhaltige Lebensmittelproduktion und gesunde Ernährung* beteiligt. 2016 hat sich das Institut auch dem *Leibniz-Forschungsverbund Wirkstoffe und Biotechnologie* angeschlossen.

Insgesamt unterhielt das IPK im Jahr 2017 95 vertragliche Kooperationen mit Hochschulen sowie 126 mit außeruniversitären Forschungseinrichtungen im In- und Ausland.

Viele Mitarbeiterinnen und Mitarbeiter sind eng in die Lehre an den agrar- und naturwissenschaftlichen Fakultäten der *MLU* und anderer Universitäten und Fachhochschulen eingebunden. Insgesamt wurden in den Jahren 2016 und 2017 28 Diplom- und Masterarbeiten sowie 20 Bachelorarbeiten am IPK erfolgreich abgeschlossen. Das IPK verfolgt das Ziel der Erhöhung gemeinsamer Berufungen, um den Zugang zu Studierenden

In order to be involved in active topics of high scientific and social relevance and to find solutions for complex social challenges, various Leibniz institutions have combined to form inter- and transdisciplinary *Leibniz Research Associations*. These are set up centrally by the *Leibniz Association* and receive financial support from the Community. These Associations represent a central contact point for politicians, the business community, financial sponsors, the media and civil society, and are open for cooperation with universities, other non-university research and infrastructure institutions, international research groups and research partners from the private sector. Since 2013, IPK has been involved in the *Leibniz Research Biodiversity Network* and since 2014 in the *Leibniz Research Sustainable Food Production and Healthy Nutrition Network*. During 2016, the Institute joined the *Leibniz Research Active Substances and Biotechnology Network*.

In 2017, IPK maintained 95 contractual cooperation agreements with universities and 126 with non-university research and service institutions in both Germany and abroad.

Many staff members are active in teaching at Agricultural and Natural Science faculties, primarily at *MLU*, but also at other universities and applied science universities. In 2016 and 2017, 28 diploma and MSc theses and 20 bachelor theses were successfully submitted by students based at IPK. To further enhance networking with universities, a cooperation agreement has been concluded with *Goettingen Georg August University*, one of Germany's largest and most research-oriented universities. IPK increasingly uses the services of the *International Association for the Exchange of Students for Technical Experience* (IAESTE) to recruit students from foreign universities. The IPK also strives to attract excellent students through industry-funded MSc scholarships.

Events, press and public relations

Scientific research and its results influence not only the everyday life of researchers, but of that of the entire population. Accordingly, the demands and expectations placed on the press and public relations operations of research institutions have increased significantly over recent years. IPK has recognized this by establishing an additional press and public relations office, as well as by making certain organizational adjustments. This has engendered an increased level of professionalization of the Institute's external image. Public relations covers communicating with a diverse range of target audiences, such as the general public, trainees/students, collaborators etc.:

- Raising awareness of biodiversity issues
- Providing information regarding methods, opportunities and risks of green genetic enginee-

zu verbessern. Zu diesem Zweck wurde eine Kooperationsvereinbarung mit der *Georg-August-Universität Göttingen* (GAU), einer der großen und forschungsstarken Universitäten in Deutschland, abgeschlossen. Weiterhin nutzt das IPK verstärkt die Angebote der *International Association for the Exchange of Students for Technical Experience* (IAESTE), um Studenten ausländischer Universitäten anzuwerben. Das IPK ist ferner bestrebt, durch industriefinanzierte Masterstipendien exzellente Studierende zu gewinnen.

Veranstaltungen, Presse- und Öffentlichkeitsarbeit

Die wissenschaftliche Arbeit und ihre Ergebnisse beeinflussen nicht nur den Alltag der Forschenden, sondern der gesamten Bevölkerung. Dementsprechend sind die Anforderungen und Erwartungen an die Presse- und Öffentlichkeitsarbeit von Forschungseinrichtungen in den vergangenen Jahren deutlich gestiegen. Dieser Entwicklung trug das IPK durch die Einrichtung einer zusätzlichen Stelle für Presse- und Öffentlichkeitsarbeit sowie organisatorischen Anpassungen Rechnung. Hierdurch wurde eine weitere Professionalisierung bei der Außendarstellung des Instituts erreicht.

Mit der Öffentlichkeitsarbeit sollen folgende kommunikativen Ziele bei unterschiedlichen Zielgruppen (Öffentlichkeit, Auszubildende/Studierende, Kooperationspartner etc.) erreicht werden:

- Sensibilisieren für Fragestellungen der biologischen Vielfalt
- Informieren über Methoden, Chancen und Risiken der Grünen Gentechnik und der neuen molekularbiologischen Verfahren als Voraussetzung für eine wissensbasierte Meinungsbildung
- Informieren über Arbeitsbereiche in MINT-Berufen, um junge Menschen für diese Berufe und Studiengänge zu begeistern

Broschüren und Filme: Um den zahlreichen Besuchergruppen einen Überblick über das Institut zu ermöglichen, wurde eine 12-seitige Institutsbroschüre erstellt, die zweisprachig Informationen hinsichtlich Organisationsstruktur und Forschungsthemen bereitstellt. Als besonderer Gewinn bei der Entwicklung von Informationsmaterialien für das Institut erwies sich die Kooperation mit Masterstudenten der *Hochschule Merseburg* aus dem Studiengang *Informationsdesign und Medienmanagement*, mit welchen im Jahr 2017 zwei Broschüren zur Darstellung der zentralen Forschungsinfrastrukturen Genbank und Pflanzenphänotypisierung entwickelt wurden. Ergänzend wurden 2017 fünf Filmmodule zur Präsentation der Pflanzenphänotypisierungsinfrastruktur des IPK erstellt und über die Website des IPK sowie den Kanal YouTube verbreitet.

ring and novel molecular biological techniques as a prerequisite for knowledge-based opinion-forming
- Providing information regarding STEM to inspire young people's study and career choices

Brochures and films: In order to give our numerous visiting groups an overview of the Institute, a 12 page bilingual brochure has been prepared, which informs the reader regarding our organizational structure and research topics. The development of information materials for the Institute benefited from the input of MSc students from the *Information Design and Media Management* programme at *Merseburg University of Applied Sciences*, with whom we were able to develop two brochures during 2017, together presenting the central research infrastructures of the Gene Bank and the plant phenotyping platforms. In addition, five films were produced during 2017 to present the plant phenotyping infrastructure; they were mounted both on the IPK website and on its YouTube channel.

Information materials: During 2016, various materials were developed to present the work of IPK at a range of scientific and media events, as well as for the general public and at trade fairs. The slogan "Crop plant diversity – Conserving ▪ Exploring ▪ Exploiting" has been included in all of these materials. In addition, roll-ups, posters and flyers, developed for other themes, have been variously used to provide relevant target groups with specific information regarding IPK.

Scientific events: During the reporting period, IPK organized a total of 30 scientific events and conferences attracting around 1,200 participants, the majority of whom came from outside Germany. The IPK acted as co-organizer for eight other scientific events, involving some 1,400 participants. The *fifth Gatersleben Talk* entitled *The Digital Revolution and its Consequences* was held at the Institute on 4-5 May 2017. Prof. Dr. Armin Willingmann, the Saxony-Anhalt Minister of Science, Economics and Digitization, along with a selection of renowned scientists from various disciplines discussed problems and perspectives of social digitization in a series of lectures, open discussions and a round table discussion. The scientific activities were accompanied by an art exhibition and a reading.

Public relations events: The central aim of science communication is to inform the general public, an activity which has been entered into within the context of various events at the Institute. A symposium was held in Groß Lüsewitz on 16 May 2017 to mark the 25th anniversary of the Sub-Collections North RG. In order to display the work and research of the Institute, open days have been organized at each of the three IPK sites. Over 3,000 guests took advantage of the opportunity to explore the facilities at Gatersleben on 4 June

Informationsmaterialien: Insbesondere im Jahr 2016 arbeitete die Geschäftsstelle daran, Materialien zur Präsentation des IPK im Rahmen wissenschaftlicher Veranstaltungen, Veranstaltungen für die Medien sowie die breite Öffentlichkeit und Messen zu entwickeln. Das Motto „Kulturpflanzenvielfalt – Erhalten ▪ Erforschen ▪ Erschließen" findet sich immer wieder an geeigneter Stelle auf den Informationsmaterialien. Zusätzlich wurde mit Hilfe von Roll-ups, Postern und Flyern, die zu verschiedenen thematischen Schwerpunkten entwickelt wurden, zu verschiedenen Anlässen zielgruppengerecht über das IPK informiert.

Wissenschaftliche Veranstaltungen: Im Berichtszeitraum wurden seitens des IPK insgesamt 30 wissenschaftliche Veranstaltungen und Konferenzen, die Mehrheit davon mit internationaler Beteiligung, für ca. 1.200 Teilnehmende organisiert. An acht weiteren wissenschaftlichen Veranstaltungen mit ca. 1.400 Teilnehmenden beteiligte sich das IPK als Mitorganisator.

Darüber hinaus wurde vom 04. bis zum 05. Mai 2017 das *5. Gaterslebener Gespräch* unter dem Titel *Die digitale Revolution und ihre Folgen* am IPK durchgeführt. Der Minister für Wissenschaft, Wirtschaft und Digitalisierung des Landes Sachsen-Anhalt, Prof. Dr. Armin Willingmann und renommierte Wissenschaftlerinnen und Wissenschaftler aus verschiedenen fachlichen Disziplinen haben sich in Vorträgen, offenen Diskussionsrunden und einem Rundtischgespräch mit den Problemen sowie den Perspektiven der gesellschaftlichen Digitalisierung auseinandergesetzt. Der wissenschaftliche Veranstaltungsteil wurde von einer Kunstausstellung und einer Lesung begleitet.

Veranstaltungen für die breite Öffentlichkeit: Zentrales Ziel der Wissenschaftskommunikation ist die Information der breiten Bevölkerung. Im Rahmen verschiedenster Veranstaltungsformate erfolgte dies am IPK. So fand beispielsweise das 25-jährige Jubiläum der Ag *Teilsammlungen Nord* (TEN) am 16. Mai 2017 im Zusammenhang mit einem Symposium in Groß Lüsewitz statt.

Um die Arbeiten und Forschungen des Instituts zu zeigen, wurden Tage der offenen Tür an den drei Standorten des IPK angeboten. Über 3.000 Gäste besichtigten die Einrichtungen am 04. Juni 2016 und 10. Juni 2017 in Gatersleben, am 21. Mai 2016 und 20. Juni 2017 in Malchow sowie am 17. Juni 2017 in Groß Lüsewitz (Fig. 6).

Messen: Das IPK präsentierte sich 2016/2017 auf insgesamt 17 Messen. Darunter waren 10 Messen zur Personalgewinnung und 7 Messen zur Präsentation des Instituts und seiner Arbeiten, wie beispielsweise die *Analytica* 2016 und die *Biotechnica* 2017.

2016 and 10 June 2017, at Malchow on 21 May 2016 and 20 June 2017, and at Groß Lüsewitz on 17 June 2017 (Fig. 6).

Fairs: IPK participated in 17 trade fairs during the reporting period; ten of these were intended for personnel recruitment and seven (including Analytica 2016 and Biotechnica 2017) in order to show-case the Institute's work.

Guided tours: During the reporting period, a total of 218 guided tours involving over 2,500 participants were organized at the IPK sites in Gatersleben, Malchow and Groß Lüsewitz (Fig. 7). The domestic and foreign guests comprised mostly researchers, students, farmers, politicians and school students, but included some special interest groups. Each guided tour was tailored to its target group, and was supported by Institute RGs.

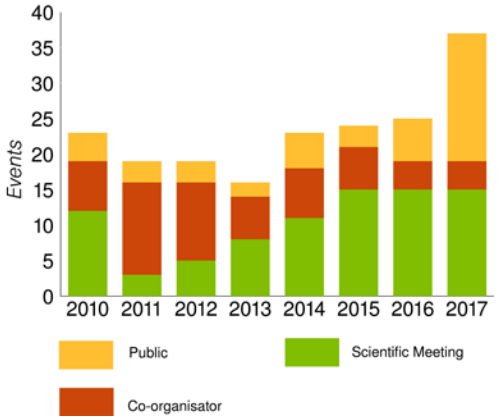


Fig. 6 Übersicht der Veranstaltungen am und mit dem IPK ▪ Events at and with IPK

Press releases and media echo: IPK retains active contact with media representatives, mainly associated with regional television broadcasters, but also including responding to the numerous inquiries which emanate from the press, film and radio. The office acts as the first point of contact and can organize a visit to the Institute, as well connect media personnel with Institute scientists. The IPK also provides information to the public via press releases, 26 of which were released during 2016 and 23 during 2017. The reach of these press releases was enhanced by the IPK's joining the Information Service Science (IDW) (Fig. 8).

The Gatersleben Biotechnology site

As its largest member institution, IPK is the focus of the *Green Gate Gatersleben* (GGG) site initiative, in which all of the campus-based plant biotechnology companies and institutions, along with the regional public sector, participate. In addition to IPK, the membership includes six companies and a student laboratory. Co-operation primarily takes the form of joint marketing of the site, joint projects and the provision of

Führungen: Im Berichtszeitraum wurden insgesamt 218 Führungen für mehr als 2.500 Teilnehmende auf dem Gelände des IPK in Gatersleben, Malchow und Groß Lüsewitz durchgeführt (Fig. 7). Bei den nationalen und internationalen Gästen handelte es sich zumeist um Forschende, Studierende, Landwirte, Politikerinnen und Politiker sowie Schülerinnen und Schüler, aber auch um weitere interessierte Besuchergruppen. Die Führungen wurden zielgruppengerecht durchgeführt und fachlich von Arbeitsgruppen aus dem Institut unterstützt.

Pressemitteilungen und Medienecho: Das IPK steht in regem Kontakt mit Medienvertreterinnen und –vertretern, aufgrund bestehender, zumeist regionaler Netzwerke, aber auch im Rahmen der vielfältigen Anfragen aus Presse, Film und Radio. Die Geschäftsstelle ist dabei erster Ansprechpartner und organisiert Besuche am IPK sowie Presse- und Medienkontakte mit Wissenschaftlerinnen und Wissenschaftlern des Instituts. Das IPK informiert die Öffentlichkeit aber auch im Rahmen von Pressemitteilungen, so wurden im Jahr 2016 26 Pressemitteilungen und 2017 23 Meldungen herausgegeben. Die Reichweite der Pressemitteilungen wurde durch den Beitritt des IPK zum *Informationsdienst Wissenschaft* (idw) erheblich verbessert. Der Pressespiegel (Fig. 8) entwickelte sich entsprechend.

Biotechnologiestandort Gatersleben

Als größte Einrichtung steht das IPK im Mittelpunkt der Standortinitiative *Green Gate Gatersleben* (GGG), in der sich alle campusansässigen Firmen und Einrichtungen der Pflanzenbiotechnologie sowie der regionalen öffentlichen Hand engagieren. Dazu gehören neben dem IPK u. a. sechs Firmen und ein Schülerlabor. Die Zusammenarbeit erfolgt in erster Linie durch ein gemeinsames Standortmarketing, die Bearbeitung gemeinsamer Projekte sowie die Bereitstellung wissenschaftlicher und infrastruktureller Serviceleistungen, wie z. B. im Rahmen des in Gatersleben durchgeführten *InnoPlanta-Forums* 2016 und 2017. Eine Neuauflage der überarbeiteten Standortbroschüre und die Präsentation des Standortes in thematisch passenden Magazinen erleichtert dabei die Arbeit.

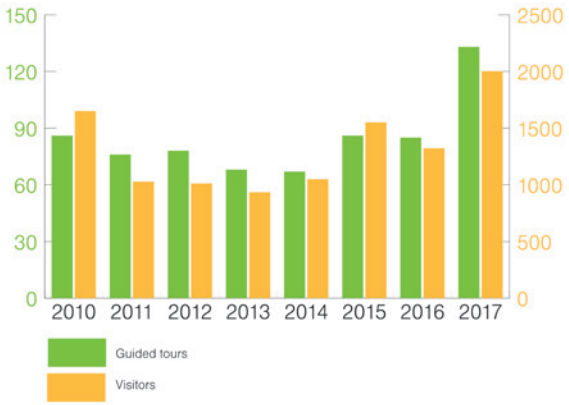


Fig. 7 Führungen am IPK und die erreichten Besucherzahlen. ▪ Guided tours and visitors

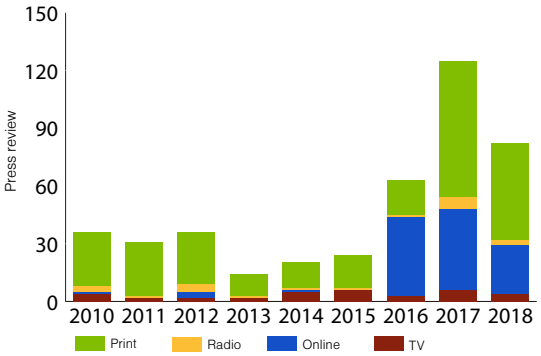


Fig. 8 Medienecho ▪ Media coverage

scientific and infrastructure services, for example the *InnoPlanta Forum*, which took place in Gatersleben both in 2016 and 2017. An updated edition of the site brochure and the presentation of the site in thematically relevant magazines have facilitated this work.

Verwaltung und Infrastruktur ▪ Administration and Infrastructure

Personal

Für den Betrieb eines großen Forschungsinstituts sind eine leistungsfähige Administration, ein wohl organisiertes allgemeines und technisches Campus-Management sowie Dienstleistungseinheiten wie die wissenschaftliche Bibliothek sowie zentrale Unterstützung des Vermehrungs- und Versuchsanbaus auf Feldflächen, in Gewächshäusern und Phytokammern, unabdingbar. Institutsleitung und Stabsfunktionen wie Justitiariat, Sicherheitskraft, Ombudsperson, Beauftragte für biologische Sicherheit und Gleichstellungsbeauftragte stehen für die Einhaltung nationaler und internationaler Standards (Fig. 9).

Qualifiziertes und motiviertes Personal ist für das IPK ein entscheidender Erfolgsfaktor. Personelle Wechsel auf der Ebene von Gruppenleitungen in wissenschaftlichen, technischen und administrativen Bereichen konnten dank entsprechender Verfahren und Angebote weitgehend gemeistert werden. Während sich das IPK bei der Suche wissenschaftlich ausgebildeter Fachkräfte schon seit langem in einem sehr kompetitiven Umfeld behauptet, wird die Gewinnung von geeignetem technischen und administrativen Personal zu einer immer größeren Herausforderung. Dem Institut ist es dennoch gelungen, die Beschäftigtenzahlen, insbesondere bei drittmittelfinanziertem Personal, nochmals zu steigern. Die Entwicklung über die letzten drei Jahre ist in der nachfolgenden Tabelle (Tab. 1) dargestellt.

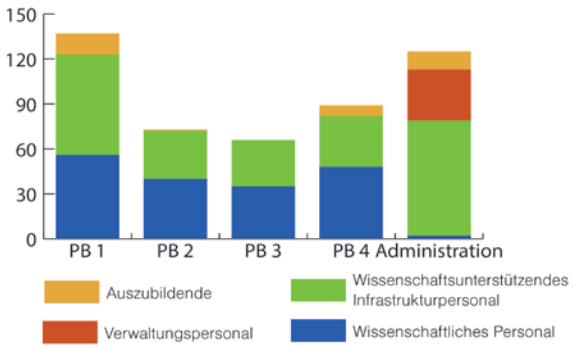


Fig. 9 Beschäftigte in den Forschungsprogrammen (vgl. auf Seite 9) und der Administration (Wissenschaftliche Dienstleistungen, Zentrale Dienste, Verwaltung, Geschäftsführung und Stabsfunktionen einschließlich Sekretariate) Stand: 31.12.2017 ▪ Employee numbers engaged in research programmes (PB, see page 9) and administration, as of 31 December 2017. | Legend: Yellow= trainees, green= Scientific infrastructure support staff, red= administrative staff, blue= scientists

Staff

The operation of a large research institute requires an efficient campus-wide administration which needs to provide services such as the scientific library and facilities to enable plants to be raised in the field, in greenhouses and in controlled environment chambers. It also ensures the necessary legal, security and workplace safety measures required to ensure compliance with national and international standards. The Institute employs an ombudsman, a biological safety officer and an equal opportunity officer (Fig. 9).

A decisive factor in ensuring success for IPK is to attract well qualified and motivated personnel. At the level of management with respect to scientific, technical and administrative activities, staff turn-over has been controlled through the use of appropriate procedures and employment offers. While IPK has faced a competitive recruitment environment for some time in its search for scientifically trained specialists, the challenge of attracting suitable technical and administrative personnel is looming ever larger. Nevertheless, the Institute has succeeded once again to grow the size of its workforce, especially the sector financially supported by external funding. Trends in employee numbers over the last three years are illustrated Table 1.

	2015	2016	2017
Haushaltsfinanziertes Personal / Internally funded staff	328	318	327
Drittmittelfinanziertes Personal / Externally funded personnel	124	141	130
Auszubildende / Trainees	24	29	34
Summen / Total	**476**	**488**	**491**

Tab. 1 Personalgesamtübersicht (Stand jeweils zum 31.12.). Die hohe Anzahl Auszubildender ist auf überlappende Ausbildungsjahrgänge zurückzuführen. ▪ Employee numbers at the Institute as of December 31 in 2015-2017. The high number of trainees reflects the overlap between training year and calendar year.

Eine herausragende Bedeutung kommt der Ausbildung des wissenschaftlichen Nachwuchses und der Karriereförderung am IPK zu. Alle Promovierenden am IPK Gatersleben sind in das *PhD Graduate Program* eingebunden. Sie profitieren im Rahmen ihrer Weiterqualifikation nicht nur von der herausragenden Forschungsinfrastruktur, der Interdisziplinarität und Internationalität des Institutes sowie den entsprechenden Netzwerken, sondern auch ganz maßgeblich von einem strukturier-

The training of young scientists and the promotion of their careers are of outstanding importance to IPK. All PhD students working at IPK Gatersleben are integrated into the *PhD Graduate Programme*. Achieving their higher qualification is assured not only by their placement within an outstanding research infrastructure, by the Institute's interdisciplinary nature, its internationality and connection with relevant networks, but also by their taking part in a mandatory structured

ten Arbeitsprogramm am Institut. Die verbindliche Teilnahme, erweitert das fachliche Know-how der Promovierenden über den Horizont ihrer eigenen Qualifikationsarbeiten hinaus und schafft die Grundlagen für Karrierewege in und außerhalb der Wissenschaft. Das *PhD Student Board* vertritt die Interessen und Anliegen der Promovierenden gegenüber der Institutsleitung und fördert damit die stetige Weiterentwicklung des Institutsangebots (Tab. 2).

work programme. Participation in the Programme extends their know-how beyond the horizon of their own research topic and creates a firmer basis for a career either in or outside of science. The *PhD Student Board* represents the interests and concerns of PhD students towards Institute's management and thus promotes positive developments in the services provided to them (Tab. 2).

	2015 (Frauen / women)	2016 (Frauen / women)	2017 (Frauen / women)
Promovierende / Postgraduates	60 (25)	46 (21)	41 (22)
Gastpromovierende / Visiting postgraduates	27 (18)	28 (19)	31 (21)
Wiss./stud. Hilfskräfte / Research assistants	11 (3)	15 (7)	18 (8)
Gaststudierende / Visiting students	8 (6)	5 (4)	8 (5)
Gesamt / Total	106 (52)	94 (51)	100 (56)

Tab. 2 Nachwuchsförderung im wissenschaftlichen Bereich (Stand jeweils zum 31.12.) ▪ The population of early career researchers in the scientific field, as of December 31 of each year.

Analog zur Förderung der Promovierenden wird die berufliche Entwicklung junger Postdocs in Forschung und Lehre unterstützt. Zur Interessenvertretung, dieser sich in der entscheidenden Phase der beruflichen Weichenstellung befindenden, Personengruppe ist ein *Postdoc-Board* etabliert, das sich eng mit dem *Direktorium* zum Status quo und zu programmatischen Aktivitäten für strukturierte Karriereentwicklungen in der Wissenschaft abstimmt. Das *Postdoc-Board* gibt Hilfestellung bei der Schaffung der eigenen beruflichen Identität. Mit Hilfe eines institutszentral zur Verfügung gestellten, selbstverwalteten Budgets werden Weiterbildungsmaßnahmen (u. a. Hochschuldidaktik, Seminare für Laborleitungen) durchgeführt und im zweijährigen Turnus eine *Summer School* organisiert.

Analogous support is given to forster the professional development of young postdoctoral fellows, involving both research and teaching activity. A *Postdoctoral Board* has been established to represent the interests of this group of researchers, who find themselves at a critical point in their professional development. The Board coordinates closely with the *Board of Directors* on the status quo and on programmatic activities supporting their development of a scientific career. The Board provides assistance in establishing a fellow's professional identity. With the help of a self-administered budget provided by the Institute, further training measures, such as studying the theory and practice of teaching and learning at the university level and attending seminars targeting laboratory managers, are offered in the form of a biennial *summer school*.

Um herausragenden Wissenschaftlerinnen und Wissenschaftlern die Möglichkeit zu geben, sich weiter im Wissenschafts- und Forschungsmanagement zu profilieren, existieren am IPK mit Stand Dezember 2017 vier unabhängige Arbeitsgruppen. Ohne in eine der vier wissenschaftlichen Abteilungen des Institutes eingegliedert und einem Abteilungsleiter unterstellt zu sein, können sich ihre Leiter mit hoher Eigenständigkeit und Sichtbarkeit auf eine spätere wissenschaftliche Leitungsfunktion vorbereiten und eigene Forschungsprojekte realisieren.

The four independent RGs active in the Institute as of December 2017 give outstanding scientists an opportunity to make their mark in science and research management. Not being integrated within one of the four formal science Departments means that the leaders of these RGs do not report to a Departmental head, and so are able to not only more easily realize their own research projects, but in so doing, can establish a spirit of independence and promote their personal scientific visibility, both of which are of value for their progression into scientific managers.

Die Zusammenarbeit mit der *MLU* soll durch die Erhöhung der Anzahl gemeinsamer Berufungen - insbesondere von Juniorprofessuren sowie von Honorar- und außerplanmäßigen Professuren - weiter gestärkt werden. Im Berichtszeitraum ist dies mit der Ernennung von Dr. Andreas Houben zum Honorarprofessor gelungen. Das Verfahren zur Besetzung einer Juniorprofessur für angewandte Chromosomenbiologie wird im März 2018 abgeschlossen und damit eine fünfte unabhängige Arbeitsgruppe am IPK geschaffen.

Cooperation with *MLU* is set to be further strengthened by raising the number of joint appointments made - especially of junior professorships and honorary and extraordinary professorships. During the review period, Dr. Andreas Houben was appointed as an honorary professor at MLU, while the filling a junior professorship in applied chromosome biology will be completed in March 2018, thereby creating a fifth independent RG at the IPK. Links to universities outside Saxony-Anhalt have also been strengthened. At the beginning of August 2017, a cooperation agreement was signed with

Die Verbindungen zu Universitäten außerhalb Sachsen-Anhalts konnten ebenfalls ausgebaut werden. Anfang August 2017 konnte eine Kooperationsvereinbarung mit der Universität

Göttingen zur Zusammenarbeit und zu einem gemeinsamen Verfahren zur Besetzung einer Professur *Genomik pflanzlicher Ressourcen* abgeschlossen werden. An der *Leibniz-Universität Hannover* habilierte Ende 2017 Frau Dr. Ljudmilla Borisjuk, Leiterin der Ag *Assimilatallokation und NMR* (AAN).

Die *Nachwuchsförderung* am IPK schließt die Berufsausbildung explizit mit ein. Über 20 junge Menschen können insgesamt sechs Berufsbilder in Theorie und Praxis kennenlernen. Mit einer Ausbildungsquote (Ausbildungsplätze bezogen auf die Anzahl der sozialversicherungspflichtigen Beschäftigten) von rund 5 Prozent liegt das IPK etwas über der Durchschnittsquote aller Einrichtungen der Leibniz-Gemeinschaft.

Darüber hinaus werden am IPK seit 2011 Ausbildungsplätze für den dualen Bachelor-Studiengang *Biotechnologie* an der *Hochschule Anhalt* (FH) in Köthen angeboten. Die Studierenden absolvieren im Institut den praktischen Teil ihrer Ausbildung (Tab. 3).

Göttingen Georg-August University and an agreement made to establish a professorship in the field of the *genomics of plant resources*. Dr. Ljudmilla Borisjuk, Head of the *Assimilate Allocation and NMR* RG, achieved her habilitation at *Hannover Leibniz University* at the end of 2017.

The promotion of young talent at IPK explicitly includes vocational training. At least 20 young people per year are familiarized, both in theory and in practice, with six job types. With a training quota (the ratio of training places to the number of employees subject to social security contributions) of around 5%, IPK lies slightly above the average quota of all institutions belonging to the Leibniz Association. In addition, since 2011, the Institute has been offering training places within a dual Bachelor's degree programme run by *Anhalt University of Applied Sciences* (FH) in Köthen in the area of *biotechnology*: the students complete the practical part of their training at IPK (Tab. 3).

Tab. 3 Auszubildende (Stand jeweils zum 31.12.) ▪ Trainee numbers at IPK, as of December 31 of each year.

Art der Auszubildenden / Type of trainee	Anzahl der Auszubildenden / Number of trainees		
	2015	2016	2017
Biologielaborant/-in / Biological lab technician	8	12	14
Bürokauffrau/-mann bzw. Kauffrau/-mann für Büromanagement / Office clerical staff	2	3	3
Gärtner/-in für Gemüsebau bzw. Pflanzentechnologin/Pflanzentechnologe / Plant technical assistants	3	2	5
Fachangestellte/-r für Medien- und Informationsdienste / Media and IT support staff	1	1	1
Köchin/Koch / Kitchen staff	2	2	3
Fachinformatiker/-in Systemintegration / IT specialists	2	2	1
Duale Studierende Biotechnologie / Dual Bachelor's degree programme	6	7	7
Gesamt / Total	**24**	**29**	**34**

Neben der Ausbildung wird am IPK ein besonderes Augenmerk auf ständige Weiterbildung des Personals gelegt. Hierzu wurde für alle technisch und administrativ Beschäftigten ein internes Weiterbildungsprogramm etabliert, das durch verschiedene Maßnahmen und Angebote weiter ausgebaut werden soll. Für Führungskräfte sind neben der jährlichen Inhouse-Schulung ebenfalls bei Bedarf individuelle weitergehende Angebote vorgesehen.

Die Förderung und Umsetzung der Chancengleichheit von Frauen und Männern auf allen Hierarchieebenen ist dem IPK ein strategisches Anliegen. Das IPK hat für eine Erhöhung des Frauenanteils flexible Zielquoten im Sinne der forschungsorientierten Gleichstellungsstandards der DFG definiert, die im Programmbudget und Gleichstellungskonzept detailliert beschrieben sind.

In addition to training, IPK places particular emphasis on promoting the ongoing training of personnel. To this end, an internal training programme has been established for all technical and administrative employees, which is to be further expanded through various measures and offers. In addition to annual in-house training, further individual training courses are provided to managers if requested.

A strategic concern of the Institute is to promote and implement equal opportunities for women and men at all levels of the organisation. In order to raise the proportion of female staff, IPK has defined flexible target rates in line with the DFG's research-oriented gender equality standards: these are described in detail in the Programme Budget and Gender Equality Concept. A period of five to eight years is assumed to be a realistic time horizon for achieving the target quotas. The goals can be flexibly adapted to the

Als realistischer Horizont für das Erreichen der definierten Zielquoten wird ein Zeitraum von fünf bis acht Jahren angenommen. Dabei können die Ziele flexibel an die realen Entwicklungen im Institut angepasst werden. Für 2018 ist die Zwischenevaluierung des für 2016 bis 2019 aufgestellten Gleichstellungskonzepts vorgesehen, mit der sowohl die Umsetzung und Wirksamkeit der vorgeschlagenen Maßnahmen beurteilt als auch die Entwicklung der Beschäftigungsstruktur dargestellt und eine entsprechende Anpassung der Zielquoten vorgenommen werden soll. Bei Letzterem ist zu berücksichtigen, dass die entsprechenden Ziele nur im Rahmen der tatsächlichen Stellenfluktuation, der Teilnahme von Frauen an Bewerbungsverfahren und unter Beachtung des Auswahlprinzips der Bestengewinnung (mindestens gleiche Eignung, Befähigung und fachliche Leistung) erreicht werden können. Als besondere Herausforderung für das IPK ist daher zu sehen, den Anteil passender Bewerbungen qualifizierter Frauen auf Ausschreibungen für wissenschaftliche Positionen zu erhöhen.

Zur Förderung der Herstellung von Chancengleichheit zwischen Frauen und Männern in Wissenschaft und Forschung konnte das Institut Mittel des *Europäischen Struktur- und Investitionsfonds* (ESI-Fonds) einwerben. Diese stehen für einen Zeitraum von vier Jahren zur Einrichtung eines Gleichstellungsbüros und zur aktiven Förderung von Forscherinnen auf ihrem Weg in Führungspositionen in der Wissenschaft zur Verfügung. Das Büro nahm im Oktober 2017 seine Arbeit auf.

Ein familienfreundliches Gesamtumfeld ist essentiell, um ein zu den Bedürfnissen möglichst vieler Lebensentwürfe passfähiges und damit attraktives Arbeitsumfeld anbieten zu können. Das IPK unterstützt alle Beschäftigten individuell mit Angeboten in Bezug auf z. B. Arbeitszeit und Arbeitsorganisation, Arbeitsort, Informations- und Kommunikationsmöglichkeiten, um Familien- und Privatleben mit der beruflichen Tätigkeit und Qualifizierung in Einklang zu bringen. Diese Ausrichtung im Institut ist als Managementinstrument durch das regelmäßige *audit berufundfamile* bereits seit 2010 verankert. Dem internationalen wissenschaftlichen Umfeld entsprechend sind darüber hinaus spezielle Angebote für ausländische Beschäftigte sowie für Forscherpaare etabliert.

Finanzierung / Budget

Dem IPK standen 2017, inklusive Fördergeldern Dritter und eigenen Einnahmen, insgesamt 54.602 TEUR an Finanzmitteln (2016: 57.403 TEUR, 2015: 55.219 TEUR) für unmittelbare Ausgaben des Instituts, d. h. ohne Einnahmen für Partner und ohne Einbehalte für Baumaßnahmen, zur Verfügung (Tab. 4). In dieser Summe sind einerseits Zuwendungen im Rahmen der Grundfinanzierung des Instituts in Höhe von 36.360 TEUR (2016: 33.664 TEUR) enthalten als auch aus dem Vorjahr

actual development of the Institute. An interim evaluation of the gender equality concept established for 2016-2019 has been planned for 2018, intended both to assess the implementation and effectiveness of the proposed measures, to present the development of the employment structure and to adjust the target quotas accordingly. Any adjustment will have to take into account that the objectives can only be achieved within the framework of actual job turnover, the participation of female applicants and the selection principle of optimal recruitment (at least equal qualification, competence and professional performance). A particular challenge at IPK is therefore to increase the proportion of suitable female applicants to scientific positions. The Institute has used the support of *European Structural and Investment Funds* to promote equal opportunities for women and men in science and research. These funds are available for a period of four years, to be used to establish an equal opportunities office and for the active promotion of female researchers into leading positions in science. The office started its work in October 2017.

A family-friendly environment is seen as essential to be able to offer an attractive working environment which fits the needs of as many lifestyles as possible. IPK strives to reconcile family and private life with professional activity and qualification by supporting all employees with respect to, for example, their choice of working times, scheduling and location, and by providing IT and communication facilities. This responsibility has been firmly fixed the Institute's management since 2010, and is audited regularly. In line with the international scientific environment, special employment offers have been possible to attract overseas personnel and couples who are both researchers.

Financial and budgetary issues

The financial resources available to cover the direct expenses of the Institute (disregarding income allocated to partners and sums withheld for construction) in the years 2017, 2016 and 2015 amounted to, respectively 54,602,000 Euro, 57,403,000 Euro and 55,219,000 Euro; these sums include both external funding and internally generated income. The 2017 and 2016 revenues totals combine grants amounting to, respectively, 36,360,000 Euro and 33,664,000 Euro, along with internal income brought forward from the previous year amounting to, respectively, 1,725,000 Euro and 451,000 Euro (Fig. 10).

In 2017, about 49% (2016: 47%) of total expenditure related to salaries and 33% (2016: 29%) to equipment. The higher operating costs (salaries and equipment) recorded in 2016 compared to 2015 reflect mostly salary increases resulting both from the outcome of the 2016 round of collective bar-

übertragene Selbstbewirtschaftungsmittel in Höhe von 1.725 TEUR (2016: 451 TEUR, Fig. 10).

Bei der Mittelverwendung entfielen 2017 rund 49 % (2016: 47 %) der Gesamtausgaben auf den Personal- und 33 % (2016: 29 %) auf den Sachmittelbereich. Der Anstieg in 2016 gegenüber 2015 bei den Betriebsausgaben (Personal- und Sachmittel) ist vorrangig auf die aus dem Abschluss der Tarifverhandlungen 2016 resultierenden Gehaltssteigerungen zurückzuführen sowie auf die allgemeine Teuerung im Zulieferbereich und im Dienstleistungssektor. Bei den Geräteinvestitionen waren 2017 die Aufwendungen für die Inbetriebnahme des Bioinformatikzentrums und des angrenzenden Gewächshauses nach der Übernahme von Gebäuden der *SunGene GmbH* in Höhe von 247 TEUR (2016: 208 TEUR), finanziert aus zusätzlichen Einnahmen aus FuE, enthalten. Daneben wurden 2.135 TEUR (2016: 1.442 TEUR) Selbstbewirtschaftungsmittel für Investitionen gebildet und im Folgejahr ausgegeben. Als Ausgaben werden auch die zum 31.12. des Jahres 2017 anerkannten Kassenmittel in Höhe von 560 TEUR (2016: 914 TEUR) für Geräteinvestitionen und 400 TEUR (2016: 687 TEUR) für Bauinvestitionen ausgewiesen. Die Entwicklung und die Struktur der Gesamtausgaben seit 2015 bis 2017 sind im Folgenden dargestellt (Tab. 4 und Fig. 11)

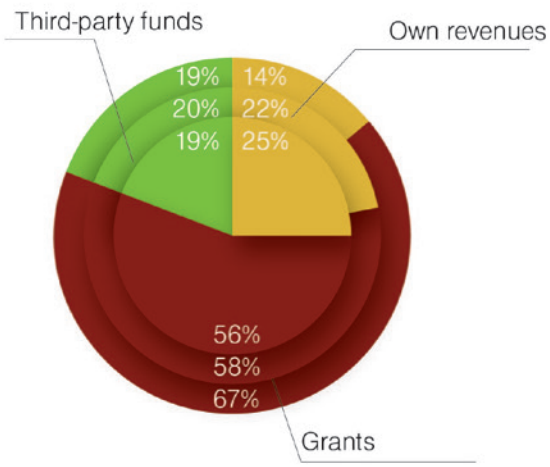


Fig. 10 Entwicklung der Gesamteinnahmen 2015–2017 (Innenkreis 2015 , Aussenkreis 2017) ▪ The composition of the Institute's revenue (2017 (outer circle), 2016 (central circle), 2015 (inner circle))

gaining and from inflation in supplier and service costs. Equipment purchases made in 2017 included a sum of 247,000 Euro (2016: 208,000 Euro) towards the commissioning of the Bioinformatics Centre and the adjacent greenhouse, following the takeover of buildings from SunGene GmbH, and was financed from additional R&D income. In addition, a sum of 2,135,000 Euro (2016: 1,442,000 Euro) of internally generated funds was set aside for investment, and released in the subsequent year. Expenditures within each year (to 31 December) also included cash and cash equivalents of 560,000 Euro (2016: 914,000 Euro) for equipment purchase and 400,000 Euro (2016: 687,000 Euro) for construction. The trends and structure of the total expenditure over the period 2015-2017 are presented in Tab. 4 and Fig. 11.

Jahr / Year	Personalausgaben / Staff costs	Sachausgaben / Materials costs	Geräteinvestitionen / Purchase of equipment	Bauinvestitionen / Investment in buildings	Gesamt / Total
2015	24.108	18.749	6.531	5.831	55.219
2016	27.073	16.397	7.053	6.880	57.403
2017	26.709	17.826	4.545	5.522	54.602

Tab. 4 Entwicklung der Gesamtausgaben in TEUR ohne Ausgaben für Partner. ▪ Total expenditure in 000 Euro (excluding funds allocated to partners).

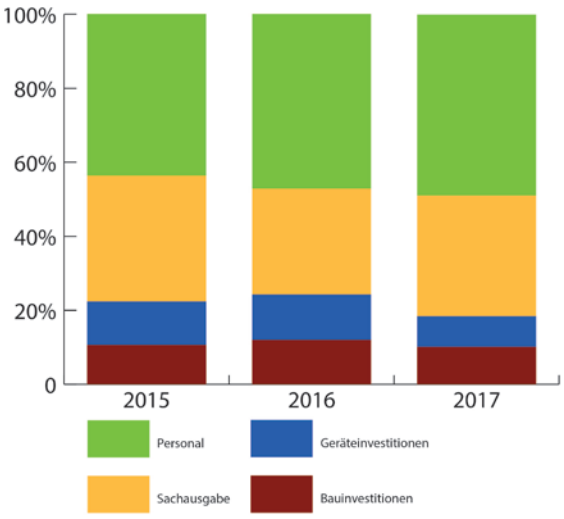


Fig. 11 Struktur der Gesamtausgaben ▪ Breakdown of the Institute's expenditure. | Legend: red=investment in buildings, blue=purchase of equipment, green=Staff costs, yellow=material costs

Drittmittel 2016/2017

In 2017 wurden aus 149 Projekten (2016: 143) leicht rückläufige Einnahmen (ohne Partner) in Höhe von insgesamt 10.574 TEUR (2016: 11.357 TEUR) erzielt. Hauptzuwendungsgeber bleiben das *Bundesministerium für Bildung und Forschung* (BMBF), die *Deutsche Forschungsgemeinschaft* (DFG) und die *Europäische Union* (EU). Die Einnahmen aus Förderlinien des BMBF resultieren überwiegend aus dem neuen Rahmenprogramm *Pflanzenbiotechnologie der Zukunft* sowie aus dem Großprojekt *Deutsches Pflanzenphänotypisierungsnetzwerk* (DPPN), in dem in Gatersleben einer von drei Knoten entstehen wird. Die Einnahmen aus DFG-Projekten sind, dem Trend der Vorjahre folgend, rückläufig.

Die Einnahmen aus Kooperationen mit Wirtschaftsunternehmen konnten 2016 dank neu eingeworbener und begonnener Projekte um ca. 7 % gesteigert werden. Der Anteil der Einnahmen aus der Wirtschaft liegt 2017 bei 18 % (im Vorjahr 27 %). Die Entwicklung der Einnahmen für Projekte über die letzten drei Jahre ist in folgender Tabelle (Tab. 5) dargestellt:

Third-party funding in 2016 and 2017

The 149 projects secured in 2017 generated an income of 10,574,000 Euro; the respective totals for 2016 were 143 projects and 11,357,000 Euro. The *Federal Ministry of Education and Research* (BMBF), *the German Research Foundation* (DFG) and the *EU* remain the Institute's major donors. Grants secured from BMBF largely lie within its new framework programme *Plant Biotechnology of the Future* and from the major project *German Plant Phenotyping Network* (DPPN), for which one of the three intended nodes will be created in Gatersleben. Income from the DFG has declined steadily in the last years. Thanks to newly secured and already started projects, income from collaborations with private sector entities increased by about 7% in 2016 over the 2015 level. The share of revenues from the economy was 18% in 2017 (27% in 2016). A breakdown of sources funding the Institute's projects over the past three years is shown in Tab. 5.

	2015	2016	2017
Bundesministerium für Bildung und Forschung / Federal Ministry of Education and Research (BMBF)	3.156	3.308	3.208
Bundesministerium für Ernährung und Landwirtschaft / Federal Ministry of Food and Agriculture (BMEL)	936	554	1.570
Bundesministerium für Wirtschaft / Federal Ministry of Economics (BMWi)	515	559	350
DFG / German Research Foundation	1.964	1.771	1.527
Land Sachsen-Anhalt / Sachsen-Anhalt state (LSA)	161	0	106
EU / European Union	845	1.312	1.193
SAW-Leibniz-Wettbewerb / SAW-Leibniz Competition	550	642	568
Sonstige Projekte / Other projects	168	161	152
Wirtschaft / Economy	2.862	3.050	1.900
Gesamt /Total	**11.157**	**11.357**	**10.574**

Tab. 5 Entwicklung der Zuwendungen (Angaben in TEUR) ▪ Grant income during 2015-2017 (in 000 Euro).

Technologietransfer

Im Berichtzeitraum wurden sieben erfindungsmäßige Technologien durch Forschende des IPK gemeldet, fünf davon wurden vom Institut in Anspruch genommen. Im gleichen Zeitraum wurden zwei Technologien vorläufig als Betriebsgeheimnis behandelt und für drei der gemeldeten Erfindungen neue Patentanmeldungen durch das Institut vorgenommen. Darüber hinaus wurden, im Sinne des Technologiescreenings, Vorrecherchen für potentielle schutzfähige und wirtschaftlich verwertbare IPK-Forschungsergebnisse (drei Technologieansätze) durchgeführt.

Im Berichtzeitraum wurde mit einem Biotech-Unternehmen ein Vertrag auf Übertragung einer zum Schutzrecht angemeldeten Gemeinschaftserfindung (mit der Hochschule Anhalt) sowie mit einem Züchtungsunternehmen ein Vertrag zur Einlizenzierung

Technology transfers

During the reporting period, IPK researchers registered seven inventions, of which five have been utilized within the Institute. Two technologies have been provisionally treated as trade secrets and patent applications have been filed for three inventions. In addition, preliminary research has been conducted focusing on the potential for the protection and commercial exploitation of three technologies. A contract has been negotiated and concluded with a biotechnology company for the transfer of a joint invention (with FH) for which an IPK patent application has been filed, and with a breeding company for the licensing of IPK results.

The income derived from licensing amounted to 104,000 Euro over the reporting period (15,000 Euro in 2017 and 89,000 Euro in 2016). In addition, a milestone payment of

von IPK-Ergebnissen verhandelt und abgeschlossen. Insgesamt wurden im Berichtszeitraum Lizenzeinnahmen in Höhe von 104 TEUR (2017: 15 TEUR, 2016: 89 TEUR) erzielt. Darüber hinaus erfolgte in 2017 für die Übertragung von Ergebnissen aus einem Kooperationsprojekt mit einem Industriepartner eine Meilensteinzahlung von 65 TEUR.

Im Berichtszeitraum wurden insgesamt 35 Kooperationsverträge (bspw. für neun Kooperationen im Rahmen des Förderprogrammes *Pflanzenzüchtungsforschung für die Bioökonomie* (*Nationale Forschungsstrategie BioÖkonomie 2030*), ein Vertrag zum Beitritt zum *Leibniz-Forschungsverbund Wirkstoffe und Biotechnologie* sowie fünf Rahmenverträge, u.a. mit dem *Agricultural Biotechnology Research Institute of Iran* (ABRII) und der *Georg-August-Universität Göttingen* (GAU), abgeschlossen. Weiterhin wurden 17 Forschungs- und Entwicklungsverträge für FuE-Vorhaben mit Wirtschaftsunternehmen mit einem Gesamtvolumen von ca. 2,3 Mio. Euro (netto), davon zwei Verlängerungsverträge und sechs Änderungsvereinbarungen für bereits laufende FuE-Vorhaben, konsolidiert und unterzeichnet.

Darüber hinaus wurden zwölf Verträge zu projektbezogenen Unteraufträgen, ein (Fördermittel-) Weiterleitungsvertrag sowie zwei Übertragungsverträge für erfindungsmäßige Technologien, zwei Lizenz- und Optionsverträge, 18 wissenschaftliche Dienstleistungsverträge (davon neun als Auftragnehmer) abgeschlossen.

65,000 Euro was paid in 2017 for transferring results from a collaborative project with an industrial partner. A total of 35 cooperation agreements were concluded, including nine under the umbrella of the *Plant Breeding Research for Bioeconomics* (*National Research Strategy Bioeconomy 2030*) funding programme and one to join the *Active Ingredients and Biotechnology* Leibniz Research Network; five framework agreements, with - among other institutions - the Agricultural Biotechnology Research Institute of Iran (ABRII) and Göttingen Georg-August University were entered into, and 17 R&D contracts with commercial enterprises, valued at about 2.3M Euro were consolidated and signed; these included two renewals and six modified agreements relating to ongoing projects. In addition, twelve project-related sub-contracts were concluded, along with one (subsidy) transfer contract and two transfer contracts for inventive technologies, two license and option contracts, and 18 scientific service contracts (in nine of which IPK acted as a contractor).

Informationen zur Infrastruktur

Infrastructure developments

Tab. 6 Baumaßnahmen 2016/2017 ▪ Construction activities during 2016/2017.

Lfd. Nr. / Lfd. No.	Maßnahme / Measure	2016 Zahlungen (TEUR) / Payments (000 Euro)	2017 Zahlungen (TEUR) Payments (000 Euro)
1	Neubau und technische Ausrüstung Pflanzenkulturhalle davon: / New building and technical equipment for the Plant Culture Hall:	3.501	1.831
1.1	aus Zuwendungen / from grants	3.004	0
1.2	aus Umwidmungen aus 2015 / from reclassification of 2015 funds	250	0
1.3	aus eigenen Einnahmen / from internal income	9	1.831
1.4	aus Drittmitteln / from external funds	238	0
2	Optimierung der energetischen Versorgung des IPK-Campus / Optimization of the energy supply for the IPK campus	83	772
3	IT-Technikzentrale / Central IT	869	192
4	Saatgutaufbereitung Geb. 1604 / Seed processing Building 1604	734	196
5	Sanierung Kleingewächshäuser Genbank / Refurbishment of small greenhouses for the Gene Bank	133	145
6	Umrüstung Phytokammer auf LED / Refurbishment of Phytochamber I	183	0
	Sanierung Phytokammernhaus I / Refurbishment of Phytochamber I	0	103
7	energetische Sanierung Teilsammlungen Nord (TEN) / Refurbishment of the energy Satellite Collections North (TEN)	20	59
8	Umbaumaßnahmen Bioinformatikzentrum (aus eigenen Einnahmen) / Rebuilding of the Bioinformatics Centre (from internal income)	446	247

Pflanzenkulturhalle: Am IPK entsteht mit der Pflanzenkulturhalle und den darin vorgesehenen Phänotypisierungsanlagen eine weltweit bisher einmalige Forschungsinfrastruktur, die gemeinsam mit bereits vorhandenen Pflanzenphänotypisierungsanlagen am IPK und weiteren Forschungsinfrastrukturen am *Forschungszentrum Jülich* (FZJ) und am *Helmholtz Zentrum München* (HMGU) im Verbund des *DPPN* gefördert werden. Die Gesamtanlage am IPK wird vollkommen neue und automatisierte Möglichkeiten bieten, sowohl ganze Pflanzen als auch Wurzelsysteme unter kontrollierten und im Tagesverlauf simulierten Licht- und Umweltbedingungen (Temperatur, CO_2, Luftfeuchtigkeit, Luftbewegung) zu beobachten und den Einfluss der Umweltbedingungen auf die genetischen Merkmalsausprägungen zu untersuchen. Die Halle wurde als bauliche und technische Grundstruktur seit 2014 mit einem Finanzvolumen von 8,25 Mio. EUR (Anteil des Bundes und des Landes: 5,8 Mio. EUR) errichtet, technisch u.a. mit aufwendiger Beleuchtungs- und Klimatechnik ausgerüstet und konnte im August 2017 durch den Ministerpräsidenten des Landes Sachsen-Anhalt und die Bundesministerin für Bildung und Forschung an die Wissenschafts-Community übergeben werden.

Optimierung der energetischen Versorgung des IPK-Campus: Bund und Land haben dem IPK im Rahmen eines Sondertatbestands 5 Mio. EUR an Finanzmitteln zur energetischen Optimierung des Campus für den Zeitraum von 2016 bis 2018 zur Verfügung gestellt. Das Vorhaben wurde planerisch in mehrere Teilprojekte zerlegt. Als erstes Teilprojekt wird eine neue Trafostation realisiert, die insbesondere die Energieversorgung der Pflanzenkulturhalle absichert. Hierfür sind Ausgaben von rund 1 Mio. EUR vorgesehen. Die Trafostation wird im Frühjahr 2018 in Betrieb gehen können. Die weiteren Teilprojekte zur Verbesserung der energetischen Versorgung und Erhöhung der Versorgungssicherheit wurden intensiv planerisch bearbeitet und das Konzept im Herbst 2017 den Gremien vorgestellt. Über die Optimierung der Versorgung mit Strom, Wärme und Kälte und die Nutzung von Einsparpotenzialen hinaus strebt die Leitung des IPK an, mittelfristig eine klimaneutrale und nachhaltige Energieversorgung des gesamten Campus sicherzustellen.

Errichtung IT-Technikzentrale: Aufgrund der Bedeutung der Bioinformatik und des IPK als weltweit zugänglichem und genutzten Archiv für pflanzengenetische und pflanzenphänotypische Daten wurde im *Konrad-Zuse-Haus* eine IT-Technikzentrale eingerichtet, um den Anforderungen an ein modernes Rechenzentrum gerecht zu werden. Hierfür wurden rund 1 Mio. EUR für Umbaumaßnahmen, technische Gebäudeausrüstung sowie für die eigentliche Ausstattung der Technikzentrale aufgewendet.

Saatgutaufbereitung: Insbesondere für die Abteilung *Züchtungsforschung*, aber auch für andere Nutzerinnen und Nutzer aus dem IPK wurde eine Saatgutaufbereitung im Betriebshof

Plant Cultivation Hall: The IPK Plant Cultivation Hall and its associated phenotyping facilities have given the Institute a globally unique research infrastructure, which, in conjunction with the existing plant phenotyping facilities at IPK and other facilities at the *Jülich Research Centre* (FZJ) and the *Munich Helmholtz Centre* (HMGU), are being funded by the *DPPN*. The unit at IPK represents a novel and automated platform for observing whole plants, as well as root systems, growing in an environment where the lighting regime, the temperature, the CO_2 concentration, the relative humidity and the movement of air can all be controlled, so that the influence of environmental factors on the phenotype can be observed. Initiated in 2014, the Hall has been established at a cost of 8.25M Euro, of which the Federal and State governmental share has been 5.8M Euro. The facility is equipped with sophisticated lighting and air-conditioning technology, and was handed over to the scientific community in August 2017 by the Prime Minister of Saxony-Anhalt and the Federal Minister of Education and Research.

Optimization of the energy supply to the IPK campus: The federal and state governments have provided IPK with 5M Euro in one-off funding to improve the energy supply infrastructure of the campus over the period 2016-2018. The project has been divided into several sub-projects. The first of these is tasked to construct a new transformer station, intended to secure the energy supply to the Plant Culture Hall, for which a spendings of around 1M Euro are foreseen. The transformer station will become operational in spring 2018. The other sub-projects, designed to improve the energy supply and enhance supply security, have been in a phase of intensive planning and concepts were presented to the committees in autumn 2017. In addition to optimizing the supply of electricity, heating and cooling and to exploit potential savings, IPK management aims in the medium term to establish a climate-neutral and sustainable energy supply for the entire campus.

Establishment of an IT technology centre: Due to the importance of bioinformatics to enable IPK to act as a globally accessible and well utilized archive for plant genetic and plant phenotypic data, an IT technology centre has been set up at the *Konrad Zuse House*. Around 1M Euro has been spent in order to meet the requirements of a modern computer centre; the funds were used for conversion measures of the building and the purchase of equipment.

Seed processing unit: A seed processing unit has been set up by converting an existing building, and has been made operational. The purpose of the unit is to aid the activities of the *Breeding Research* Department, as well as those of other users of IPK. The costs for this construction, inclu-

durch Umbau und Umnutzung eines Bestandsgebäudes eingerichtet und in Betrieb genommen. Die Kosten für diese Baumaßnahme einschließlich Geräteausstattung betrugen im Berichtszeitraum 930 TEUR.

Phytokammernhaus I: In der Kammer 18 des Phytokammernhauses I des IPK wurde Ende 2015 begonnen, die bislang installierte Beleuchtungstechnik mit Leuchtstoffröhren auf LED-Technik umzurüsten. Der Umbau soll durch eine spektral deutlich flexiblere und energetisch optimierte Beleuchtungsanlage sowohl wissenschaftlich als auch wirtschaftlich Vorteile bringen. Die Kosten hierfür betrugen 183 TEUR.

Energetische Sanierung TEN: Für die Außenstellen wurden seitens des Sitzlandes Mecklenburg-Vorpommern in 2016 für Malchow 60 TEUR und in 2017 für Groß Lüsewitz 80 TEUR für energetische Maßnahmen als Sondertatbestand bereitgestellt. In Malchow wurden die geplanten Mittel vollständig für den Umbau der Heizung auf Erdgas sowie für die Sanierung des Bürogebäudes mit dem Ziel der Energieoptimierung verwendet. 2017 wurden Maßnahmen zur Optimierung der Kühlkapazität in Groß Lüsewitz weiterverfolgt.

Umbau Bioinformatikzentrum: Am 30. Juni 2014 erfolgte der Besitzübergang des *SunGene-Gebäudes* (neu *Bioinformatikzentrum*) an das IPK. Sowohl Erwerb als auch Umbau wurde ausschließlich aus eigenen Mitteln des Instituts finanziert (zusätzliche Einnahmen aus FuE). Mit erheblichem finanziellen Aufwand (693 TEUR im Berichtszeitraum) und persönlichem Engagement aller Beteiligten konnten die Bioinformatik-Gruppen, die Ags *Pathogenstress-Genomik* (PSG), *Assimilatallokation und NMR* (AAN) sowie, mit einem Funktionsraum Rasterelektronenmikroskopie, die Ag *Strukturelle Zellbiologie* (SZB) schrittweise ab Ende 2016 bis Juni 2017 das Gebäude beziehen.

Planung Besucherzentrum und Besucherlabor: Bereits heute besuchen mehr als 8.000 Menschen jährlich das, in unmittelbarer Nachbarschaft zum IPK angesiedelte, *Grüne Labor* sowie das IPK selbst. Die Vermittlung von Pflanzenforschung, genetischen Grundlagen und Basiswissen zur Pflanzenzüchtung ist mit den derzeitigen Formaten und Möglichkeiten des Instituts nur in sehr eingeschränktem Umfang möglich. Das IPK hat daher 2016 ein erstes Grobkonzept für ein auf dem Campus angesiedeltes Besucherzentrum, einschließlich Schaugarten und Schülerlabor, entwickelt. Dort sollen die Domestikation von Pflanzen, züchterische Methoden und MINT-relevante Inhalte pflanzenforschungsbezogen präsentiert und vermittelt werden.

Inzwischen wurden Anregungen und Ideen nach intensiven Kontakten u.a. zum *Museum für Vorgeschichte* in Halle, zum *Museum für Naturkunde* Berlin, zu *Wissenschaftsscheune* und *Max-Planck-Institut für Pflanzenzüchtungsforschung* (MPIPZ)

ding the purchase of equipment, amounted to 930,000 Euro during the reporting period.

Phytochamberhouse I: Conversion works began at the end of 2015 to replace the fluorescent lights in chamber 18 to LED bulbs. The conversion is expected to deliver both scientific and economic benefits, since LED lighting is significantly more flexible in spectral terms and is more energy efficient. The costs of the conversion were 183,000 Euro.

Energy infrastructure: The government of Mecklenburg-Western Pomerania state granted a sum of 60,000 Euro In 2016 to Malchow and 80,000 Euro in 2017 to Groß Lüsewitz in order to address the energy infrastructure at these two sites. In Malchow, the funds were dedicated to converting the heating system to natural gas and to renovate the office building with a view to reducing energy consumption. In 2017, measures were initiated to improve refrigeration at the Groß Lüsewitz site.

Reconstruction of the Bioinformatics Centre: On 30 June 2014, ownership of the *SunGene GmbH* building (now the *Bioinformatics Centre*) was transferred to IPK. Both its acquisition and conversion were financed from the Institute's own funds, derived from R&D income. The bioinformatics staff, along with the *Pathogen Stress Genomics* (PSG), and *Assimilate Allocation and NMR* (AAN) RGs occupied the building over the period Dec 2016-June 2017, and the *Structural Cell Biology* (SZB) RG has established a scanning electron microscopy room. The cost of this exercise has been considerable (693,000 Euro during the review period). All of the parties involved were fully committed to the process.

Planning of a visitor centre and a laboratory: Every year, over 8,000 people visit the Green Laboratory. The Institute's physical capacity to teach plant research, genetic principles and the basics of plant breeding practice is rather restrictive. So, in 2016, a preliminary concept for an on campus visitor centre was initiated; this is proposed to include both a demonstration garden and a visitor laboratory. The intention is to both present and teach the principles of crop domestication, plant breeding and STEM topics of relevance to modern plant research. In the meantime, intensive discussions with staff from, among others, the Halle *Prehistory Museum*, the *Berlin Natural History Museum*, the *Science Barn*, the Cologne-based *Max Planck Institute for Plant Breeding Research* and the *Leibniz Institute for Science and Mathematics Education* (IPN) have been used to refine the concept. An evaluation of the concept during 2018 is expected to firm up the establishment of the IPK Visitor Centre.

in Köln sowie zum *IPN* (Leibniz-Institut für die Pädagogik der Naturwissenschaften und Mathematik) aufgenommen und das Konzept stark verfeinert und präzisiert. Wesentliche Weichenstellungen für das Besucherzentrum werden aus der Beurteilung des Konzepts im Evaluierungsjahr 2018 erwartet.

Versuchsfeld und Gärtnerei

Im Zentrum der Arbeiten der Ag *Versuchsfeld und Gärtnerei* stehen die Unterstützung des Reproduktionsanbaus der Genbank sowie die gärtnerische und feldwirtschaftliche Betreuung von wissenschaftlichen Versuchen im Freiland, in Gewächshäusern und Phytokammern. Durch die Hinzunahme von gepachteten Flächen, dem ehemaligen SunGene-Gewächshaus sowie Phytokammern im Bioinformatikzentrum stehen nun ca. 65 ha an Freiflächen, etwa 7.100 m^2 Gewächshausflächen sowie rund 220 m^2 in Phytokammern zur Verfügung.

Eine zentrale Rolle kommt der Optimierung der Nutzung der Flächen und Kapazitäten durch eine koordinierte Versuchsplanung zu, die durch die Arbeitsgruppe über Bedarfsabfragen und Koordination in entsprechenden Arbeitskreisen sichergestellt wird. Auch die Nutzung von GPS-gesteuerter Feldversuchstechnik und entsprechender Planungssoftware trägt zur Optimierung des Versuchsanbaus bei. Das IPK hat 2017 begonnen, wie bereits bei Züchtungsunternehmen verbreitet, eine Drohnen- und GPS-gestützte Versuchsüberwachung und Bonitierung zu etablieren.

In Bezug auf die seit längerem verfolgte Versuchsfeldfächenerweiterung um 12 ha westlich des heutigen Institutsgeländes zeichnet sich eine sehr ermutigende Entwicklung ab. Das Land Sachsen-Anhalt hat Neuerungen in das Haushaltsgesetz für 2017 und 2018 eingebracht, die eine unentgeltliche Überlassung von gemeinsam mit dem Bund geförderten Einrichtungen mit Grund und Boden zur Erfüllung ihrer Aufgaben vorsehen. Zu den gemeinsam geförderten Einrichtungen zählen auch die Institute der *Leibniz-Gemeinschaft*. Das IPK wird alles tun, damit das *Ministerium für Wirtschaft, Wissenschaft und Digitalisierung* die hierfür notwendigen administrativen und rechtlichen Verfahren einleiten und durchführen kann.

Informationstechnologie

Anzahl und Funktionsumfang der wissenschaftlichen Fachanwendungen nehmen stetig zu. Praktisch alle wissenschaftlichen Geräte werden inzwischen über einen Steuerungs-PC bedient und sind zum Datenaustausch vernetzt. Inzwischen sind über 1.500 Geräte im Netzwerk registriert und über 800 davon dauerhaft online. Die permanente Aktualisierung aller Betriebssysteme und der Schutz vor Schadsoftware und Attacken aus dem Internet sind eine ständige Herausforderung für den IT-Service.

Experimental field and nursery

Regenerating the Gene Bank's collection and managing plants used in field-based, greenhouse-based and controlled environment chamber-based experiments is central to the Institute's research activities. The acquisition of leasehold land, the former SunGene GmbH greenhouse and phytochambers means that approximately 65 hectares of land, 7,100 m^2 of greenhouse space and 220 m^2 phytochamber space has been added to the Institute's portfolio. The experimental field and nursery staff work to ensure the optimization of the usage of these areas by their involvement in the design of experiments proposed by the scientists.

The use of GPS-guided agricultural equipment and the necessary software makes a further contribution to the optimization of plant trials. As is increasingly becoming common practice in the plant breeding sector, IPK began in 2017 to experiment with drone and GPS technology to monitor trials and harvest operations. A particularly encouraging development has been the 12 hectare expansion of the Institute's experimental field area on the western side of the present IPK site, the acquisition of which has been pursued for some time. The Saxony-Anhalt government has introduced amendments to its 2017 and 2018 budget which provide institutions jointly funded by the Federal government to fulfil their tasks to benefit from the provision of land free of charge; institutes which are members of the *Leibniz Association* qualify under these provisions. IPK will do its utmost to enable the *Ministry of Economy, Science and Digitization* to initiate and implement the required administrative and legal procedures.

IT infrastructure

The number and range of scientific applications are growing. Virtually all scientific equipment is now controlled by computers, and most are linked into an IT network to allow for data exchange. Over 1,500 devices are currently registered on the IPK network, of which at least 800 are permanently online. Updating operating systems and protecting the network from malware and cyberattacks are a constant challenge for the IT service.

With the renewal of the network switch technology in 2016, all buildings on the campus are now networked at 2 x 10 Gbps to provide a redundant and high performance environment. The expansion of the wifi network is ongoing. Over 89 access points on the campus allow network access with a mobile device. In order to provide both employees and national and international guests from educational or research institutions with straightforward network access, three service zones (SSIDs) have been provided in the WLAN, each providing a separate security zone, one for for IPK emplo-

Durch die Erneuerung der Netzwerk-Switchtechnik im Jahr 2016 sind nun alle Gebäude auf dem Campus mit 2 x 10 GBit/s redundant und performant vernetzt. Der Ausbau des drahtlosen Netzwerks wird kontinuierlich betrieben. Über 89 Access-Points auf dem IPK-Campus sind Netzwerkzugriffe mit mobilen Geräten möglich. Um sowohl den Beschäftigten als auch nationalen wie internationalen Gästen aus dem Bildungs- und Forschungsumfeld einen unkomplizierten Netzwerk-Zugang zu verschaffen, werden im WLAN drei Servicezonen (SSIDs) bereitgestellt, die für IPK-Beschäftigte, Mitglieder im *eduroam*-Verbund und Gäste jeweils getrennte Sicherheitszonen zur Verfügung stellen.

Das *Hierarchical-Storage-Management-System* (HSM) als zentraler Datenspeicher für Massendaten wurde auf eine neue Servergeneration aktualisiert. Es speichert Daten parallel auf drei verschiedene nachgelagerte Speichermedien, darunter Magnetbänder, so dass keine weitere Archivierung notwendig ist. Durch die zuvor erfolgte Anschaffung eines leistungsfähigen Bandroboters im Jahr 2016 ist nun eine Skalierung bis in den Petabyte Bereich möglich. Über HSM sind momentan rund 250 Terabyte an Daten im Online-Zugriff.

Im Berichtszeitraum wurde die neue IT-Technikzentrale in Betrieb genommen. Die zentralen IT-Komponenten sind nun in einer nach aktuellen Standards konzipierten Betriebsumgebung untergebracht, die die Verfügbarkeit und Betriebssicherheit weiter erhöht.

Wissenschaftliche Bibliothek und Informationsdienste

Die *Wissenschaftliche Bibliothek* des IPK verfügt über einen Bestand über 82.000 Medieneinheiten zu den Forschungsschwerpunkten des Instituts. Die Hauptaufgabe der Bibliothek ist die Literaturversorgung der am IPK Forschenden. Als öffentliche Einrichtung steht sie mit ihrem Serviceangebot auch externen Nutzern zur Verfügung. Insgesamt nutzen die Bibliothek seit Jahren stabil rund 900 Personen.

Auf Anregung der *Hochschulrektorenkonferenz* (HRK) hat die *Allianz der deutschen Wissenschaftsorganisationen*, zu der auch die Leibniz-Gemeinschaft gehört, das Projekt *DEAL* – bundesweite Lizenzierung von Angeboten großer Wissenschaftsverlage – ins Leben gerufen. Das IPK hat sich dieser Initiative angeschlossen.

Die Verhandlungen der HRK mit den großen naturwissenschaftlich orientierten Verlagen wie *Elsevier Springer/Nature* und *Wiley* sind derzeit noch nicht beendet. Für das IPK ist dennoch die Versorgung mit aktueller Forschungsliteratur durch Interim-Regelungen bzw. Vertragsverlängerungen gewährleistet.

yees, one for members of the *eduroam* network and one for guests.

The *Hierarchical Storage Management System* (HSM) used as the central storage facility for massive data sets has been updated to a new generation server, which stores the data in parallel in three different media (including magnetic tape), so that no further archiving is necessary. With the purchase of a powerful tape robot in 2016, scaling up to the petabyte range has become now possible. Currently 250 terabytes of data are accessible online via HSM.

The new IT technology centre was put into service during the reporting period. The central IT components are now housed in an operating environment designed according to current industry standards, which further increases availability and operational reliability.

IPK library and information services

The IPK's *research library* has a collection of more than 82,000 items relating to the Institute's major research foci. The main task of the library is to provide IPK researchers with ready access to the scientific literature, but as a public institution, a range of services is available to external users. For many years a stable basis of around 900 individual users is registered in the library.

At the suggestion of the German Rectors' Conference (HRK), the *Alliance of German Science Organizations*, to which the Leibniz Association also belongs, launched the *DEAL* project - a nationwide licensing of materials published by the major science publishers. The IPK has joined this initiative. The HRK's negotiations with leading scientific publishers such as *Elsevier Springer/Nature* and *Wiley* are not yet over. For IPK, however, the supply of current research literature is guaranteed by interim regulations or by contract extensions.

The library holdings of IPK are electronically registered in the *Common Library Network* (GBV) and in the information portals *ViFaBio* and *LIVIVO*, thereby making them available at the national level.

The IPK supports the Leibniz Association's Open Science initiative. With regard to publications, an open access (OA) publication strategy has been adopted and a publication fund set up to support the OA publication of the Institute's scientific work. In 2017, 54 articles were published in fully OA journals and 31 in hybrid journals; the corresponding figures for 2016 were 45 and 17.

Since December 2016, IPK has become a member of the *Open Researcher and Contributer ID* (ORCID)-Germany

Der Bibliotheksbestand des IPK ist im *Gemeinsamen Bibliotheksverbund* (GBV) sowie in den Informationsportalen *ViFaBio* und *LIVIVO* elektronisch erfasst und steht damit auf nationaler Ebene zur Verfügung.

Das IPK unterstützt die Open-Science-Inititativen der Leibniz-Gemeinschaft. In Bezug auf Publikationen wurde eine Open-Access-Publikationsstrategie verabschiedet und zur Unterstützung unmittelbarer Open-Access-Veröffentlichung wissenschaftlicher Arbeiten ein Publikationsfonds eingerichtet. 2017 wurden 54 (Vorjahr: 45) Artikel in genuinen und 31 Publikationen (Vorjahr: 17) in hybriden Journalen veröffentlicht.

Seit Dezember 2016 ist das IPK Teil des durch die *Technische Informationsbibliothek* (TIB) Hannover geführten *ORCID-Deutschland-Konsortiums*. Die *Open Researcher and Contributer ID* (ORCID) sichert einen einheitlichen, allgemeinen und offenen Standard der Autorenidentifikation. Durch aktive institutsinterne Informations- und Unterstützungsangebote gehört die *ORCID* inzwischen faktisch zur Visitenkarte der am IPK Forschenden. Über 85 Prozent der wissenschaftlich Aktiven am IPK sind bei www.orcid.org registriert.

consortium led by the *German National Library of Science and Technology* (TIB) in Hannover. *ORCID* ensures an uniform, general and open standard of author identification. Through the active internal information and support services offered within the Institute, *ORCID* has become the business card for IPK researchers: over 85% of the active scientists at IPK are registered at www.orcid.org.

Abteilung Genbank ▪ Department of Genebank

Leiter ▪ Head
Prof. Dr. Andreas Graner

Allgemeine Forschungsziele

Pflanzengenetische Ressourcen stellen eine wichtige Grundlage für die Erforschung der Evolution und Merkmalsausprägungen von Kulturpflanzen sowie ihre züchterische Nutzbarmachung dar. Die kontinuierliche Verbesserung des Erhaltungsmanagements der *Bundeszentralen ex situ-Genbank* sowie der Ausbau und die Vernetzung der digitalen Informationsangebote befördern die Weiterentwicklung der Genbank in ein biologisch-digitales Ressourcenzentrum. Wichtige Beiträge hierzu werden in den beiden institutsweiten Forschungsschwerpunkten *Erschließungskonzepte für pflanzengenetische Ressourcen* sowie *Genomdiversität und Evolution* erarbeitet.

Stand der Forschungsarbeiten und wichtige Ergebnisse

Die *ex situ-Genbank* ist das zentrale Strukturelement der Abteilung, welche in drei Forschungsbereiche gegliedert ist. Über die Einbindung in das *Nationale Fachprogramm für pflanzengenetische Ressourcen* werden wichtige Beiträge zur Umsetzung der *Nationalen Strategie zur biologischen Vielfalt* geliefert. Die Vernetzung auf europäischer Ebene wurde mit dem Betrieb und der Weiterentwicklung des *Europäischen Suchportals für pflanzengenetische Ressourcen* (EURISCO) gefestigt. Mit der Etablierung einer neuen Arbeitsgruppe zur *Genomik Genetischer Ressourcen* (GGR), in deren Zuständigkeit auch die Leitung der institutsweiten DNA Sequenzierungsplattform fällt, wurden die Voraussetzungen zur systematischen Genotypisierung von Genbankollektionen weiter verbessert. Die Standorte Malchow und Groß Lüsewitz konnten durch die Schaffung einer weiteren Wissenschaftlerstelle gestärkt werden. Insgesamt lieferten die Forschungsarbeiten im Berichtszeitraum eine Reihe wichtiger Beiträge und Erkenntnisse für die Charakterisierung der Sammlungen, die Verbesserung des Sammlungsmanagements und die Erforschung und Nutzbarmachung der genetischen Vielfalt.

Sammlungsmanagement

Der Bestand der *Bundeszentralen ex situ-Genbank* umfasst 150.751 Akzessionen aus 2.933 Arten und 776 Gattungen. Der Erhalt der Sammlung erfolgt in Gatersleben und den beiden

General Research Goals

Plant genetic resources form an important basis for studying the evolution and characteristics of crop plants, at the same time providing a resource for crop improvement. Ongoing improvements in conservation management at the *Federal ex situ Genebank*, along with the expansion and networking of digitized data promises to develop the *Genebank* into becoming a virtual biological resource centre. Important contributions are being made in the two institute-wide research foci *Concepts for the Valorization of Plant Genetic Resources* and *Genome Diversity and Evolution*.

Research Statement and Major Achievements

The *ex situ Gene Bank* is the core of the Department, which is organized into three research areas. Through its integration within the *National Programme for Plant Genetic Resources*, important contributions are being made to the implementation of the *National Biodiversity Strategy*. Networking at the European level has been strengthened by the operation and further development of the *European Search Catalogue for Plant Genetic Resources* (EURISCO). The prerequisites for undertaking systematic genotyping of the Genebank's collection have been put in place by establishing a new working group focussing on *Genomics of Genetic Resources*, which is simultaneously tasked with the management of the institute-wide DNA sequencing facility. Research carried out at the Malchow and Gross Lüsewitz sites will be supported by the creation of a new scientific post. Overall, the research pursued during the reporting period has provided a number of important contributions and insights relevant to the characterization of the collection, to improvements in the management of the collection and to the uncovering and exploitation of genetic diversity.

Collection Management

Currently the *Federal ex situ Gene Bank* curates 150,751 accessions, covering 2,933 species and 776 genera. The main collection is housed at Gatersleben, with outlying locations at Malchow (curating the oilseed and fodder species collec-

Außenstandorten Malchow (Öl- und Futterpflanzen) und Groß Lüsewitz (Kartoffelsortiment). Zur Vermehrung bzw. Charakterisierung wurden im Berichtszeitraum über 21.500 Akzessionen im Feld bzw. Gewächshaus angebaut sowie, zur Kontrolle der Saatgutqualität, 33.800 Keimprüfungen durchgeführt.

Neben den Lebendsammlungen verfügt die Genbank über ein Herbarium mit über 436.000 Belegen, 107.000 Referenzmustern von Samen und Früchten sowie 55.000 Getreideähren. In den vergangenen zwei Jahren wurden 78.911 Muster abgegeben. Damit hat die Genbank seit 1948 insgesamt 1.076.179 Muster an Nutzer im In- und Ausland bereitgestellt (Fig. 12). Eine Zusammenstellung der Sortimentsbestände und der Abgaben ist Tab. 7 und Fig. 12 zu entnehmen. Mit der Einführung einer Nutzergebühr im Jahr 2016 ging der Umfang der Bestellungen und Materialabgaben zurück. Hierdurch konnten notwendige zusätzliche Kapazitäten für die Erhaltungsarbeiten und den Vermehrungsanbau bereitgestellt werden.

Das IPK beherbergt eine der weltweit größten Kryosammlungen zur Sicherung vegetativ zu erhaltender Genbankmuster. Die Kollektion umfasst 1.538 Kartoffelakzessionen sowie 148 Minze und 142 Knoblauchmuster. Die Sicherheitssammlung im Saatgutlager des *Global Diversity Trust* auf Spitzbergen wurde weiter aufgestockt und umfasst jetzt 48.655 Akzessionen.

Forschung

Die Forschungsarbeiten im Bereich *Sammlungsmanagement und Evaluierung* zielen auf die weitere Verbesserung des Erhaltungsmanagements ab. Dies schließt die Optimierung interner Arbeitsabläufe sowie den Erhalt und die Weiterentwicklung der Sammlung ein.

Im Hinblick auf vegetativ vermehrte Arten wurde vorrangig an der Entwicklung bzw. Optimierung von Protokollen zur Kryokonservierung von Kartoffel, *Allium* und *Menta* gearbeitet. Mit Hilfe von Transkriptomanalysen und biochemischen Ansätzen wurde begonnen, die Funktion ausgewählter Transkriptionsfaktoren während des Einfriervorgangs zu erforschen (Ag *CSB*). Der für samenbürtige Arten erforderliche Erhaltungsaufwand wird in hohem Maße von der maximalen Einlagerungsdauer des Saatguts bestimmt. In diesem Zusammenhang konnten im Rahmen genetischer Analysen bei Weizen eine Reihe von QTLs für Samendormanz identifiziert werden. Darüber hinaus konnte gezeigt werden, dass dem Lipidstoffwechsel eine entscheidende Rolle bei der Langlebigkeit von Weizensamen zukommt (Ag *RGR*).

Zur weiteren Verbesserung des Sammlungsmanagements wurde mit dem systematischen DNA- Fingerprinting umfangreicher Genbankkollektionen (Gerste, *Phaseolus*, Kartoffel) begonnen, um Duplikate zu identifizieren (Ags *GED*, *GGR*, *TEN*). In diesem

tion) and at Gross Lüsewitz (the potato collection). Over the reporting period, the multiplication and characterization activities involved growing out 21,500 accessions either in the field or under glass, while 33,800 accessions were monitored for seed viability using a germination test.

In addition to the living collection, the Genebank also curates a herbarium comprising over 436,000 sheets, 107,000 reference seed and fruit samples and 55,000 cereal ears. Over the past two years, 78,911 samples have been provided to users, so since 1948, the Genebank has dispatched 1,076,189 samples to users based both in Germany and overseas (Fig. 12). A summary of the status of the collection and the distribution of the recipients of samples is given in Tab. 7 and Fig. 12. The introduction of a handling charge in 2016 has decreased the volume of orders and the number of samples dispatched. This has freed capacity to be redeployed into conservation and multiplication activities.

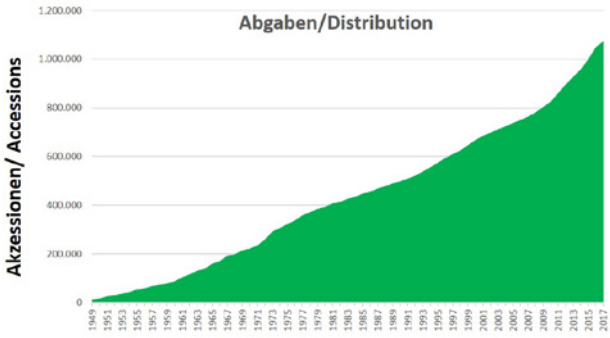
The IPK houses one of the world's largest collections of cryo-preserved vegetatively reproduced gene bank accessions. The collection includes 1,538 potato entries, along with 148 of mint and 142 of garlic. The back-up collection housed in the *Global Diversity Trust's Svalbard Global Seed Vault* on Spitzbergen Island has been expanded to 48,655 accessions.

Research

The research activity focussing on *Management and Evaluation* is tasked with making improvements to germplasm maintenance procedures. As well as focussing on the conservation and development of the collection, this activity also includes optimizing internal operations. With regard to vegetatively propagated species, priority has been given to developing and perfecting protocols needed for the cryo-conservation of potato, *Allium* and *Menta*. Transcriptomic and biochemical characterization approaches have been applied to investigate the role of certain transcription factors activated during the freezing process (RG *CSB*). Interventions required for species which set seed are largely determined by the maximum length of storage beyond which seed viability is lost. In this context, genetic analysis has been used to identify a number of QTLs underlying variation in grain dormancy in wheat. In addition, it has been demonstrated that the grains' lipid metabolism is a very important determinant of their longevity (RG *RGR*).

A systematic programme of DNA fingerprinting has been initiated, targeting the collections of barley, *Phaseolus* and potato, with a focus on identifying duplicated accessions (RGs *GED*, *GGR*, *TEN*). This activity has been accompanied by the development of homozygous inbred lines, since these mate-

Fig. 12 Kumulierte Abgaben von Genbankakzessionen seit 1949. ▪ Cumulative distribution of accessions since 1949.



Zusammenhang erfolgte auch die Entwicklung von homozygoten Inzuchtlinien. Im Gegensatz zu herkömmlichen Akzessionen, die häufig ein Gemisch verschiedener Genotypen darstellen, ermöglichen Inzuchtlinien eine eindeutige Zuordnung von genotypischen und phänotypischen Informationen. Die so entwickelten *Präzisionssammlungen* stellen eine wichtige Erweiterung der Genbanksammlungen dar und sind eine wertvolle Ressource für zukünftige Forschungsarbeiten.

Im Forschungsbereich *Taxonomie und Evolution* konzentrieren sich die Arbeiten auf phylogenetische Klassifizierung und die Untersuchung von Artbildungsprozessen innerhalb ausgewählter Pflanzengattungen. Von besonderer Bedeutung ist die Aufklärung zwischen- und innerartlicher Anpassungsmechanismen im Hinblick auf ökologische Umgebungsvariablen.

Die Tribus *Triticeae* ist durch eine große evolutionäre Vielfalt bezüglich der Genomgröße (diploide, tetraploide, hexaploide Arten) gekennzeichnet. Hierbei konnten neue Erkenntnisse über die Entstehung polyploider Arten gewonnen, und bestehende, phylogenetische Inkonsistenzen aufgelöst werden. Im Hinblick auf die Aufklärung rezenter Artbildungsprozesse in der Gattung *Hordeum* wurde gezeigt, dass die phylogenetischen Beziehungen zwischen *H. capense* und *H. secalinum* erheblich komplexer sind als bisher angenommen und eine Revision der bisherigen Taxonomie erforderlich ist. Ähnliche Ergebnisse lieferten die Arbeiten zur molekularen Phylogenie der Gattung *Crocus*.

Der Forschungsbereich *Charakterisierung und Dokumentation* befasst sich mit der Untersuchung von Genbankmaterial auf DNA-Ebene und mit der Entwicklung und Pflege von Genbankinformationssystemen. Die experimentellen Arbeiten konzentrieren sich auf die Kartierung qualitativer und quantitativer Merkmale sowie die Klonierung agronomisch relevanter Gene bei Gerste, Weizen und Roggen.

Bei der Erstellung der genomischen Referenzsequenzen bei Gerste und Weizen (Emmer, Hart- und Brotweizen) wurden maßgebliche Fortschritte in der Assemblierung proximaler Chromosomenbereiche erzielt, die durch supprimierte Rekombination gekennzeichnet sind (Ag *GGR*). Die Arbeiten zur systematischen, sequenzbasierten Genotypisierung der gesamten Gerstenkollektion am IPK wurden fortgeführt. Neben der *Genbank* (Ags *GGR*, *GED*, *RGR*, *DOK*) sind an diesem zentralen Projekt auch Gruppen aus der Abteilung *Züchtungsforschung* (Ag *QG*, *BIT*) sowie eine unabhängige Ag (*DG*) beteiligt.

rials, unlike conventional gene bank accessions which frequently comprise a mixture of different genotypes, facilitate the acquisition of unambiguous genotypic and phenotypic data. These so-called “precision collections” are regarded as an important extension of the Genebank’s collection and will increasingly represent a valuable resource for research.

In the area of *Taxonomy and Evolution*, the research activity is focussed on phylogenetic classification and the investigation of speciation within selected plant genera. Of particular importance is the elucidation of the mechanistic basis of inter- and intra-specific adaptation to environmental variation.

The *Triticeae* tribe is characterized by extensive evolutionary diversity with respect to genome size (it comprises diploid, tetraploid and hexaploid species). Some new information pertinent to the formation of polyploid species has been obtained, and some existing phylogenetic inconsistencies have been resolved. With regard to investigations of recent speciation in the genus *Hordeum*, it has been shown that the phylogenetic relationship between *H. capense* and *H. secalinum* is considerably more complex than has been previously assumed, making a taxonomic revision necessary. Similar results have arisen from the application of molecular phylogeny in the genus *Crocus*.

The *Characterization and Documentation* research area is concerned with the description of Genebank materials at the DNA level, along with the development and maintenance of the Genebank’s IT system. Experimental work is focussed on the genetic mapping of qualitative and quantitative traits in barley, wheat and rye, and the isolation of genes which encode agronomically important traits.

Further to the acquisition of whole genome reference sequences for barley and wheat (emmer, durum and bread wheat), significant advances have been made in assembling proximal chromosomal regions, which are characterized by a suppression in the rate of genetic recombination (RG *GGR*). The systematic, sequence-based genotyping of the entire IPK barley collection is ongoing. In addition to the Genebank’s contribution (RGs *GGR*, *GED*, *RGR*, *DOK*), groups belonging to the Department of *Breeding Research* (RGs *QG*, *BIT*) and the independent *DG* group are also involved in this core project.

Tab. 7 Übersicht zum Bestand und den Abgaben der Genbank nach Fruchtarten ▪ Overview of collection and transfers from the Gene Bank by crop species

Sortimente / Assortments	Bestand/ Accessions	Abgaben / Distribution 2016	2017
Getreide und Gräser / Cereals and Grasses	**65,897**	**20,115**	**14,429**
Weizen / wheat	28,206	4,122	2,785
Gerste / barley	23,607	13,402	10,160
Hafer / oat	4,849	826	134
Roggen / rye	2,410	395	210
Triticale / Triticale	1,593	9	16
Mais / maize	1,537	902	706
Aegilops / Aegilops	1,526	165	160
Hirsen / millets	845	156	55
Sonstige Gräser / other grasses	1,324	138	203
Leguminosen / Legumes	**27,819**	**4,692**	**3,509**
Phaseolus / Phaseolus	8,979	942	2,004
Erbsen / pea	5,312	634	206
Ackerbohnen / field beans	3,096	267	117
Lupinen / lupines	2,768	416	366
Wicken / vetches	1,845	426	85
Kleearten / clover species	1,929	540	285
Sojabohnen / soybeans	1,493	351	134
Bohnen-Sonderkulturen / other beans	618	225	34
Lathyrus / vetchling	516	217	80
Kichererbsen / chickpea	527	206	41
Linsen / lentils	460	409	44
Sonstige / others	276	59	113
Cucurbitaceae	**2,658**	**1,429**	**323**
Kürbisse / pumpkins	1,067	627	100
Melonen / melons	725	202	134
Gurken / cucumbers	713	502	63
Sonstige / others	153	98	26
Gemüse (+Rüben) / Vegetables	**18,394**	**10,108**	**4,895**
Tomaten / tomatoes	3,725	1,985	734
Allium	2,761	432	136
Beta / Beta beets	2,293	592	247
Brassica / Brassica	2,185	1,328	838
Paprika / pepper	1,535	978	367
Salat / lettuce	1,136	390	77
Quinoa / Quinoa	953	1,458	1,271
Raphanus / Raphanus	753	346	442
Zichorie / chicory	682	249	42
Möhren / carrots	493	301	68
Sellerie / celery	255	283	29
Spinat / spinach	214	312	18
Sonstige / others	1,409	1,454	626

Sortimente / Assortments	Bestand/ Accessions	Abgaben / Distribution 2016	2017
Öl-, Faser-, Farbpflanzen / Oil, Fibre, Dye Plants	**5,478**	**2,637**	**1,484**
Lein / flax	2,321	441	537
Sonnenblumen / sunflower	682	252	206
Ölpflanzen / oil plants	552	690	67
Farbpflanzen / dye plants	460	596	333
Faserpflanzen / fibre plants	190	392	300
Sonstige / others	1,273	266	41
Arznei-, Gewürzpflanzen / Medicinal, Spice Plants	**5,478**	**2,637**	**1,484**
Mohn / poppy	2,321	441	537
Tabak / tobacco	682	252	206
Sonstige / others	552	690	67
Mutanten / Mutants	**1,706**	**198**	**70**
Soja / soybean	530	13	1
Tomaten / tomato	744	185	61
Antirrhinum	432	0	8
Kartoffeln / Potatoes	**6,217**	**3,948**	**733**
Öl- und Futterpflanzen / Oil and Forage Crops	**14,388**	**3,195**	**2,224**
Gräser / grasses	10,548	1,139	63
Raps und Futterkohl / rapeseed, feeding kale	2,525	1,719	2,117
Rotklee und Luzerne / red clover, alfalfa	1,315	337	44
Gesamt/Total	**150,751**	**50,438**	**28,473**

Research Group: Genome Diversity (GED)

Head: Prof. Dr. Andreas Graner

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Keywords

Precision Phenotyping

Trait Mapping

Biomass Development

Drought tolerance

Highlights

Alqudah AM, et al. (2016) The Genetic Architecture of Barley Plant Stature. Front. Genet. 7:117. DOI: 10.3389/fgene.2016.00117.

Schmidt M, et al. (2016) Prediction of malting quality traits in barley based on genome-wide marker data to assess the potential of genomic selection. Theor Appl Genet, DOI 10.1007/s00122-015-2639-1.

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Youssef HM, et al. (2017) VRS2 regulates hormone-mediated inflorescence patterning in barley. Nat. Genet. 49: 157-161.

Thirulogachandar V, et al. (2017) Leaf primordium size specifies leaf width and vein number among row-type classes in barley. Plant J. (2017) Epub ahead of print. dx.doi.org/10.1111/tpj.13590.

Neumann K, et al. (2017) Genetic architecture and temporal patterns of biomass accumulation in spring barley revealed by image analysis. BMC Plant Biol. DOI: 10.1186/s12870-017-1085-4.

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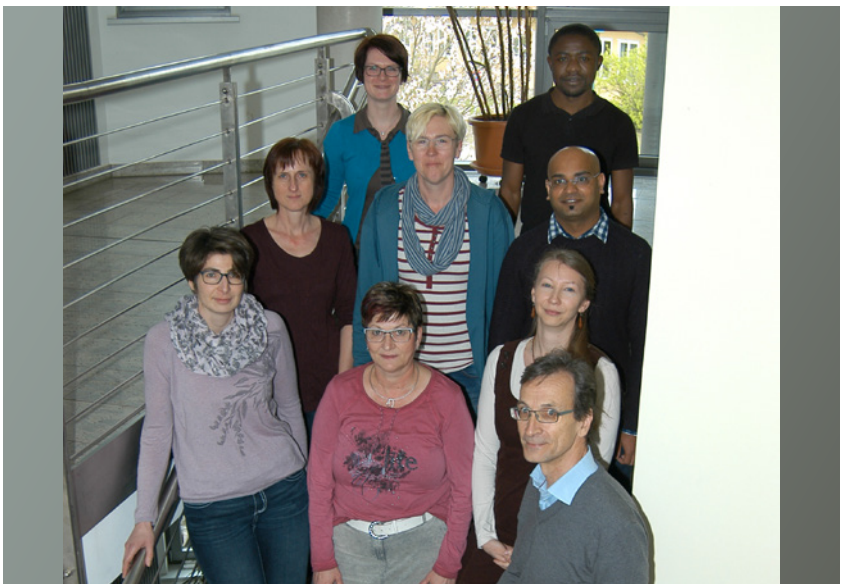

Our research focusses on genetic analysis of agronomic traits, mainly in barley (*Hordeum vulgare),* by studying the allelic diversity present in the germplasm pool of the *ex situ* collection. To this end, several customized mapping panels have been developed. These mirror the genetic diversity of two- and six rowed landraces of spring barley and are used as a resource for genome wide association analyses. In addition to morphological traits and yield components, we are interested in the genetics of biomass formation. As photo-assimilates are translocated from vegetative parts of the plant to developing seeds a deeper understanding of biomass formation is expected to contribute to further increases in yield potential.

Research Statement and Major Achievements

The genetic dissection of agronomic traits in barley has been a major objective of the research group, which has spearheaded the development of genomics resources for more than a decade. Agronomic traits were mapped and major genes conferring disease resistance and several mutant characters were isolated to investigate their allelic diversity present in the Gene Bank collection. To support trait mapping and gene isolation a set of customized populations was developed, which since has been employed within the Institute and beyond. In this context, we started to study the genetics of biomass accumulation using non-destructive imaging technologies. With the reorganization of the research group in 2015 the focus now rests on exploiting the genetic and phenotypic diversity of traits and characters. To assist the conservation management of the Gene Bank we contribute to the activation and molecular characterization of selected collections.

To initiate the genetic dissection of biomass formation in barley automated imaging technologies were employed for trait analyses in a population of two-rowed spring barley accessions. The correlations (R^2) of the model-derived traits digital biomass (DB) and fresh weight averaged 0.84 under control conditions and 0.74 under drought stress. Broad sense heritabilities ranged from 0.6 to 0.9 and increased with progres-

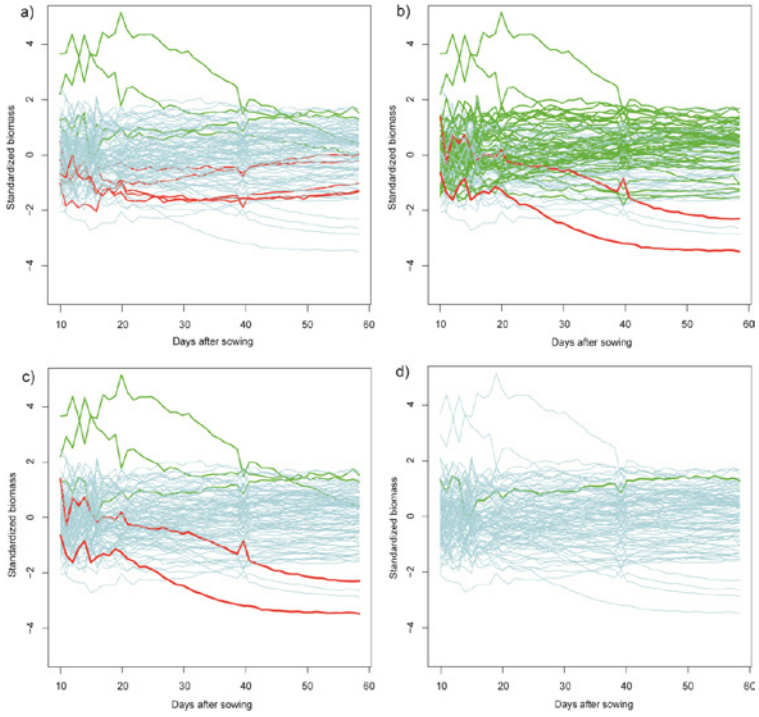

Fig. 13 Standardized digital biomass of barley accessions highlighting favorable and non-favorable QTL allele combinations over time. Biomass was standardized each day according to the population average. Values below zero indicate genotypes with biomass values lower than the average for the population; values above zero represent genotypes with biomass values higher than the average. Genotypes that carry the positive marker alleles for each QTL set are highlighted in green, those carrying the non-favorable alleles are shown in red. The remaining allelic combinations for all other genotypes are shown in grey a) QTL for early biomass (3 QTL) b) QTL for late biomass (4 QTL) and c) QTL for early and late biomass (7 QTL) d) QTL for early and late biomass and for the inflection point (9 QTL) (K. Neumann, J. Reif)

sing plant development. By performing genome-wide association analysis for DB on a daily basis up to 58 days after sowing a dynamic, bimodal pattern of QTL was observed. The first set of QTL peaked during early growth stages and disappeared with progressing plant development while the second set of QTL only peaked at later growth stages. Importantly, optimal results of marker assisted selection was achieved only after both early and late QTL were combined (Neumann et al. 2017, Fig. 13). In comparison to plant growth under well-watered conditions, drought stressed plants revealed a different pattern. Here, the first set of QTL was detected only during the drought stress phase, while the second set of QTLs emerged only at later stages after plants had entered the recovery phase, upon re-watering. A comparison of QTLs observed under well-watered and under drought-stressed conditions revealed that only two of the QTL were significant under both conditions while the remaining 10 QTL were stress responsive (in collaboration with RG *Quantitative Genetics*).

Malting quality is an important end-use trait in barley. The complex inheritance of malting quality has prevented its efficient manipulation in breeding programs. A genomic prediction approach for malting quality traits was devised that revealed a high potential of applying genomic selection for malting quality and speed up the breeding process (Schmid et al. 2016). QTL were detected for any of the 10 malting quality components investigated. A QTL hotspot was detected on chromosome 3H. Further analyses are required to clarify if the QTL hotspot is due to pleiotropy or linkage.

The populations that were developed for association mapping continued to represent a valuable resource for trait mapping and gene identification. In collaboration with the research group Plant Architecture, a GWAS approach helped to elucidate the molecular function and pleiotropic effects of the two paralogous genes Vrs1 and Vrs2 which are major regulators of spike morphology (row type) (Alqudah et al. 2016, Youssef et al. 2017, Thirulogachandar et al. 2017).

Embedding in Departmental and IPK Research Strategy

The research activities of the group integrate with research theme 1, *Concepts for the Valorization of Plant Genetic Resources*. Genetic characterization of barley and Phaseolus germplasm contributes to the activation of the Gene Bank collections by the generation of precision panels consisting of homozygous, genetically fingerprinted genotypes, by the identification of redundancies within the collections and by providing information on their genetic structure. Trait mapping contributes to the valorization of genetic resources both for research and breeding.

Plans, opportunities and future challenges

Genome wide association analysis using customized diversity panels provides ample opportunities to study agronomic traits. Further fine mapping of QTL in bi-parental populations and integration of sequence information available for the barley genome will be performed to identify and/or validate candidate genes and their allelic diversity. The feasibility of this approach has been successfully demonstrated for major genes conferring virus resistance (Yang et al. 2017). In this regard, we will aim at unlocking the allelic diversity of genes underlying quantitative traits such as biomass formation.

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Resequencing Genetic Resources
Pan-Genome Analysis
Molecular Cloning

Highlights

Avni R, et al. Wild emmer genome architecture and diversity elucidate wheat evolution and domestication. Science (2017) 357:93-97.

Mascher M, et al. A chromosome conformation capture ordered sequence of the barley genome. Nature (2017) 544:427-433.

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Russell J, et al. Exome sequencing of geographically diverse barley landraces and wild relatives gives insights into environmental adaptation. Nat Genet (2016) 48:1024-1030.

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We build genomic resources for the systematic and comprehensive capturing, interpreting and presenting of the globally available genomic diversity of Triticeae crop species. Based on high-quality reference sequences we aim at unlocking gene bank collections of barley, wheat, and rye and making these data available for research and application. We systematically use this data to unravel the genes controlling (i) soil-borne virus disease in barley, (ii) cytoplasmic male sterility restoration in all Triticeae crops and (iii) chloroplast differentiation and maturation.

Research Statement and Major Achievements

Sequencing Triticeae genomes: The research group *GGR* takes a leading role in sequencing the genomes of barley, wheat, and rye. As a major achievement a first version of the barley reference genome sequence, generated by an international effort under the umbrella of the *International Barley Genome Sequencing Consortium* (IBSC) and led by IPK, could be finalized and published in the prestigious journal Nature (Mascher et al. 2017). One of the most important breakthroughs for the physical ordering of the barley genome sequence, even through regions of the genome that don't contain genetic recombination, was the adaptation of methods for three dimensional (3D-) conformation capture sequencing in cereals by Dr. Axel Himmelbach. Based on this specific know-how our group could also contribute essential data sets to three wheat genome sequencing projects: (i) wild emmer wheat, (ii) durum wheat, (iii) bread wheat. In the meantime, the high-quality reference sequence of wild emmer wheat was published with IPK participation in the journal *Science* (Avni et al. 2017) and manuscripts for durum and bread wheat are under preparation. In a BMEL funded project IPK research groups *GGR*, *DG* and *BIT* collaborate with *Helmholtz-Center Munich* on the sequencing of German winter wheat cultivar '*Julius*'. The sequence assembly produced by company *NRGene* has been finished and annotation of the sequence is ongoing. This project is part of an international collaboration towards pan-genome analysis in wheat (http://www.wheatinitiative.org/activities/associated-programmes/10-wheat-genomes-project). Since November 2016 similar activities

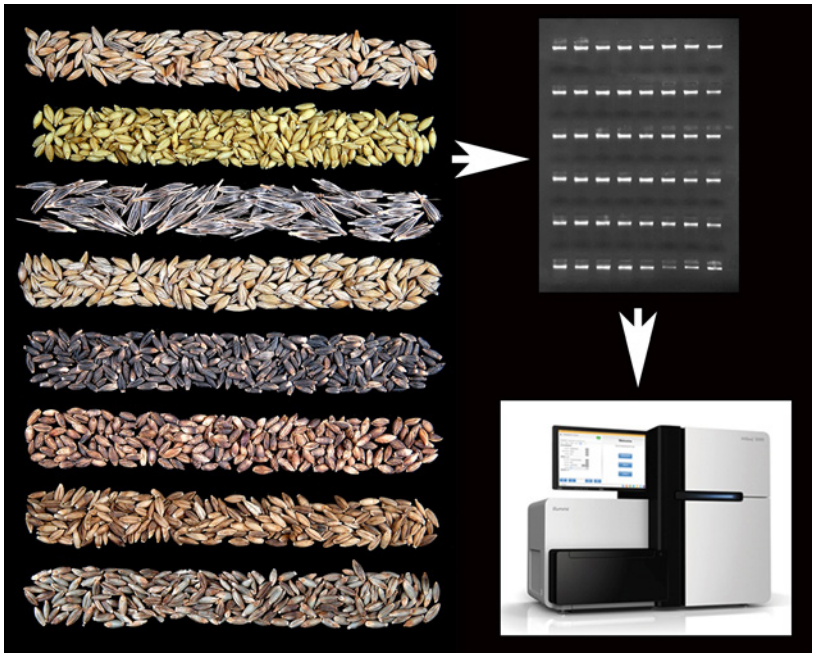

Fig. 14 Genetic diversity of the barley germplasm collection is systematically captured in the BRIDGE project through genotyping-by-sequencing (GBS). Individual plants per accession are grown for DNA extraction to be sequenced on the Illumina Hiseq2500 system of IPKs central next generation sequencing (NGS) service platform. (seed variation images taken by B. Schäfer)

are underway based on BMBF funded project *SHAPE*, which allows us to develop three additional reference quality genome sequence assemblies of diverse haplotypes.

In the case of rye, *GGR* has taken the lead to organize international joint funding for whole genome sequencing based on the approach of the company NRGene, which relies on high-coverage short read sequencing-by-synthesis. This effort has reached the phase of collaboration agreement finalization and it is expected that all data required for assembly will be generated before the end of 2017.

Unlocking barley genetic resources: The development of fundamental genomic resources for cereal crop species like barley is enabling the efficient and enhanced characterization of global genomic diversity. As a result, IPK research groups *GGR* and *DG* as well as additional national and international collaborators used exome capture based re-sequencing of a diverse panel of geo-referenced landrace and wild barley accessions to resolve the relationship of global genome diversity and regional or climatic adaptation (Russel et al. 2016). A unique opportunity of collaboration with archaeologists from Israel and ancient DNA experts from the *Max Planck Institute for the Science of Human History* in Jena, allowed us to unravel the diversity of 6,000-year-old barley grains from the Judean desert (Mascher et al. 2016).

In the frame of the *The Joint Initiative for Research and Innovation* project *BRIDGE*, *GGR* is leading the pilot flagship project (including partners from research groups *GED*, *DOK*, *RGR*, *DG*, *BIT*, *QG*) for re-sequencing entire species collections of IPK's gene bank (Fig. 14). End of July 2017 the genotyping-by-sequencing of >20,000 barley accessions was accomplished. Data is still under analysis.

Embedding in Departmental and IPK Research Strategy

Activities of *GGR* reported above are contributing fundamental information for underpinning the research areas 1 (*Concepts for the Valorization of Plant Genetic Resources*) and 2 (*Genome Diversity and Evolution*) of IPKs Research Strategy. Reference genome sequences for and re-sequencing of the lead crop species at IPK, wheat and barley, are essential components for unlocking the genetic diversity represented in entire gene bank collections. Innovations in genome sequencing and assembly will facilitate future evolutionary studies in wild relatives or entire genera.

Plans, Opportunities and Challenges

The research group *GGR* will continue its activity in structural genome analysis of the crop species barley, wheat and rye, mainly in the areas of pan-genome analysis, analysis of structural variation, developmental and tissue specific 3D organization of large cereal genomes as well as the systematic characterization of globally available genomic diversity. The direct access to IPK`s *Next Generation Sequencing* (NGS) platform and its continued equipping with complementing innovative technology (PacBio Sequel, 10XGenomics Chromium Controller, Illumina NovaSeq, etc.) is providing excellent opportunities for this kind of research and provides us also with excellent opportunities for international collaboration and networking.

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YOUSSEF, H.M., M. MASCHER, M.A. AYOUB, N. STEIN, B. KILIAN & T. SCHNURBUSCH: Natural diversity of inflorescence architecture traces cryptic domestication genes in barley (*Hordeum vulgare* L.). Genet. Resour. Crop Evol. 64 (2017) 843-853.

Additional Publications 2015

PEROVIC, J., C. SILVAR, D. PEROVIC, N. STEIN & F. ORDON: Fluorescence-based CAPS multiplex genotyping on capillary electrophoresis systems. Bio-protocol 5 (2015) e1472.

Other Papers

2017

JOST, M.: Cloning of the plant development regulatory genes *MANY NODED DWARF* (*MND*) and *LAXATUM-A* (*LAX-A*) by taking advantage of on improved barley genomics infrastructure. 18. Kurt von Rümker-Vorträge. Vortr. Pflanzenzücht. 86 (2017) 51-58.

Theses

2016

JOST, M.: Cloning of the plant development regulatory genes *MANY NODED DWARF (MND)* and *LAXATUM-A (LAX-A)* by taking advantage of an improved barley genomics infrastructure. (PhD Thesis) Martin-Luther-Universität Halle-Wittenberg, Institut für Agrar- und Ernährungswissenschaften der Naturwissenschaftlichen Fakultät III, Halle/S. (2016) 184 pp.

WENDLER, N.: Unlocking the secondary gene pool of barley for breeding and research. (PhD Thesis, kumulativ) Martin-Luther-Universität Halle-Wittenberg, Institut für Agrar- und Ernährungswissenschaften der Naturwissenschaftlichen Fakultät III, Halle/S. (2016) 111 pp.

Patents

2016

HOUBEN, A., R. KARIMI ASHTIYANI, T. ISHII, N. STEIN & J. KUMLEHN: Generation of haploid plants. (Industrieanmeldung), Veröffentlichung: 03.03.2016, IPK-Nr. 2014/01. EP 14182719.6 (2016).

Research Group: Genebank Documentation (DOK)

Head: Dr. Helmut Knüpffer

Scientists

Stefanie Kreide

Markus Oppermann

Michael Ulrich

Dr. Stephan Weise

Keywords

EURISCO

Genebank Information System (GBIS)

Plant Genetic Resources (PGR)

Phenotypic Data

Taxonomic Databases

Weather Data

Highlights

The 8th International Triticeae Symposium with more than 120 participants was organized in collaboration with the EUCARPIA Cereals Section in Wernigerode, 12–16 June 2017, with support from DFG and GPZ.

An article showing the progress of EURISCO was published in the annual database issue of Nucleic Acids Research (Weise et al. 2017).

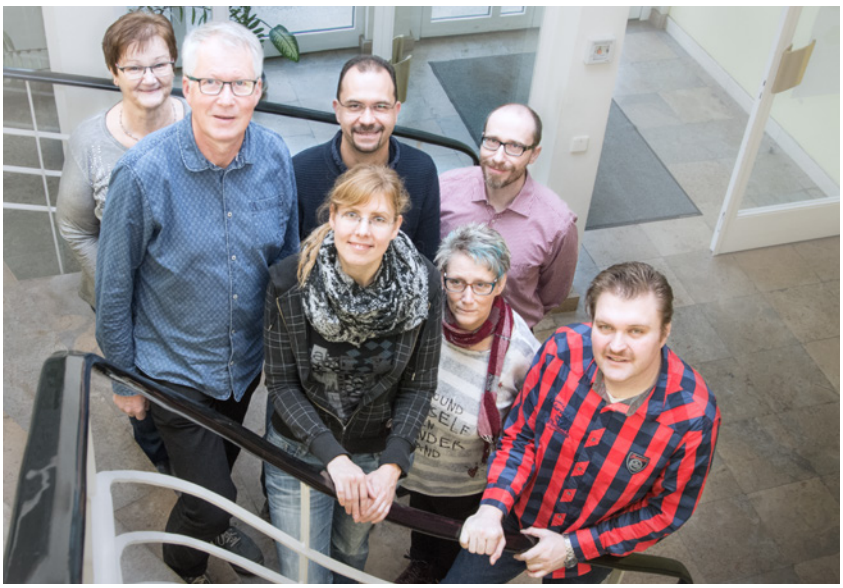
GBIS now supports the newly introduced handling fee for gene bank material requests.

The research group participates in two Horizon 2020 projects approved during the reporting period.

The EURISCO team was enlarged by a BLE-funded project.

Funding

ECPGR, H2020, BLE,
conferences: DFG, GPZ



The activities of the research group cover a large variety of aspects of gene bank data handling (Fig. 15). We focus on all kinds of support and development of the *Genebank Information System* (GBIS) and the *European Search Catalogue for Plant Genetic Resources* (EURISCO), thus assuring the long-term availability of PGR-related data. In addition, we assist other groups with advice and a helping hand in the use of gene bank-related databases. We are involved in international collaborations regarding PGR documentation and biodiversity informatics.

Research Statement and Major Achievements

The *Genebank Information System* (GBIS) is the central system supporting all processes related to the maintenance of gene bank accessions. In order to guarantee performance and efficiency of the system, it is indispensable to continuously maintain and develop the different components of *GBIS*. In connection with the introduction of a handling fee for gene bank material requests, various adaptations of GBIS were implemented and completed in summer 2016.

In parallel, a new version of the public web interface – *GBIS2/I* – is being developed in order to improve the usability of the system and to cope with the technological progress. The new component will be finished by the end of 2017, with special emphasis on a straightforward design and a variety of new features and will be available in 2018.

Another central task of the research group is the continuous processing and improvement of historic and current data on gene bank accessions. Triggered by the needs of different ongoing research activities at IPK, a strong focus during the reporting period was on cleansing and availability of phenotypic data of cereals covering a period of seven decades of gene bank multiplication.

The research group has the mandate to maintain and host the *European Search Catalogue for Plant Genetic Resources* (EURISCO) as well as to coordinate the

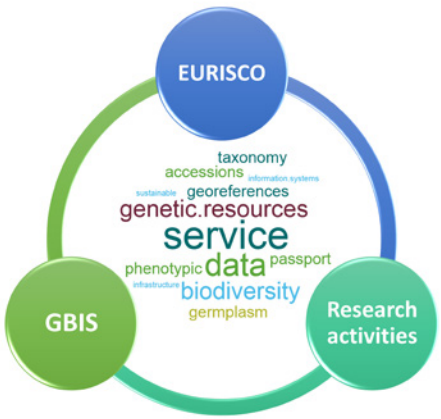


Fig. 15 Illustration of the main areas of activity of the research group Genebank Documentation.

underlying network in the member countries, on behalf of the *European Cooperative Programme for Plant Genetic Resources* (ECPGR). *EURISCO* provides a central entry point for data about 2 million germplasm accessions, which are preserved in almost 400 collections in 43 countries. In the reporting period, *EURISCO* was continuously improved in close collaboration with *ECPGR*. In this context, priority was given to the extension for phenotypic data. In order to strengthen the network, *EURISCO* was presented at several conferences. A series of annual international training workshops for data providers was initiated.

In May 2017, the *EURISCO* team was extended through a one-year project focusing on the improvement of the taxonomic backbone as well as the user interface of *EURISCO*, funded by the *German Federal Office for Agriculture and Food* (BLE).

The *8th International Triticeae Symposium* was organized in collaboration with the *EUCARPIA Cereals Section* in Wernigerode from 12-16 June 2017. It brought together more than 120 participants from 26 countries. Considerable funding was provided by the *Deutsche Forschungsgemeinschaft* (DFG).

A DFG-funded project for digitizing IPK herbarium specimens was finished in 2016. A herbarium web application for exploring these data was developed, bringing together the label data of the specimens with passport data of related gene bank accessions.

In addition, the research group manages or hosts a variety of international databases.

Embedding in Departmental and IPK Research Strategy

The Genebank Information System provides the IT basis of most of the preservation processes of the gene bank collection. In the frame of Research Theme 1, the research group processes, integrates and provides gene bank accession-related data for numerous projects, such as *BRIDGE* and *Genebank 2.0*, to name a few.

The research group will cooperate with other IPK bioinformatics research groups in establishing a PGR Data Warehouse.

Plans, Opportunities and Challenges

As a result of the networking activities, *EURISCO* will participate in two *Horizon 2020* projects, which were approved during the reporting period.

The identification of duplicate accessions of the gene bank collection provides a challenging task. Especially for strategies based on non-genomic accession-related data, the research group is predestined to assume a leading role.

Citizen-science approaches are becoming increasingly popular in different areas of biodiversity informatics. This comprises both the collection of new data and the processing of existing data. In parts, citizen-science approaches are also promising for gene banks. Thus, the research group will focus on the acquisition of resources for solutions ranging from simply capturing data from digitized documents, via enriching accession passport data to developing a tool enabling the community to comment and describe the use of gene bank material. These activities will successively increase the value of gene bank data.

Peer Reviewed Papers

2016

BADAEVA, E.D., A.S. RUBAN, S.A. ZOSHCHUK, S.A. SURZHIKOV, H. KNÜPFFER & B. KILIAN: Molecular cytogenetic characterization of *Triticum timopheevii* chromosomes provides new insight on genome evolution of *T. zhukovskyi*. Plant Syst. Evol. 302 (2016) 943-956.

ĆWIEK-KUPCZYŃSKA, H., T. ALTMANN, D. AREND, E. ARNAUD, D. CHEN, G. CORNUT, F. FIORANI, W. FROHMBERG, A. JUNKER, C. KLUKAS, M. LANGE, C. MAZUREK, A. NAFISSI, P. NEVEU, J. VAN OEVEREN, C. POMMIER, H. POORTER, P. ROCCA-SERRA, S.-A. SANSONE, U. SCHOLZ, M. VAN SCHRIEK, Ü. SEREN, B. USADEL, S. WEISE, P. KERSEY & P. KRAJEWSKI: Measures for interoperability of phenotypic data: minimum information requirements and formatting. Plant Methods 12 (2016) 44.

KNÜPFFER, H.: Plant genetic resources from the Balkan Peninsula in the world's genebanks. J. Agric. Food Environ. Sci. 69 (2016) 53-68.

SHAAF, S., R. SHARMA, F.S. BALOCH, E.D. BADAEVA, H. KNÜPFFER, B. KILIAN & H. ÖZKAN: The grain *Hardness* locus characterized in a diverse wheat panel (*Triticum aestivum* L.) adapted to the central part of the Fertile Crescent: genetic diversity, haplotype structure, and phylogeny. Mol. Genet. Genomics 291 (2016) 1259-1275.

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BOLGER, M., R. SCHWACKE, H. GUNDLACH, T. SCHMUTZER, J. CHEN, D. AREND, M. OPPERMANN, S. WEISE, M. LANGE, F. FIORANI, M. SPANNAGL, U. SCHOLZ, K. MAYER & B. USADEL: From plant genomes to phenotypes. J. Biotechnol. 261 (2017) 46-52.

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WEISE, S., M. OPPERMANN, L. MAGGIONI, T. VAN HINTUM & H. KNÜPFFER: EURISCO: The European search catalogue for plant genetic resources. Nucleic Acids Res. 45 (2017) D1003-D1008.

Articles in Compilations

2017

BADAEVA, E.D., H. KNÜPFFER, O.P. MITROFANOVA & B. KILIAN: Karyotype diversity of emmer wheat helps reconstructing possible migration routes of the crop. In: Proc. 13th International Wheat Genetics Symposium, April 23-28, 2017, Tulln, Austria. (2017) 129-131.

VELCHEVA, N., H. KNÜPFFER & S. WEISE: Bulgarian national inventory in international plant genetic resources databases. In: CHOLAKOV, T. & K. UZUNDZHALIEVA (Eds.): Proceedings, International Conference "135 Years Agricultural Science in Sadovo and 40 Years Institute of Plant Genetic Resources – Sadovo", Plovdiv, Bulgaria, 29–30 May 2017. (2017) 137-144.

Other Papers

2016

JALLI, M., M. BENKOVÁ, S. WEISE, A. LEISTRUMAITÉ, D. PLACINTA, L. LEGZDINA, M. ZACZYŃSKI, M. ŠVEC, A. DIDIER, N. NEYKOV, H. KNÜPFFER, A. JAHOOR & J. SVENSSON: Identification and updating of C&E data in EBDB of AEGIS *Hordeum* (HordEva). Activity Report. ECPGR Activity Grant Scheme – First Call, 2014. European Cooperative Programme for Plant Genetic Resources (ECPGR) (2016) 20 pp.

WEISE, S.: EURISCO Newsletter. August 2016. IPK Gatersleben, Germany. (2016) 2 pp.

WEISE, S.: EURISCO Newsletter. December 2016. IPK Gatersleben, Germany. (2016) 2 pp.

2017

WEISE, S.: EURISCO Newsletter. August 2017. IPK Gatersleben, Germany. (2017) 2 pp.

WEISE, S.: EURISCO Newsletter. Dezember 2017. IPK Gatersleben, Germany. (2017) 3 pp.

WEISE, S., H. KNÜPFFER, L. MAGGIONI & A.F. ADAM-BLONDON (Eds.): Report of the EURISCO Training Workshop 2016, National Focal Points Regional Training Workshop for Western Europe, 12–14 October 2016, Angers, France. European Cooperative Programme for Plant Genetic Resources, Rome, Italy http://www.ecpgr.cgiar.org/working-groups/documentation-information/eurisco-training-workshop-2016/. (2017) 13 pp.

WEISE, S. & M. OPPERMANN (COMPILERS) (Eds.): Report of the EURISCO Training Workshop 2017, National Focal Points Regional Training Workshop for Central Europe, 12–14 September 2017, Gatersleben, Germany. European Cooperative Programme for Plant Genetic Resources, Rome, Italy http://www.ecpgr.cgiar.org/working-groups/documentation-information/eurisco-national-focal-points-training-workshop-2017/.(2017) 13 pp.

Additional Publications 2015

WEISE, S.: EURISCO Newsletter. December 2015. IPK Gatersleben, Germany. (2015) 2 pp.

Theses

2017

MAEßE, M.: Entwicklung eines Prototyps zur Erfassung und Verarbeitung von inhomogenen phänotypischen Daten. (Bachelor Thesis) Hochschule Harz, Wernigerode (2017) 79 pp.

Research Group: Resources Genetics and Reproduction (RGR)

Head: PD Dr. Andreas Börner

Scientists

Dr. Ulrike Lohwasser

Dr. Natalia Tikhenko

Matias Schierenbeck

Rasha Tarawneh

Keywords

Long-term Seed Storage

Reproduction of Genebank Collections

Characterisation and Evaluation

Seed Longevity

Genetic Mapping

Abiotic Stress

Highlights

Andreas Börner elected as President Designate of EUCARPIA (European Association for Research on Plant Breeding).

Granting of DFG project: Complex study and physical mapping of genes in hexaploid wheat responsible for embryo development of wheat-rye hybrids.

Bayer Science and Education Foundation Fellowship: Genetic studies on drought stress tolerance in wheat.

Nagel M et al. Barley seed ageing: genetics behind the dry elevated pressure of oxygen ageing and moist controlled deterioration. Front. Plant Sci. 7 (2016) 388.

Funding

DFG, EU, BMEL, GIZ, DAAD, Leibniz, Industry (Bayer)

The research group is responsible for the conservation, regeneration and distribution management of the Gatersleben gene bank collection, which comprises the long-term storage, multiplication and distribution of the germplasm. The major research focus concerns seed longevity but also germplasm evaluation and genetic characterisation. In cereals, a number of bi-parental mapping populations and association mapping panels have been established to allow for the genetic analysis of various traits. In addition to these genetic studies, seed material is also used for various physiological and biochemical surveys in collaboration with partners within and outside of IPK.

Research Statement and Major Achievements

The total number of accessions maintained at the Gatersleben site comprises 130,146 samples. Safety duplicates are available for 48,655 accessions (about 32% of the whole collection). They are kept at the *Global Seed Vault*, Svalbard, Norway. In the last two years 23,294 germination tests have been performed. July 1, 2016, a handling fee for the delivery of gene bank accessions was introduced. The annual distribution decreased from 43,295 (01.07.2015 – 30.06.2016) to 25,516 (01.07.2016 – 30.06.2017) accessions, excluding the External Branch. During the regeneration seasons 2015/2016 and 2016/2017 totals of 9,346 and 9,921 accessions were cultivated, respectively, including 1,193 and 1,357 samples grown for evaluation only.

Research on seed longevity and dormancy as the main focus of the group was continued. Dormancy parameters were investigated on seeds of the EcoSeed association mapping panel compromising 116 two-row and 68 six-row barleys from 23 countries. Pre-harvest sprouting was strongly affected by the year of cultivation (Fig. 16). At maturity, pre-harvest sprouting was highly correlated with germination at 20°C. Interestingly, six-row Ethiopian genotypes did not develop any dormancy but accumulated significant higher amounts of nitric oxide than six-row genotypes from USA or Greece. Combining eight traits, genome-wide association mapping revealed 376 associations

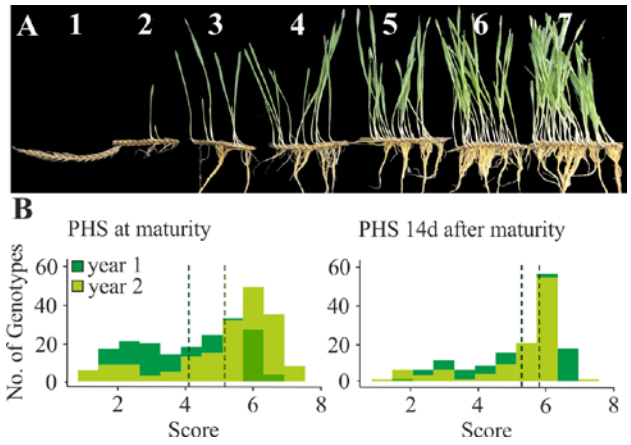

Fig. 16 Pre-harvest sprouting (PHS) was different in two experimental years and increased after a period of 14 days. Panel A) Evaluation scheme of sprouted spikes in moistened sand from 1 (no sprouting) to 7 (complete sprouting). Panel B) Distribution plots show differences between years and treatments.

predominantly located on chromosomes 2H and 5H. This reconfirms the strong quantitative nature of dormancy (in collaboration with RG *CSB*).

The molecular basis of seed deterioration is investigated in collaboration with the RG *HET* (D. Riewe, J. Wiebach, T. Altmann). Metabolite profiling of central metabolites using gas-chromatography mass-spectrometry (GC-MS) in 90 seed stocks of wheat naturally aged for 6 to 15 years identified glycerol and glycerol-phosphate as highly negatively correlated (R = -0.82) to germination, pointing to lipid hydrolysis in the aging seed. Lipidomic profiling using high resolution liquid-chromatography mass-spectrometry (LC-MS) led to the discovery and quantification of 365 oxidized lipids (and 221 non-oxidized lipids) in these seeds. Several hundreds of these lipids were significantly correlated to the germination (max R = -0.89). Intact storage and membrane lipids like triacylglycerols, phospholipids and galactolipids were exclusively positively correlated to the germination. Oxidized variants of these lipids and hydrolytic degradation products like (oxidized) diacylglycerols, monoacylglycerols, lysophospholipids and fatty acids were virtually all negatively correlated. These significant results provide striking evidence that during seed aging, ROS oxidize lipids, thereby triggering hydrolytic lipid degradation, resulting in membrane and cellular damage, and as a consequence, loss in viability of the whole organism.

Research to improve the utilisation of gene bank collections is focused on agronomic traits of cereals (wheat, barley, rye). In collaboration with the RG *GGK* genetic studies on anther extrusion in wheat were performed. Panels of spring and winter wheat accessions were used for genome wide association studies. Genotypic data included about 12,000 SNP markers for each of the panels. In total, 23 significant marker trait associations were detected, i.e. anther extrusion behaved as a complex trait.

Embedding in Departmental and IPK Research Strategy

The research group is responsible for the conservation management of the Gatersleben gene bank collections, which comprises the long-term storage, multiplication and distribution of the germplasm. The experimental work of the research group belongs to the IPK research theme 1: *Concepts for the Valorization of Plant Genetic Resources*. In collaboration with other research groups within the *Genebank* department but also in the other departments of the IPK we use gene bank accessions for phenotypic (morphological, physiological and biochemical traits) and genetic studies.

Plans, Opportunities and Challenges

Studies on seed longevity will be the main focus of the research. In addition to genetic studies, seed material will be also used for various physiological and biochemical surveys. In cereals (wheat, barley, rye) bi-parental mapping populations and association mapping panels have been established. They will be used for further genetic analysis of agronomic traits with major emphasis on abiotic stress tolerance (drought, pre-harvest sprouting, lodging).

Peer Reviewed Papers

2016

AGACKA-MOŁDOCH, M., M.A. REHMAN ARIF, U. LOHWASSER, T. DOROSZEWSKA, C.O. QUALSET & A. BÖRNER: The inheritance of wheat grain longevity: a comparison between induced and natural ageing. J. Appl. Genet. 57 (2016) 477-481.

AREND, D., M. LANGE, J.-M. PAPE, K. WEIGELT-FISCHER, F. ARANA-CEBALLOS, I. MÜCKE, C. KLUKAS, T. ALTMANN, U. SCHOLZ & A. JUNKER: Quantitative monitoring of *Arabidopsis thaliana* growth and development using high-throughput plant phenotyping. Scientific Data 3 (2016) 160055.

MOSTEK, A., A. BÖRNER & S. WEIDNER: Comparative proteomic analysis of beta-aminobutyric acid-mediated alleviation of salt stress in barley. Plant Physiol. Biochem. 99 (2016) 150-161.

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NAGEL, M., J. KODDE, S. PISTRICK, M. MASCHER, A. BÖRNER & S.P.C. GROOT: Barley seed ageing: genetics behind the dry elevated pressure of oxygen ageing and moist controlled deterioration. Front. Plant Sci. 7 (2016) 388.

OSIPOVA, S., A. PERMYAKOV, M. PERMYAKOVA, T. PSHENICHNIKOVA, V. VERKHOTUROV, A. RUDIKOVSKY, E. RUDIKOVSKAYA, A. SHISHPARENOK, A. DOROSHKOV & A. BÖRNER: Regions of the bread wheat D genome associated with variation in key photosynthesis traits and shoot biomass under both well watered and water deficient conditions. J. Appl. Genet. 57 (2016) 151-163.

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THORMANN, I., P. REEVES, A. REILLEY, J.M.M. ENGELS, U. LOHWASSER, A. BÖRNER, K. PILLEN & C.M. RICHARDS: Geography of genetic structure in barley wild relative *Hordeum vulgare* subsp. *spontaneum* in Jordan. PLoS One 11 (2016) e0160745.

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CHESNOKOV, Y.V., G.V. MIRSKAYA, E.V. KANASH, N.V. KOCHERINA, U. LOHWASSER & A. BÖRNER: QTL mapping of bread wheat (*Triticum aestivum* L.) grown under controlled conditions of an agroecobiological testing ground. Russ. J. Plant Physiol. 64 (2017) 48-58.

DOBRIKOVA, A.G., E.K. YOTSOVA, A. BÖRNER, S.P. LANDJEVA & E.L. APOSTOLOVA: The wheat mutant DELLA-encoding gene (*Rht-B1c*) affects plant photosynthetic responses to cadmium stress. Plant Physiol. Biochem. 114 (2017) 10-18.

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GLAGOLEVA, A., N. SHMAKOV, O. SHOEVA, G. VASILIEV, N. SHATSKAYA, A. BÖRNER, D. AFONNIKOV & E.K. KHLESTKINA: Metabolic pathways and genes identified by RNA-seq analysis of barley near-isogenic lines differing by allelic state of the *Black lemna and pericarp* (*Blp*) gene. BMC Plant Biol. (Suppl. PlantGen 2017 conference) 17 (2017) 182.

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Research Group: Cryo and Stress Biology (CSB)

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Keywords

Cryopreservation

Low-Temperature Stress

Desiccation and Osmotic Stress

Mint Slow-Growth Storage

Potato Vitrification Protocols

Allium

Highlights

Mint completely cryopreserved.

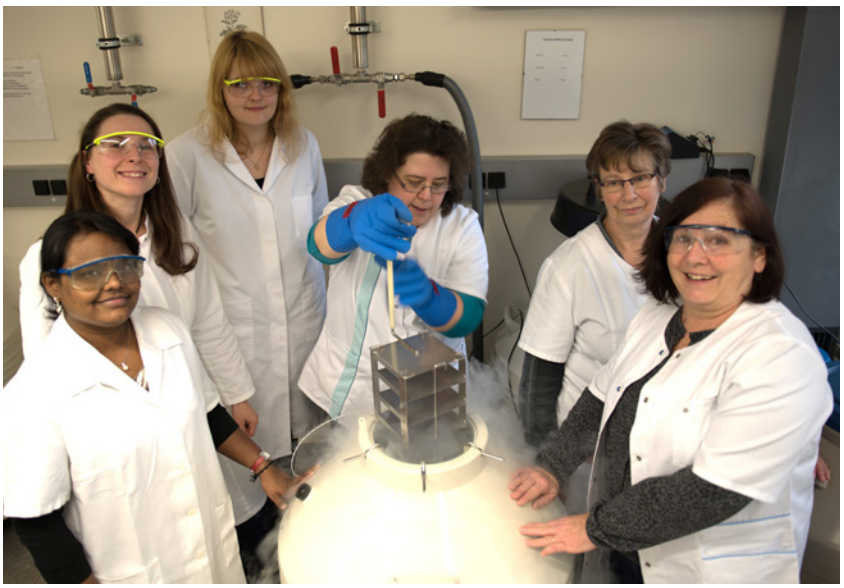
Improved potato cryopreservation.

Wheat pollen project started.

KAIT project elucidates cryostress regulators.

Funding

Leibniz, DAAD



The Cryo and Stress Biology research group is responsible to back up accessions of the federal *ex situ* collections that can only be vegetatively propagated. Under slow-growth conditions, 280 accessions of mint, *Antirrhinum* and *Allium* are maintained as *in vitro* plants and are available for distribution. The long-term maintenance is ensured by cryopreservation whereby 148 mint, 132 garlic and 1,538 potato accessions represent one of the world's largest collections in cryo. Thereby, desiccation, low temperature and endophytic microorganisms affect cryopreservation success and set the main research focus for long-term maintenance of plant genetic resources.

Research Statement and Major Achievements

CSB focuses on the ongoing cryopreservation of genetic resources, the slow-growth storage management and cryogenic research. In order to improve the security status of the cryo collections research achievements were integrated in the routine work:

Vegetatively propagated mint collection is completely cryopreserved and methods intensively compared: Two cryopreservation methods using *Plant Vitrification Solution 2* (PVS2) and PVS3 were applied to cryopreserve 27 mint accessions. Significant faster regrowth and reduced accumulations of endophytic microorganisms were observed for plantlets treated with PVS3 and explained higher percentage of plant regrowth. The vitrification-based protocols were finally used to back up the complete *in vitro* collection (Fig. 17).

Vitrification-based protocols improve cryopreservation results of potato: Regrowth results, sugar accumulation and ATP concentration were compared between dimethyl-sulfoxide (DMSO) droplet freezing and PVS3 droplet vitrification. Both protocols lead to a drastic increase of sucrose and ATP was significantly reduced after shoot tips isolation. For PVS3, again, faster plantlet regrowth and reduced endophyte accumulation were observed. To prove the success in a routine procedure, DMSO and PVS3 protocols were applied to 26 accessions and revealed, again, significant

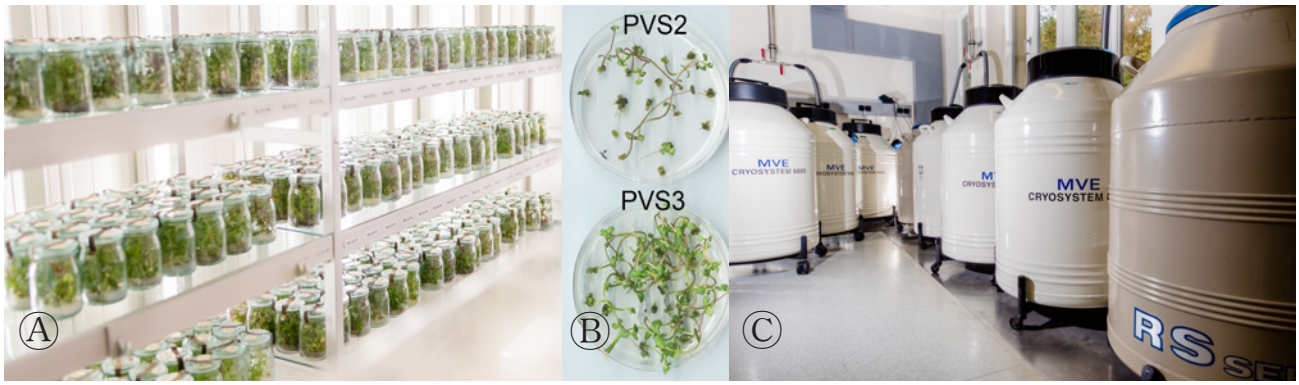


Fig. 17 Long-term maintenance of vegetatively propagated mint. A) Mint are kept in slow-growth storage at 10°C for about 1.5 years. B) Comparison of regrowth after PVS2 and PVS3 cryopreservation shows reduced explant development after PVS2. C) Mint is safely cryopreserved at -196°C (Pictures: Lynne Main, Angelika Senula, Manuela Nagel)

higher regrowth and less callus formation after cryopreservation with PVS3. Hence, PVS3 is now routinely applied to cryopreserve potato genetic resources.

***Allium* cryopreservation can be applied to different organs but regrowth is still affected during the treatments:** *Allium* cryopreservation focuses on garlic and shallot. For routine application, PVS3 vitrification is successfully applied to garlic shoot tips derived from bulbils, cloves, unripe and ripe inflorescences from the field. Here, shoot tips are isolated, precultured at 10% sucrose, cryoprotected by PVS3 and frozen in liquid nitrogen. Current results have shown that each step reduces regrowth success from 100% over 90 - 100%, 30 – 65% to 0 – 65%, respectively. Thereby, the highly hypoxic PVS3 is assumed to affect regrowth. However, comparative analysis between aerated and hypoxic solution did not reveal differences and reinforced the relevance of osmotic and cold stress.

The Leibniz Pakt Project *KAIT* reveals deep insights in cryostress mechanism: In collaboration with RG *ABC*, ATP was investigated and responded to increased low-temperature and osmotic stress conditions and acts as a marker for post-cryogenic viability in Arabidopsis. To decipher regulators of cryostress, multiple functions of *WRKY22* were investigated by transcriptomic approach and revealed that *WRKY22* is induced during dehydration and involved in the phytohormone-mediated defence response. *WRKY22* is assumed to be involved in the regulation of the stomatal closure during cryoprotection and in SA and JA-mediated defence response.

Wheat pollen storage experiments begin with appropriate viability assessment: To support plant genetic resources preservation and hybrid wheat production, physiological, biochemical and genetic mechanisms of wheat pollen growth and storage are under investigation. Mature wheat pollen loses rapidly viability after anther extrusion. To investigate pollen tube growth, a range of protocols and media have been evaluated and used to compare different genotypes. Up to 50% pollen tube growth could be observed in repeatable experiments and are the basis for further storability assessment.

Embedding in Departmental and IPK Research Strategy

To back-up vegetatively propagated plant genetic resources, *CSB* coordinates in detail material exchange, field multiplication and data management within the *Gene Bank* (RGs *RGR*, *TEN*, *ETX*, *DOK*) and is supported in LIMS data management by RG *BIT*. Based on the ideas of research *theme 1*, RGs *CSB*, *ETX* and RG *RGR* consider activities to evaluate garlic and mint resources. To elucidate mechanism of desiccation, low-temperature and biotic stress, *CSB* contributes to *theme 5* and collaborates with RGs *ABC*, *SZB*, *QG* and *GR*.

Plans, Opportunities and Challenges

We expect that the potato, garlic and shallot collections be in cryo at the latest in 20 years. A challenge is to achieve this target faster. Therefore, efficiency of protocols, workflows, number of plantlets in cryo and optimization of data input and handling are under review.

Cryogenic research will focus on fundamental cryo-stress mechanism in order to guaranty the long-term security of the collections and to investigate/evaluate new species/organs as possible targets for long-term conservation. To this end, an international network of plant cryobanks is envisaged to support decision-making, efficiency and coordination.

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2016

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Articles in Compilations

2016

BÖRNER, A., A.J. WORLAND, C.N. LAW, V. KORZUN, E.K. KHLESTKINA, T.A. PSHENICHNIKOVA, S. CHEBOTAR, S. LANDJEVA, B. KOBILJSKI, E. PESTSOVA, S.V. OSIPOVA, A.F. BALINT, A. GIURA, K. KOWALCZYK, M. AGACKA-MOLDOCH, M.R. SIMON, A.M. CASTRO, Y. CHESNOKOV, N. TIKHENKO, M.A. REHMAN ARIF, M. NAGEL, K. NEUMANN, S. NAVAKODE, U. LOHWASSER & M.S. RÖDER: EWAC – the past 25 years (1991-2015). In: BÖRNER, A. & K. KOWALCZYK (Eds.): Proceedings of the 16th International EWAC Conference, 24 - 29 May 2015, Lublin, Poland. (Series: European Wheat Aneuploid Co-operative newsletter, Vol. 16) Gatersleben: Leibniz-Institut für Pflanzengenetik und Kulturpflanzenforschung (2016) 15-26.

KELLER, E.R.J., M. GRÜBE, M.-R. HAJIREZAEI, M. MELZER, H.-P. MOCK, H. ROLLETSCHEK, A. SENULA & K. SUBBARAYAN: Experience in large-scale cryopreservation and links to applied research for safe storage of plant germplasm. In: LAMBARDI, M. & S. HAMILL (Eds.): Proceedings of the XXIX IHC - Int. Symp. on Micropropagation and In Vitro Techniques, Brisbane, Australia, August 17-22, 2014. (Series: Acta Horticulturae, Vol. 1113) Leuven: ISHS (2016) 239-249.

KELLER, E.R.J. & A. SENULA: Recent aspects of *Allium* cryopreservation in the federal German genebank. In: GOKCE, A.F. (Ed.): Proceedings of the VIIth International Symposium on Edible Alliaceae: Nigde, Turkey, May 21-25, 2015. (Series: Acta Horticulturae, Vol. 1143) Leuven: ISHS (2016) 35-44.

Other Papers

2017

BÖRNER, A., M. AGACKA-MOŁDOCH, D.Z. ALOMARI, M.G. CARDELLI, A.M. CASTRO, Y.V. CHESNOKOV, A.K. CHISTYAKOVA, M. DELL' ARCIPRETE, J.I. DIETZ, K. EGGERT, G.S. GERARD, D. GIMÉNEZ, K. JOŃCZYK, U. LOHWASSER, G. LORI, I. MALBRÁN, E.V. MOROZOVA, Q.H. MUQADDASI, M. NAGEL, S.V. OSIPOVA, H.M. PARDI, A.E. PERELLÓ, L. PERELLO, A.V. PERMYAKOV, M.D. PERMYAKOVA, T.A. PSHENICHNIKOVA, M.A. REHMAN ARIF, M.S. RÖDER, S.V. RUDAKOV, A.S. RUDAKOVA, E.G. RUDIKOVSKAYA, A.V. RUDIKOVSKY, L. SALDÚA, M. SCHIERENBECK, U. SKOMRA, L.V. SHCHUKINA, S. SHOKAT, M.R. SIMÓN, A.V. SIMONOV, R. TARAWNEH, J.P. URANGA, M.E. VICENTE, N. VON WIRÉN, M. YANNICCARI & C.D. ZANKE: Items from Germany. Ann. Wheat Newsl. 63 (2017) 8-16.

Theses

2016

MARTHE, A.: Einfluss von chemisch induzierten Trockenstress auf eine Sommerweizen-Kollektion. (Bachelor Thesis) Martin-Luther-Universität Halle-Wittenberg, Naturwissenschaftliche Fakultät III, Institut für Agrar- und Ernährungswissenschaften, Halle/S. (2016) 30 pp.

2017

BEHRENS, A.: Assoziationsgenetische Untersuchungen zur Trockentoleranz bei Sommerweizen. (Master Thesis) Martin-Luther-Universität Halle-Wittenberg, Naturwissenschaftliche Fakultät III, Institut für Agrar- und Ernährungswissenschaften, Halle/S. (2017) 57 pp.

FEUERHAHN, S.: Genetische Untersuchungen zur Langlebigkeit von natürlich und künstlich gealtertem Saatgut bei Weizen (*T. aestivum* L.). (Master Thesis) Martin-Luther-Universität Halle-Wittenberg, Naturwissenschaftliche Fakultät III, Institut für Agrar- und Ernährungswissenschaften, Halle/S. (2017) 81 pp.

KÖPNICK, C.: Einfluss der Kryokonservierung auf primäre Metabolite und den Energiehaushalt von Kartoffelsprossspitzen. (Master Thesis) Hochschule Neubrandenburg, Fachberreich Agrarwirtschaft und Lebensmittelwissenschaften, Neubrandenburg (2017) 77 pp.

SCHERER, A.: Statistische Analysen zur Regenerationswahrscheinlichkeit von kryokonservierten Kulturpflanzenexplantaten. (Bachelor Thesis) Technische Hochschule Mittelhessen, Fachberreich Mathematik, Naturwissenschaften und Informatik, Giessen (2017) 56 pp.

WANG, S.: Qualitative und quantitative Bestimmung der Entwicklungseigenschaften von Kartoffelexplantaten auf verschiedenen Regenerationsmedien. (Bachelor Thesis) Hochschule Anhalt, Studiengang Biotechnologie, Köthen (2017) 39 pp.

Research Group: Satellite Collections North (TEN)

Head: Dr. Klaus J. Dehmer

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Keywords

Genetic Diversity

Plant Genetic Resources

Potato

Forages

Oil Plants

Phenotyping and Genotyping

Highlights

Research on four externally funded projects, among these the EU funded GrassLandscape project.

Participation in Leibniz Science Campus Phosphorus Research Rostock

Distribution of 10,100 accessions to 546 requesters.

11,942 accessions (86% of the active oil and forage crop collections) deposited at the Svalbard Global Seed Vault.

Funding

BMEL/BLE, ERA-NET/FACCE-JPI, FNR

The Satellite Collections North maintain plant genetic resources of potatoes, oil and fodder crops at the Gross Luesewitz and Malchow/Poel sites of the IPK *Genebank* and conduct research on them. Here, our topics comprise – among others - genetic diversity, resistance/tolerance to diseases, content of valuable ingredients, as well as drought and nutrient use efficiency. Regarding classical gene bank work, we are responsible for the collection, preservation, characterization, evaluation, documentation and distribution (including C&E data) of appr. 20,500 accessions.

Research Statement and Major Achievements

The *Satellite Collections North* focus on elucidating the phenotypic and genotypic diversity of our plant genetic resources in order to maximize the level of accession-specific information available to our customers.

As a flagship project regarding the molecular diversity of our collections, fingerprinting of appr. 3,400 potato accessions via SSR and plastid markers not only confirmed the higher diversity present in the Andean sub-collection (Fig. 18), but also that 5% of our clonal material might be duplicated. In addition, a constant and thorough monitoring of the material maintained *in vitro* was identified as key to preserving the identity of our accessions.

Within the *GrassLandscape* project, 537 *Lolium* accessions from the entire European distribution range of the genus were phenotyped using IPK's automated phenotyping platform. Here, correlation analyses of re-growth rates obtained from digital height and digital leaf area variables and spring growth rates of sward plots in the field showed that predictions of sward growth from greenhouse re-growth are not yet possible. However, strong correlation between dry weight of green house grown plants and digital leaf area demonstrates that the estimation of biomass in *L. perenne* principally works using high-throughput phenotyping. Above that we could identify digital leaf area as the most promising variable to predict biomass increase of swards for it showed a

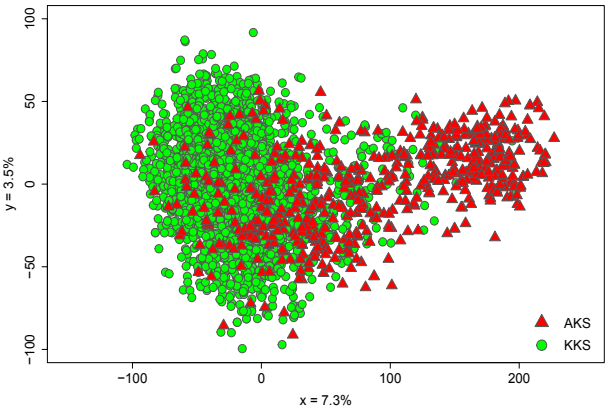

Fig. 18 Principal component analysis of 2,928 clonally propagated accessions of the Andean (red triangles) and Cultivated Potato Collections (green dots) based on 15 SSR markers (K. Diekmann).

moderate association with sward growth across three trial sites in France, Belgium and Northern Germany. Finally, first analyses of spring growth at all three trial sites gave evidence of a strong interaction between accessions and trial sites regarding the timing of spring growth.

Analyses of variance of C&E-data on 366 *Lolium* accessions collected in four European countries showed significant correlations between geographic origin and productivity in spring and rust susceptibility (Bulgarian material), aftermath heading and growth after winter (accs. from Ireland) or all growth parameters evaluated (Spanish and Croatian material) during cultivation at Malchow/Poel.

With respect to the maintenance of our potato collections, we currently preserve 6,217 accessions from 140 tuber bearing *Solanum* species.

In 2016 and 2017, 765 accessions were multiplied in the field and phenotyped for 15 traits, while in the greenhouse, 354 wild potato accessions were successfully regenerated. In both years, germination rates for 2,432 seed lots were determined. Via *in vitro* culture, 2,928 potato entries are maintained clonally, while more than 1,500 accessions are cryopreserved at IPK Gatersleben (CSB).

A total of 4,681 potato accessions (2016: 3,948; 2017: 733) was distributed to 310 requesters (233; 77).

GLKS accessions were evaluated for resistance to *Globodera pallida* (cooperation with *LALLF Rostock*; 32 accessions/144 genotypes tested; no acc./5 genotypes resistant to Pa2/3), *Phytophthora* infestans on leaves (JKI/ZL; 198 accs.; 105 accs. very resistant, 53 accs. resistant) and tubers (JKI/ZL; 53 accs./226 genotypes; 6 accessions/28 genotypes very resistant; 39 accs./124 genotypes resistant) and *Synchytrium endobioticum* (JKI/A; 40 accs., 4 resistant to race 18). 144 entries were evaluated for their taste, 598 for tuber starch content.

14,389 accessions belonging to 20 genera and 129 species are maintained at the Malchow Oil Plants and Fodder Crops Collections.

In 2016 and 2017, 1,149 accessions were characterized and multiplied in the field. In addition to evaluation trials on 145 accessions for research purposes, three-year field evaluations were carried out for *Lolium perenne* (47 accs. as recently bred material in co-operation with LFA). Germination rates for 13,624 seed lots were determined. Based on successful multiplications, 86% of the active collections (11,942 accs.) are saved at the Svalbard Global Seed Vault.

Seeds of 5,419 accessions (2016: 3,195; 2017: 2,224) were provided to 236 users (187; 49).

Embedding in Departmental and IPK Research Strategy

Focusing on potatoes, oil and fodder crops, the research of the Satellite Collections North feed into IPK's research theme 1, *Concepts for the Valorization of Plant Genetic Resources*. Aiming at constantly enhancing the information available on our germplasm, we strive to pheno- and genotype our accessions as comprehensively as possible in order to add to the overall goal of a biological digital resource centre.

Plans, Opportunities and Challenges

As a member of the *Leibniz ScienceCampus Phosphorus Research Rostock*, an intensified characterization of our PGR for nutrient efficiency is aimed at during the coming years, employing - besides others - hydroponic systems. These also can be employed to assess drought stress as a major aspect of climate change in Europe.

The seed and *in vitro* management will be continuously improved by e.g. employing non-destructive techniques to assess seed viability or treatment with cold plasma to influence the germination rate of seed lots (cooperation with INP Greifswald).

Molecular research on general and functional diversity will continue. Regarding the first aspect, especially the legume fodder crops as currently 'neglected' collection shall be included, while potatoes and grasses will be screened for gene diversity concerning traits of interest.

In order to reach the goal of a complementation of our biological resources with as comprehensive digital information as possible, the technical, edificial and personal infrastructure of the research group has to be improved in order to safeguard the sustainable conservation of our collections.

Peer Reviewed Papers

2016

MALYSHEV, A.V., M.A.S. ARFIN KHAN, C. BEIERKUHNLEIN, M.J. STEINBAUER, H.A.L. HENRY, A. JENTSCH, J. DENGLER, E. WILLNER & J. KREYLING: Plant responses to climatic extremes: within-species variation equals among-species variation. Global Change Biol. 22 (2016) 449-464.

2017

DIEKMANN, K., K.M. SEIBT, K. MUDERS, T. WENKE, H. JUNGHANS, T. SCHMIDT & K.J. DEHMER: Diversity studies in genetic resources of *Solanum* spp. (section Petota) by comparative application of ISAP markers. Genet. Resour. Crop Evol. 64 (2017) 1937-1953.

OERTEL, A., A. MATROS, A. HARTMANN, P. ARAPITSAS, K.J. DEHMER, S. MARTENS & H.-P. MOCK: Metabolite profiling of red and blue potatoes revealed cultivar and tissue specific patterns for anthocyanins and other polyphenols. Planta 246 (2017) 281-297.

Articles in Compilations

2016

BOTHE, R., S. NEHRLICH, E. WILLNER & K.J. DEHMER: Phenotyping genetic diversity of perennial ryegrass ecotypes (*Lolium perenne* L.). In: ROLDÁN-RUIZ, I., J. BAERT & D. REHEUL (Eds.): Breeding in a World of Scarcity: Proceedings of the 2015 Meeting of the Section “Forage Crops and Amenity Grasses” of Eucarpia. Cham: Springer (2016) 21-27.

Other Papers

2016

DEHMER, K.J.: Groß Lüsewitzer Kartoffel-Sortimente der IPK-Genbank (GLKS). Kartoffelbau 67 (2016) 54.

MEISE, P., S. SEDDIG, A. SCHUM, A. JOSEFOWICZ, H.-P. MOCK, K. DEHMER, C. BÜNDIG & T. WINKELMANN: Trocken- und Stickstoffmangel - Stressreaktionen der Stärkekartoffel. Untersuchungen auf morphologischer, physiologischer und proteomischer Ebene im Projekt PROKAR. Kartoffelbau 67 (2016) 40-45.

WACKER, K., K.J. DEHMER, B. EICHLER-LÖBERMANN, R. UPTMOOR: Phosphoreffizienz und genetische Regulation der Phosphataseproduktion und -aktivität bei Kartoffel (*Solanum tuberosum* L.). Mitt. Ges. Pflanzenbauwiss. 28 (2016): 276-277.

WILLNER, E. & K.J. DEHMER: IPK-Sortimente für Öl- und Futterpflanzen in Malchow/Poel (SÖF). Raps 3 (2016) 82.

ZACHER, A., C. BAUM, F. DE MOL, B. GEROWITT, K.J. DEHMER, A. GRANER: Potentielle Wirkung von Unkräutern auf die P-Mobilisierung unter Mais. Mitt. Ges. Pflanzenbauwiss. 28 (2016): 102-103.

2017

WACKER, K., M. KAVKA, K.J. DEHMER, B. EICHLER-LÖBERMANN & R. UPTMOOR: Unterschiede in der Phosphoreffizienz und Phosphoraneignung verschiedener *Solanum tuberosum* L. Genotypen aus in vitro- und Knollen-Kultur. Mitt. Ges. Pflanzenbauwiss. 29 (2017) 269-270.

ZACHER, A., C. BAUM, F. DE MOL, K.J. DEHMER & B. GEROWITT: Wirkung der Vergesellschaftung von Mais mit Unkräutern auf die P-Mobilisierung im Boden im Gefäßversuch. Mitt. Ges. Pflanzenbauwiss. 29 (2017) 174-175.

Theses

2017

DITTMANN, A.: Mikrosatelliten gestützte Identitätsüberprüfung potentieller Duplikate bei Kartoffel-Akzessionen der IPK-Genbank. (Bachelor Thesis) Universität Rostock, Institut für Biowissenschaften, Abteilung Pflanzengenetik & IPK Groß Lüsewitz, (2017) 39 pp.

Research Group: Experimental Taxonomy (ETX)

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Keywords

Taxonomy

Triticeae

Hordeum

Crocus

Systematics

Reference Collections

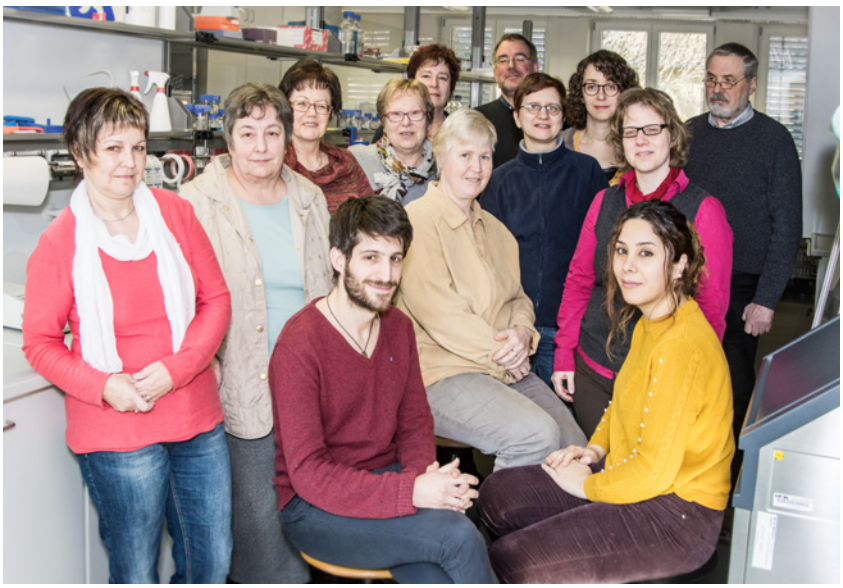
Highlights

Bernhardt, N, et al. Dated tribe-wide whole chloroplast genome phylogeny indicates recurrent hybridizations within Triticeae. BMC Evol. Biol. 17 (2017) 141.

Mahelka, V, et al. Multiple horizontal transfers of nuclear ribosomal genes between phylogenetically distinct grass lineages. Proc. Natl. Acad. Sci. USA 114 (2017) 1726-1731.

Funding

DFG



The research group works on the phylogenetic classification and evolution of crops and their wild relatives. We use experimental studies to link molecular markers and phylogenetic data with ecological and morphological traits, and to analyse plant–environment interdependency on and below the species level in an evolutionary framework. The other important part of the work of the group regards curatorial management of the taxonomic collections and to arrive at nomenclaturally suitable treatments of crops and their wild relatives.

Research Statement and Major Achievements

Within a DFG project aiming at clarifying the phylogeny of di- and polyploid Triticeae we use hybridisation-captured genes sequenced on the *Illumina NGS platform*. Phylogenetic analyses of on- and off-target sequences of this approach provide a much better idea about species relationships within the wheat group of the tribe but also show that large but differing parts of the genomes are shared among the taxa, even between different genera. We arrived at a comprehensive dated maternal phylogeny of the studied taxa (Bernhardt et al. 2017) by assembling the entire chloroplast genomes for 183 individuals from 53 species out of 15 Triticeae genera. The analyses of this dataset (*i*) identified recent and ancient cases of hybridisation resulting in chloroplast exchanges among different species and genera, and (*ii*) is able to explain inconsistencies regarding dating of Triticeae nodes in earlier analyses. We now expand the analyses from the wheat group to all Triticeae taxa.

In the barley genus *Hordeum* we published the most comprehensive species phylogeny up-to-date (Brassac and Blattner 2015) that resolves for the first time relationships for all di- and polyploid taxa within a single multi-locus analysis. Based on the results of this study we are currently trying to understand the evolution of narrow groups of polyploid species. Thus we use genotyping-by-sequencing to disentangle the relationships between the two tetraploids *H. capense* and *H. secalinum*. First results indicate that instead of (one or) two species there are four different taxa summarised under these names, two in central and southern Europe and two in South Africa. In

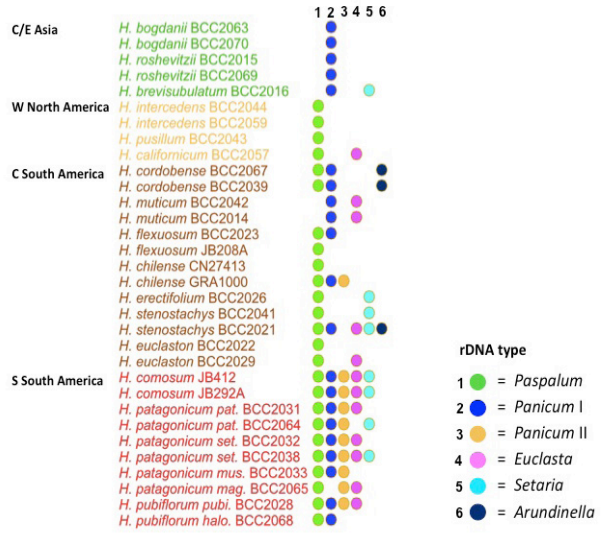


Fig. 19 Occurrence of ribosomal DNA (rDNA) derived from six different groups of panicoid grasses in the diploid species of *Hordeum* section *Stenostachys*. A study by Mahelka et al. (2017) indicates that horizontal gene transfer happened at least nine times independently between members of the Panicoideae and Triticeae, introducing partly large pieces of foreign genomic DNA into the genomes of these *Hordeum* and some closely related Triticeae species.

Hordeum we found a striking example for horizontal gene transfer (Mahelka et al. 2017). Asian and American Hordeum species received multiple times genome parts from panic grasses (Fig. 19) when they colonized areas already inhabited by these taxa.

The number of recognised species in *Crocus* nearly doubled during the last years and we estimate that roughly 200 species might occur. For them, we work on a comprehensive phylogenetic hypothesis that will finally result in a new taxonomic treatment of the genus. Through whole-genome shotgun sequences, we inferred single-copy genes to be used as phylogenetic markers. We recently got DFG funding to use 20 of these marker regions to study relationships among all *Crocus* groups and taxa.

Within another DFG project, we try to uncover the parental species of saffron (*Crocus sativus*), an assumed allotriploid, male-sterile taxon that can only be propagated vegetatively. Our results indicate that saffron is a segmental allopolyploid that most probably originated within *C. cartwrightianus* in Greece and the Aegean Islands.

For *Allium* subgenus *Melanocrommyum* a taxonomic revision was published, summarising the current knowledge. As an extension of our internet-searchable database on *Allium* we are currently taxonomically updating all Gene Bank entries of sequences published by us during the last 25 years. Providing the correct names, if changes occurred in-between, together with the inclusion of geo-referenced collection sites will support the barcoding efforts in *Allium* that recently started in Central Asian countries. A first estimation resulted in about 30% of the more than 1000 gene bank entries that need updates, and provided 400 non-submitted ITS sequences, which were produced during the last years in the context of the revision of subg. *Melanocrommyum*.

As a follow-up study of an earlier analysis that showed that *Hordeum* species endured ice-age climate changes *in situ* in the Patagonian steppe, we are analysing the reaction of woody taxa of the steppe on Pleistocene cold cycles. We here developed a method we call SSR-seq, where microsatellites are not only analysed for changes in fragment lengths but instead are sequenced in multiplex on next-generation sequencing platforms to resolve changes in the microsatellite motive and their flanking regions. This method results in better resolution in comparison to traditional microsatellite analyses.

The herbarium of the IPK currently holds a collection of 436,000 vouchers, with additional 107,000 samples in the seed and fruit collection and 55,600 in the spike collections. New specimens added to the collection consist of reference materials of gene bank accessions, but also the important type specimens for newly described *Allium* and *Crocus* taxa could be included. Thus, the herbarium is an integral part for documenting biodiversity-related research within the IPK. In a DFG-funded project specimens of crops and wild plants of the IPK herbarium have been digitized and are accessible online via the *Virtual Herbaria* portal of the Vienna-based database system *JACQ*. The digitisation of herbarium vouchers will go on for the next years.

Embedding in Departmental and IPK Research Strategy

Our research on phylogenetic classification and evolution of crops and their wild relatives is an important part of the research theme 2 *Genome Diversity and Evolution* of the IPK research strategy.

Plans, Opportunities and Challenges

During the next years we will contribute with our experience in phylogeographic analysis of plant taxa to two international cooperation projects. One is intended to understand vegetation history of the Eurasian steppe belt (DFG and FWF funded), the other deals with evolution at the dry limit (DFG-SFB 1211).

Peer Reviewed Papers

2016

BAGHERI, A., A.A. MAASSOUMI, M.R. RAHIMINEJAD & F.R. BLATTNER: Molecular phylogeny and morphological analysis support a new species and new synonymy in Iranian *Astragalus* (Leguminosae). PLoS One 11 (2016) e0149726.

BLATTNER, F.R.: *TOPO6*: a nuclear single-copy gene for plant phylogenetic inference. Plant Syst. Evol. 302 (2016) 239-244.

HARPKE, D., H. KERNDORFF, E. PASCHE & L. PERUZZI: Neotypification of the name *Crocus biflorus* Mill. (Iridaceae) and its consequences in the taxonomy of the genus. Phytotaxa 260 (2016) 131-143.

LUNAU, K., S. KONZMANN, J. BOSSEMS & D. HARPKE: A matter of contrast: yellow flower colour constrains style length in *Crocus* species. PLoS One 11 (2016) e0154728.

MILJKOVIĆ, M., V. RANĐELOVIĆ & D. HARPKE: A new species of *Crocus* (Iridaceae) from southern Albania (SW Balkan Peninsula). Phytotaxa 265 (2016) 39-49.

PETERSON, A., D. HARPKE, I.G. LEVICHEV, S. BEISENOVA, M. SCHNITTLER & J. PETERSON: Morphological and molecular investigations of *Gagea* (Liliaceae) in southeastern Kazakhstan with special reference to putative altitudinal hybrid zones. Plant Syst. Evol. 302 (2016) 985-1007.

2017

BAGHERI, A., F. GHAHREMANINEJAD, A.A. MAASSOUMI, M.R. RAHIMINEJAD & F.R. BLATTNER: Nine new species of the species-rich genus *Astragalus* L. (Leguminosae). Novon 25 (2017) 266-281.

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BARTOLUCCI, F., G. DOMINA, M. ADORNI, A. ALESSANDRINI, N.M.G. ARDENGHI, E. BANFI, G.A. BARAGLIU, L. BERNARDO, A. BERTOLLI, E. BIONDI, L. CAROTENUTO, S. CASAVECCHIA, P. CAUZZI, F. CONTI, M.A. CRISANTI, F.S. D'AMICO, V. DI CECCO, L. DI MARTINO, G. FAGGI, F. FALCINELLI, L. FORTE, G. GALASSO, R. GASPARRI, L. GHILLANI, G. GOTTSCHLICH, F. GUZZON, D. HARPKE, L. LASTRUCCI, E. LATTANZI, G. MAIORCA, D. MARCHETTI, P. MEDAGLI, N. OLIVIERI, M. PASCALE, N.G. PASSALACQUA, L. PERUZZI, S. PICOLLO, F. PROSSER, M. RICCIARDI, G. SALERNO, A. STINCA, M. TERZI, D. VICIANI, R.P. WAGENSOMMER & C. NEPI: Notulae to the Italian native vascular flora: 3. Italian Botanist 3 (2017) 29-48.

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EROL, O., D. HARPKE & A. CIFTCI: *Crocus heilbronniorum*, a new Turkish species of Series *Lyciotauri* (Iridaceae). Phytotaxa 298 (2017) 173-180.

FRITSCH, R.M.: Validation of *Allium tashkenticum*. Turczaninowia 20 (2017) 125-126.

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ŠARHANOVÁ, P., T.F. SHARBEL, M. SOCHOR, R.J. VAŠUT, M. DANČÁK & B. TRÁVNÍČEK: Hybridization drives evolution of apomicts in *Rubus* subgenus *Rubus* - evidence from microsatellite markers. Ann. Bot. 120 (2017) 317-328.

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Abteilung Züchtungsforschung ▪ Department of Breeding Research

Leiter ▪ Head
Prof. Dr. Jochen C. Reif

Allgemeine Forschungsziele

Der Pflanzenzüchtung kommt eine Schlüsselrolle bei der Ernährungssicherung der wachsenden Weltbevölkerung zu. In der Abteilung *Züchtungsforschung* (BR) werden Erkenntnisse und innovative Ansätze erarbeitet, um die Kulturpflanzenvielfalt für zukünftige Züchtungsaufgaben zu erschließen. Dabei wird an der Verfahrenskette eines Zuchtgangs entlang geforscht: der Schaffung genetischer Variation, der Fixierung von Sorteneltern und der Auswahl überlegener Genotypen sowie der Erhaltungszüchtung.

Stand der Forschungsarbeiten und wichtige Ergebnisse

Die Forschungsaktivitäten der Abteilung *Züchtungsforschung* reichten von Arbeiten in der Chromosomenbiologie zur schnellen Fixierung von Sorteneltern über neue Ansätze der Präzisionszucht bis hin zur Optimierung der Zuchtmethodik von Pre-Breeding-Programmen. Die Abteilung *Züchtungsforschung* trägt mit ihren Arbeiten zu allen fünf abteilungsübergreifenden Forschungsschwerpunkten des IPK bei. Entsprechend ihrer Forschungsaktivitäten sind ihre Arbeitsgruppen (Ag) in die drei Bereiche *Züchtungsinformatik*, *Chromosomenbiologie* und *Genomanalyse* gegliedert. Die Ag *Apomixis* (APM) wurde zum Juni 2017 und die Ag *Genomplastizität* (GP) zum August 2017 geschlossen. Die Studien der ehemaligen Ag *Karyotypevolution* (KTE) werden im Rahmen einer Projektgruppe weitergeführt.

Unter den 2016/2017 erbrachten Forschungsleistungen sind die Folgenden besonders hervorgehoben:

Wissensbasiertes Aufbrechen von unerwünschten Merkmalskorrelationen: Eine Weizensorte sollte exzellente Qualität und ausgeprägte Resistenz gegen biotischen und abiotischen Stress mit hohem Ertrag kombinieren. Häufig weisen die unterschiedlichen Merkmale allerdings unerwünschte Korrelationen auf. Die Aufgabe der Pflanzenzüchtung besteht daher darin, Gene in Sorten zu kombinieren, die es erlauben diese unerwünschten Merkmalskorrelationen aufzubrechen. In enger Zusammenarbeit zwischen der Ag *Gen- und Genomkartierung* (GGK) und der Ag *Quantitative Genetik* (QG) wurde ein innovativer Ansatz entwickelt und an einem umfangreichen Weizendatensatz validiert, der es erlaubt, auf molekularer Ebene uner-

General Research Goals

Breeding plays a key role in achieving food security in the context of an increasing global population. Scientists in the department of *Breeding Research* are aiming to generate insights and develop innovative approaches to allow the genetic diversity of crop plants to be better exploited as a way of achieving future breeding goals. The research spans the entire breeding process, from the induction of genetic variation, through the identification of parental material to the selection of superior genotypes and maintenance breeding.

Research Statement and Major Achievements

The activities ranged from research on chromosomal biology facilitating the rapid fixation of genotypes, novel approaches of precision breeding to the optimization of breeding methodology for pre-breeding. The department of *Breeding Research* contributes to all of the five trans-departmental research themes of the IPK. As a consequence of their research focuses, the research groups (Ag) of the department of *Breeding Research* are structured into the three programs *Breeding Informatics*, *Chromosome Biology* and *Genome Analysis*. The RG of *Apomixis* (APM) have been closed down since June 2017 and the RG of *Genome Plasticity* (GP) since August 2017. The research conducted within the previous group *Karyotype Evolution* (KTE) is continued as a project team.

The following scientific achievements are considered as highlights in 2016/2017:

Knowledge-based breaking of undesired trait correlations: A wheat variety should combine excellent quality, pronounced resistance against biotic and abiotic stresses, and high grain yield. Nonetheless, traits show often undesired correlations which have to be broken by plant breeding. The RGs *Gene and Genome Mapping* (GGK) and *Quantitative Genetics* (QG) developed an approach to reduce undesired trait correlations. The statistical toolbox was expanded to differentiate between pleiotropy and linked genes in association mapping. The toolbox was successfully evaluated

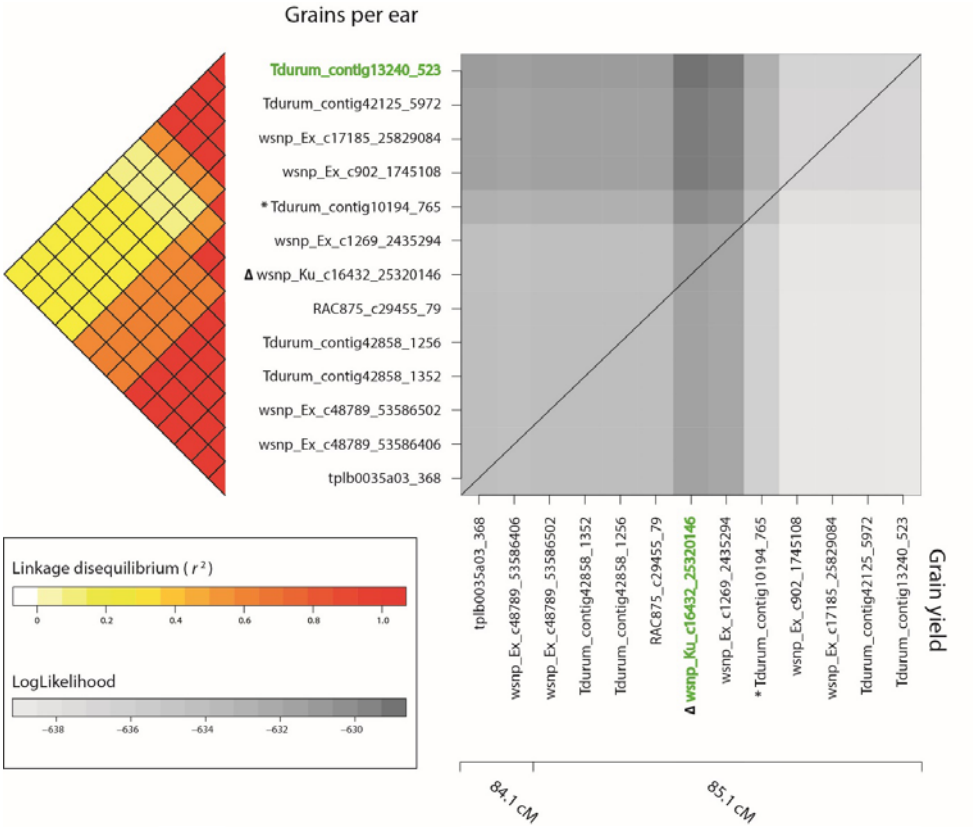

Fig. 20 Landscape of bivariate likelihoods to distinguish close linkage from pleiotropy for grain yield and grains per ear on chromosome 6A (Albert W. Schulthess, Marion Röder und Jochen C. Reif, IPK Gatersleben). ▪ Landscape of bivariate likelihoods to distinguish close linkage from pleiotropy for grain yield and grains per ear on chromosome 6A (Albert W. Schulthess, Marion Röder und Jochen C. Reif, IPK Gatersleben).

wünschte Merkmalskorrelationen zu reduzieren. Hierzu wurde erfolgreich die statistische Werkzeugkiste für die Differenzierung von Pleiotropie und enger Kopplung von Genen in Assoziationskartierungsstudien erweitert (Fig. 20). Ungewünschte Merkmalskorrelationen können nun im Falle von enger Kopplung markergestützt reduziert werden – ein wichtiger Schritt für die Entwicklung von Sorten, die gute Qualität, Resistenz und hohen Ertrag kombinieren.

Roggen betritt die genomische Ära: Roggen ist eine Modellkulturpflanze für die abiotische Stressforschung. Allerdings waren die genomischen Ressourcen für Roggen bisher unterentwickelt. Die Ag *Bioinformatik und Informationstechnologie* (BIT) hat wesentlich dazu beigetragen, diese Lücke im Rahmen eines vom BMBF geförderten Gemeinschaftsprojekts zu schließen. Mehr als 6,1 Milliarden Sequenzabschnitte der Lo7-Roggenlinie wurden assembliert, die als Grundlage für die Entwicklung eines hochdichten Genotypisierungs-Arrays dienten (Fig. 21). Dieser wurde dringend für die genombasierte Roggenzüchtung benötigt. Um den erreichten Meilenstein an Forscher und Züchter weiterzugeben, hat die Ag *BIT* notwendige Methoden konzipiert und entwickelt, damit die etablierte genomische Infrastruktur entsprechend einer nachhaltigen Forschung (OPEN data policy) zur Verfügung gestellt werden kann. Mit den entwickelten genomischen Ressourcen, die von der Ag *BIT* verwaltet und angeboten werden, hat Roggen einen großen Schritt in die genomische Ära gemacht. Diese genomische Infrastruktur fungiert als Grundlage und ist für weitere Genomprojekte in der Gerste und im Weizen in Anwendung.

using a comprehensive wheat data set (Fig. 20). Marker-assisted selection can now be used to reduce the undesired trait correlations in the case of close linkage – an important step towards breeding varieties which combine good quality, resistance and high grain yield.

Rye enters the genomic era: Rye is a model crop for abiotic stress research but genomic resources were so far underdeveloped. The RG *Bioinformatics and Information Technology* (BIT) substantially contributed to close this gap in the frame of a collaborative project funded by the BMBF. Over 6.1 billion sequence reads of the Lo7 rye inbred line were assembled (Fig. 21), which laid the foundation to develop a high-density genotyping array urgently needed for genomics-based rye breeding. To release this milestone to researchers and breeders the *BIT* group designed methods which assimilate the established genomic infrastructure following the OPEN data policy. With the developed genomic resources managed by *BIT*, rye has made a huge step into the genomic era. The genomic infrastructure is applicable and serves as a basis for other genome projects in barley or wheat.

Live cell imaging of multiple genomic loci: Elucidating the spatial-temporal organization of the genome inside the nucleus is imperative to understand the regulation of genes and non-coding sequences during development and environmental changes. Emerging techniques of chromatin imaging promise to bridge the gap between sequencing studies and imaging studies that provide spatial and temporal

Fig. 21 Ein komprimierter Blick auf die Diversität des Roggengenoms. Auf abstrakte Art und Weise illustriert die Abbildung diverse (rot) und konservierte (blau) Regionen der sieben Roggenchromosomen (J.-M. Pape and T. Schmutzer, IPK Gatersleben). ▪ A condensed view on the diversity discovered in the rye genome. In an abstract way the circus plot illustrates diverse (red) and conserved (blue) regions throughout the seven rye chromosomes (J.-M. Pape and T. Schmutzer, IPK Gatersleben).

Lebendbeobachtung multipler genomischer Sequenzen: Zum Verständnis der Regulation von Genen und nicht-kodierenden Sequenzen im Verlauf der Entwicklung und bei Umweltveränderungen ist es erforderlich, die räumliche und zeitliche Organisation des Genoms innerhalb des Zellkerns zu verstehen. Neue bildgebende Techniken zur Darstellung des Chromatins ermöglichen es, die Lücke zwischen Sequenzierung und dem Verständnis der räumlichen und zeitlichen Interphase-Chromatin-Organisation zu erforschen. So wurde unter Leitung der Ag *Chromosomenstruktur und –funktion* (CSF) eine bildgebende Technik, die auf dem CRISPR/Cas9 System basiert, für Pflanzen entwickelt. Durch die Fusion von eGFP/mRuby2 mit der katalytisch inaktiven Modifikation der Nuklease Cas9 von *Streptococcus pyogenes* und *Staphylococcus aureus* konnte die Dynamik der Telomere in lebenden Zellkernen von *Nicotiana benthamiana* visualisiert werden (Fig. 22). Im Verlauf von 30 Minuten wurden Telomer-Bewegungen von bis zu 2 µm beobachtet. Zusätzlich konnte gezeigt werden, dass CRISPR-dCas9 mit fluoreszenz-markierten Proteinen kombiniert werden kann, um DNA-Protein Interaktionen *in vivo* sichtbar zu machen. Durch die parallele Nutzung von zwei verschiedenen dCas9-Varianten ebnen die Arbeiten den Weg, um mehrere verschiedene DNA-Sequenzen gleichzeitig zu identifizieren. CRISPR-imaging ermöglicht somit, die Dynamik von Chromatin-Segmenten in Interphase-Kernen lebender Pflanzenzellen besser zu verstehen.

information of defined genomic regions. Coordinated by the RG *Chromosome Structure and Function* (CSF) an imaging technique based on the CRISPR/Cas9 system has been developed for plants. By fusing eGFP/mRuby2 to the catalytically inactive version of *Streptococcus pyogenes* and *Staphylococcus aureus* Cas9, a robust visualization of telomere repeats was shown in live leaf cells of *Nicotiana benthamiana* (Fig. 22). By tracking the dynamics of telomeres visualized by CRISPR-dCas9, long range telomere movements of up to 2 µm were revealed within 30 minutes during interphase. Furthermore, it was shown that CRISPR-dCas9 can be combined with fluorescence-labelled proteins to visualize DNA-protein interactions *in vivo*. By simultaneously using two dCas9 orthologues, the way was paved for imaging of multiple genomic loci in live plants cells. CRISPR-imaging bears the potential to significantly improve our understanding of the dynamics of chromosomes in live plant cells.

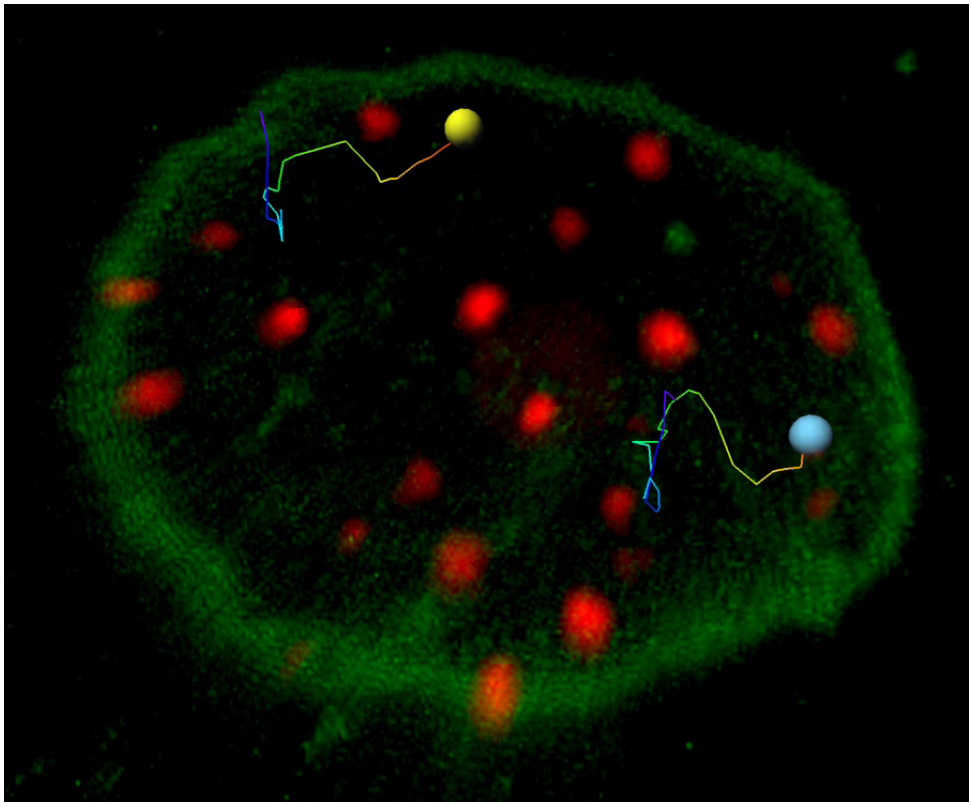

Fig. 22 CRISPR-basierte Kennzeichnung von Telomer-Repeats (in rot) in einem lebenden Zellkern (in grün) von *Nicotiana benthamiana* (S. Dreissig, S. Schiml, P. Schindele, O. Weiss, T. Rutten, E. Gladilin, V. Schubert, M. F. Mette, H. Puchta and A. Houben: Plant J. (2017)) ▪ CRISPR-based labelling of telomere repeats (in red) in a living interphase nucleus (in green) of *Nicotiana benthamiana* (S. Dreissig, S. Schiml, P. Schindele, O. Weiss, T. Rutten, E. Gladilin, V. Schubert, M. F. Mette, H. Puchta and A. Houben: Plant J. (2017)).

Perspektiven und Herausforderungen

Das Ziel der Abteilung ist in den kommenden Jahren die Forschungsarbeiten in den Bereichen (Vor-)Züchtungsmethodik, angewandte Quantitative Genetik und Chromosomenbiologie weiter auszubauen. Hierbei liegt der Schwerpunkt auf folgenden Forschungsgebieten: (1) Entwicklung und Evaluierung neuer Vorzüchtungsstrategien im Weizen, (2) Forschung für die Hybridweizenzüchtung und (3) Fixierung von Genotypen und Beeinflussung der Meiose. Für letzteres ist das Verständnis der Mechanismen der Chromosomenstruktur und -regulation bei der Zellteilung wichtig, da somit diese Prozesse gezielt beeinflusst und für eine schnellere Züchtung eingesetzt werden können. Die Zusammensetzung der Abteilung ist unikal und kombiniert die für die Umsetzung der oben gelisteten Schwerpunkte notwendige Expertise.

Plans, Opportunities and Challenges

The plan is to further strengthen the research activities in the areas of (pre)breeding methodology, applied quantitative genetics, and chromosome biology. We will put major emphasis in (1) developing and evaluating novel prebreeding strategies in wheat, (2) hybrid wheat breeding research, and (3) fixing of genotypes and manipulating of meiosis. For the latter the understanding of mechanisms of chromosomes assembly and regulation of cell divisions will allow manipulating these processes and will contribute to accelerate the plant breeding process. The composition of the department is unique and combines all necessary expertise.

Research Group: Quantitative Genetics (QG)

Head: Prof. Dr. Jochen C. Reif

Scientists

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Maria Yuli Gonzalez

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Zuo Li

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Keywords

Hybrid Breeding in Selfing Species

Prebreeding Methodology in Wheat

Hybrid Prediction Approaches

Genome-wide Mapping of Correlated Traits

Highlights

BMBF funds research on exploiting wheat genetic resources: QG coordinates Genebank2.0 project involving ten scientific partners and two breeding companies.

Third generation of Syngenta fellowships launched for best students at the MLU for joint research activities with QG.

The master thesis of Ulrike Beukert is honoured with the Hans H. Ruthenberg Award 2017.

Hybrid prediction models were successfully transferred to pearl millet (Nature Biotechnology 35:969-976).

A quantitative genetic framework highlights the role of epistatic effects for grain-yield heterosis in bread wheat (Nature Genetics 49:1741-1746).

QG developed a strategy to disentangle pleiotropy from close linkage (Journal of Experimental Botany DOI:10.1093/jxb/erx214).

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The *Quantitative Genetics* research group is interested in devising and evaluating *omics*-based breeding strategies to boost selection gain in (pre)breeding programs. The model crop is wheat, but research activities also encompass barley, pearl millet, rice, soybean, maize, rye, and rapeseed.

Research Statement and Major Achievements

Improved quantitative genetic models to predict hybrid performances: A challenge in hybrid breeding is to select superior hybrids out of millions of potential crosses. We developed genome-wide hybrid prediction approaches considering additive, dominance, and epistatic effects. These models were successfully applied in wheat, barley, rapeseed, pearl millet (Fig. 23), and rice populations. We observed stronger interactions of environments with dominance and epistatic than with additive effects. Consequently, the development of hybrid prediction models, including dominance and epistatic effects, require intensive phenotyping. Another challenge in hybrid prediction is to estimate precisely marker effects for lines originating from diverse population. Marker effects were estimated in the past either specific for each subpopulation or for the total population. Both approaches have major drawbacks. Therefore, we devised an improved genome-wide prediction model (GSA-BLUP) considering general but also subpopulation specific marker effects. The GSA-BLUP increased prediction accuracies of barley hybrids.

Using genomic selection in wheat breeding: Breeding for complex traits such as grain yield is challenging because of the complex genetic architecture. Genomic selection is a promising tool to cope with the situation and replace the traditional marker-assisted selection. Enhanced prediction accuracy, which is central for the application of genomic selection, can be achieved by applying more suitable statistical models. Instead of the usually used marker-based models, we implemented haplotype-based genomic prediction and successfully applied it to a large elite winter wheat population. The model is expected to exploit interaction effects among genes within a short range on the chromosome, which will last for generations due to tight

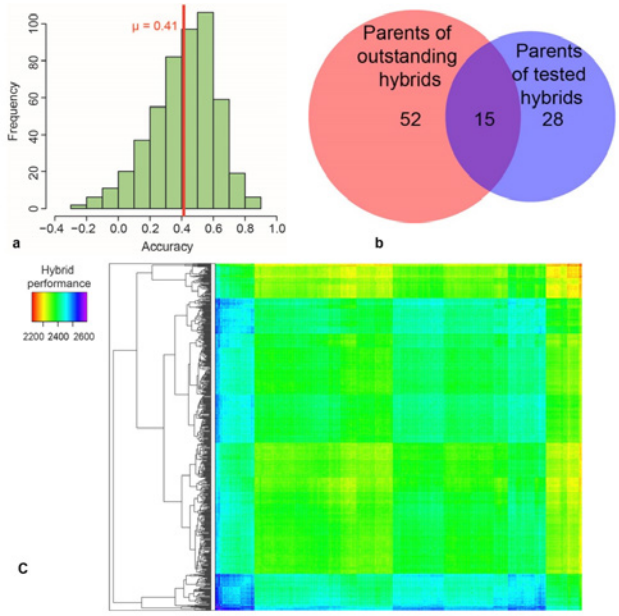

Fig. 23 Prediction of hybrid performance in pearl millet (Nature Biotechnology, in press). a) Prediction accuracy of hybrids b) Promising hybrid combination identified with novel yet untapped parental lines c) Heat map of heterotic groups formed.

linkage. Therefore, our haplotype-based model is an attractive tool for applied breeding. In terms of selection strategy, pure genomic selection was only recommended when high prediction accuracy is achieved. We developed a new selection strategy integrating genomic prediction and phenotyping. The key to this new strategy is the reliability criterion, which estimates the genomic prediction accuracy for each genotype. Genotypes with reliable and high genomic predicted values can be directly put into the official variety testing, and those with low to medium reliabilities deserve further intensive phenotyping. This integrated approach significantly improves the selection gain of breeding programs.

Implementing multiple-trait genome-wide mapping and prediction: Understanding the mechanisms which underlie trait correlations is not only an attractive biological topic, but also drives decisions in marker-assisted breeding. Distinguishing if an undesired trait correlation is due to closely linked loci instead of pleiotropy would indicate that efforts have to be allocated into breaking trait correlations by recombination. Multiple-trait mapping provide the statistical framework to disentangle pleiotropy and close-linkage, but has not been explored for genome-wide association mapping. We implemented multiple-trait association mapping in a diverse wheat population focusing on grain yield and correlated traits. Pleiotropy remained as the main explanation for these trait associations. We used the multivariate statistical tool box for further applications. For instance, the methodology was applied for genome-wide dynamic mapping in barley, wheat, and maize. In addition, multiple-trait genomic selection boosted the accuracy of Fusarium head blight resistance prediction up to 26% if information on plant height was included as correlated trait in the genomic prediction model.

Embedding in Departmental and IPK Research Strategy

The studies on *omics*-based breeding approaches are a central component of the research strategy of the Department of *Breeding Research*. The research of the Ag QG contributes mainly to the research theme 1 *Concepts for the Valorization of Genetic Resources*.

Plans, Opportunities and Challenges

The goal is to further strengthen the research activities in the area of (pre)breeding methodology and quantitative genetics in wheat. We will focus on (1) hybrid breeding methodology, (2) redesigning the exploitation of wheat genetic resources, and (3) expanding the toolbox of statistical genomics. The large data sets accumulated in the past five years offer great opportunities for developing and evaluating algorithms for Big Data Analyses in the context of quantitative genetics.

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Theses

2016

BEUCHEL, C.F.: Potential and limits of marker-assisted selection and genome-wide prediction for powdery mildew and tan spot resistance in a large European elite winter wheat population. (Master Thesis) Martin-Luther-Universität Halle-Wittenberg, Naturwissen-schaftliche Fakultät III, Institut für Agrar- und Ernährungswissenschaften, Halle/S. (2016) 36 pp.

WANG, Y.: Genome-wide prediction of testcross performance and phenotypic stability for important agronomic and quality traits in elite hybrid rye (*Secale cereale* L.). (PhD Thesis, kumulativ) Landessaatzuchtanstalt der Universität Hohenheim, Stuttgart (2016) 35 pp.

2017

BEUKERT, U.: Genome-based identification of heterotic patterns in rice. (Master Thesis) Martin-Luther-Universität Halle-Wittenberg, Naturwissenschaftliche Fakultät III, Institut für Agrar- und Ernährungswissenschaften, Halle/S. (2017) 31 pp.

HE, S.: Potentials and limits of genomics-assisted wheat breeding. (PhD Thesis) Martin-Luther-Universität Halle-Wittenberg, Naturwissenschaftliche Fakultät III, Institut für Agrar- und Ernährungswissenschaften, Halle/S. (2017) 43 pp.

MILKER, S.: Untersuchung von männlicher Sterilität und Selbstinkompatibilität bei *Matricaria chamomilla* L. zur Bestäubungslenkung. (Bachelor Thesis) Ernst-Abbe-Hochschule Jena, Fachbereich Medizintechnik und Biotechnologie, Studiengang Biotechnologie, Jena (2017) 56 pp.

REMBE, M.: Genome-wide association mapping and genome-wide prediction of anther extrusion in a Nested Association Mapping (NAM) population of wild x cultivated barley. (Master Thesis) Martin-Luther-Universität Halle-Wittenberg, Naturwissenschaftliche Fakultät III, Institut für Agrar- und Ernährungswissenschaften, Halle/S. (2017) 60 pp.

SANDMANN, M.: Functional characterization of AtKNL2 reveals the path for its centromere localization and its impact on the centromere environment. (PhD Thesis, kumulativ) Friedrich-Schiller-Universität Jena, Biologisch-Pharmazeutische Fakultät, Jena (2017) 165 pp.

Project Group: Karyotype Evolution (KTE)

Head: Prof. Dr. Ingo Schubert

Scientists

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Keywords

Cytogenomics

DNA Double Strand Break Repair

Genome Size Evolution

Karyotype Evolution

Highlights

Holistic approach linking genome (size) and karyotype evolution (Schubert & Vu, Trends in Pl. Sci. 2016).

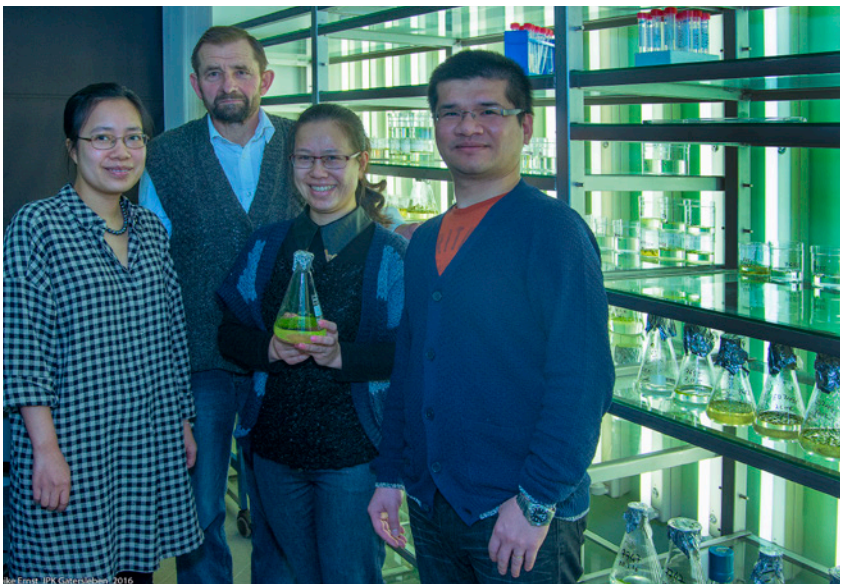
DSB repair outcome depends on genome size (Vu et al. New Phytol. 2017).

Endogenous sequence patterns predispose the repair modes of DSB repair (Vu et al. Plant J. 2017).

Chromosome rearrangements between the most ancestral duckweed species resolved (Hoang & Schubert, Chromosoma 2017).

Funding

DFG, MOET Vietnam



We focus on the evolution of genomes and karyotypes in closely related species with large variation in nuclear DNA content. We study possible reasons and consequences of genome size variability at the genomic and the chromosomal level by testing for whole genome duplication and karyotype rearrangements, e.g. between duckweed species. Because DNA double-strand break (DSB) repair mechanisms are essential for the evolutionary balance between genomic stability and variation, we quantify the outcome of DSB-repair at the sequence and chromosomal level within small and large genomes and in dependence of the sequence context.

Research Statement and Major Achievements

Karyotype evolution between duckweed species: The monocotyledonous, aquatic, neotenic and mostly asexual duckweed species are becoming a crop for life-stock feeding and biofuel application. The ancestral duckweed genus Spirodela comprises only two species: *S. polyrhiza* (n=20) and *S. intermedia* (n=18). After establishing a chromosomally integrated map for *Spirodela polyrhiza* (Cao et al., 2016), we resolved the evolutionary chromosome rearrangements between both species by serial multicolor FISH with 96 BACs which were anchored before to the cytogenomic maps of the 20 *S. polyrhiza* chromosomes. Eight chromosome pairs of *S. intermedia* were found to be involved in inversions and/or translocations which also mediate the observed dysploid chromosome number alteration (Hoang & Schubert, 2017).

DSB repair modes in relation to genome size and sequence context: Based on our and other's previous results we attempted a unifying hypothesis that links genome size and karyotype evolution with DSB repair (Fig. 24). Sequencing the repair products from three identical target sequences of *A. thaliana* and barley, and quantitative assessment of DNA gain and loss through DSB repair processes suggests deletion-biased DSB repair causing ongoing genome shrinking in *A. thaliana* (157 Mb/1C), whereas genome size in barley (~5500 Mb/1C) remains nearly constant. Phylogenomic comparisons between *A. thaliana* and two related species revealed

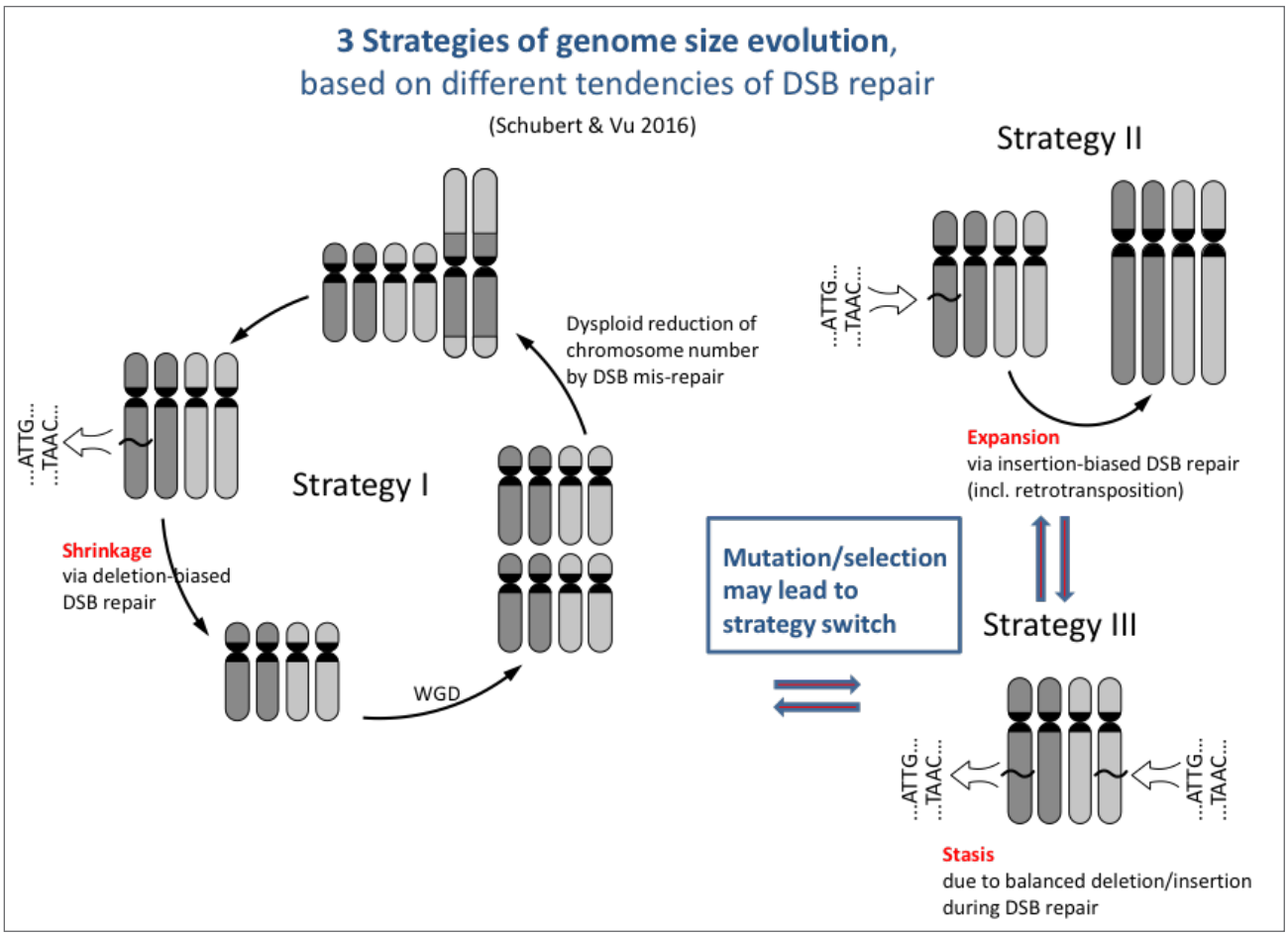


Fig. 24 Three strategies of genome size evolution based on different tendencies of DSB repair and related to karyotype evolution are hypothesized. Mutations within and/or selection of DSB repair pathways may lead to the consolidation of a strategy or to a switch between the strategies.

footprints of naturally occurring deletions during the evolution of the *A. thaliana* genome (Vu et al., 2017). These experimental results support our above mentioned hypothesis.

Sequencing the repair products of CRISPR/Cas9-induced DSBs at selected endogenous *A. thaliana* sequences showed that the sequence context predisposes repair modes. For instance: i) single-strand annealing-mediated deletions depend on the presence and distance of repeats flanking DSBs, ii) frequency and size of insertions increase if a sequence with high similarity to the target site is available in *cis*, iii) most of the mutagenic repair events are linked with pre-existing or *de novo*–generated (micro)homology, if not completed by blunt end-ligation (Vu et al., 2017).

Embedding in Departmental and IPK Research Strategy

The cytogenomic work of our project group fits well into IPK's research theme 2 *Genome Diversity and Evolution*.

Plans, Opportunities and Challenges

Our expertise and facilities should contribute to the future elucidation of genome and karyotype evolution within the duckweed family, and to resolve pathways as well as genomic and evolutionary consequences of erroneous DSB repair in plants.

For references see RG *QG*.

Research Group: Bioinformatics and Information Technology (BIT)

Head: Dr. Uwe Scholz

Scientists

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Keywords

Data Management
Databases and Data Warehouses
Research Data Publication
Plant Genomics and Phenomics Research Data Repository
Crop Genomes and Diversity

Highlights

Providing the genomic infrastructure for the chromosome conformation capture ordered sequence of the barley genome published in Nature (http://dx.doi.org/10.1038/nature22043).

Release of the first whole-genome draft sequence for rye (Plant Journal http://dx.doi.org/10.1111/tpj.13436).

The PGP repository was accepted by the data journals GigaScience and Nature Scientific Data.

First research data publications accepted in Nature Scientific Data (http://dx.doi.org/10.1038/sdata.2016.55 and http://dx.doi.org/10.1038/sdata.2017.44).

Co-development of the standard for interoperability of phenotypic data - MIAPPE (http://dx.doi.org/10.1186/s13007-016-0144-4).

Funding

BMBF, BMEL, DFG

The research group is engaged in the management of research data, in the implementation of integrated biological information systems/data warehouses for performing *in silico* analyses, in the development of systems for information retrieval, research data publication as well as in the provision of bioinformatics tools, especially for sequence analysis.

Research Statement and Major Achievements

The research group supports the concept of Open Data and established broad expertise in the publication and management of research data. We developed the *Phenomics Research Data Repository* (PGP), which is the first productive instance of the e!DAL infrastructure. Currently, we published over 140 cross-domain data records with a total volume of over 2.2 TB that follow the FAIR principals (Findable, Accessible, Interoperable, and Re-usable) and were accessed on average over 15,000 times per month. One important example is the publication of the first MIAPPE conform dataset of a high-throughput plant phenotyping experiment in the *Nature Scientific Data Journal*.

The *BIT* research group is involved in several collaborations that investigate complex crop genomes by high-throughput sequencing. Recently, we contributed to the map-based pseudomolecule sequence of the barley genome. Our strategy was highlighted in combining resources from more than 80,000 assemblies from individual sequences of BAC clone inserts (roughly 60,000 assemblies were produced with the BAC pipeline by Beier et al. 2016). These BAC assemblies were used to generate a non-redundant sequence of 4,265 scaffolds of overlapping BAC clusters which were converted to 4.79 Gbp of non-redundant sequence of the barley genome. All this information has been deposited on public archives and can be accessed through the BARLEX portal (http://barlex.barleysequence.org).

In the frame of the RYE-Select project, we recently published a whole-genome draft sequence of rye (*Secale cereale* L.). With the constructed scaffolds, covering a total length of 2.8 Gbp, this genomic resource captures nearly the entire low-copy portion

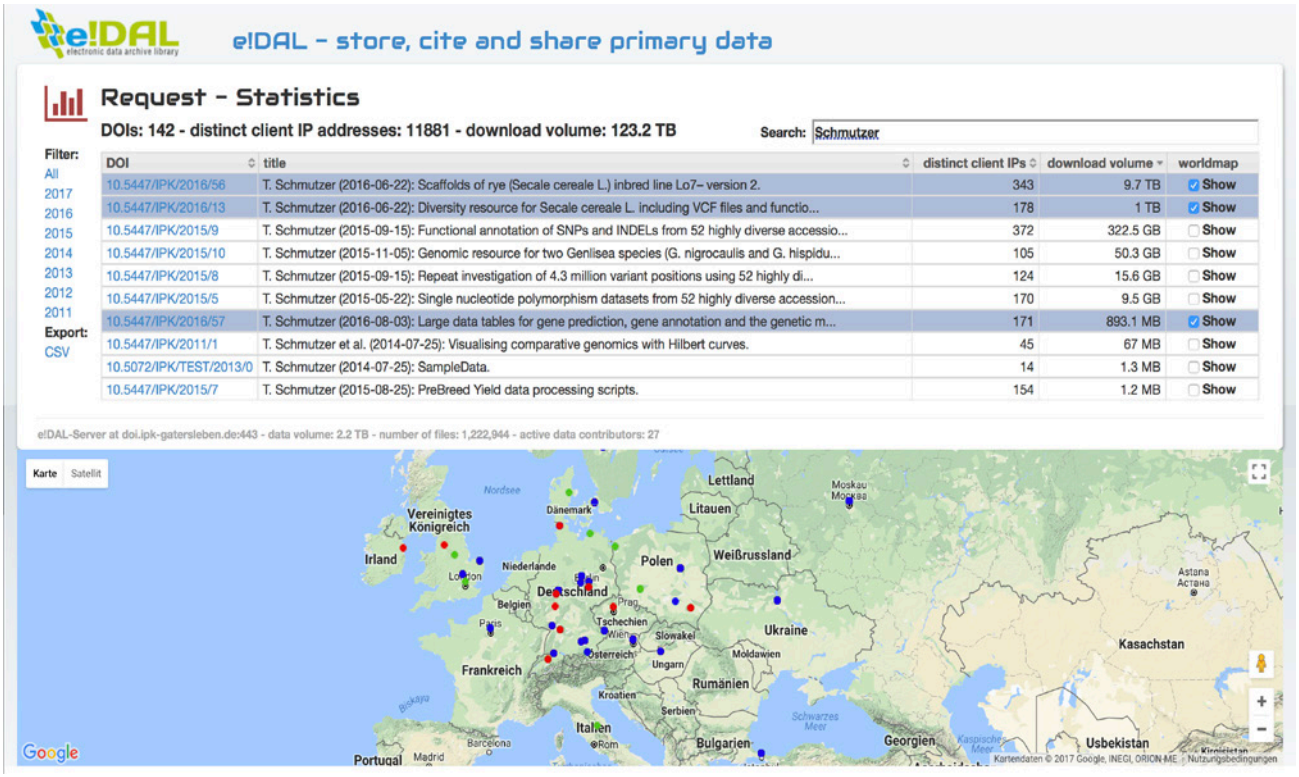

Fig. 25 Excerpt of the usage statistics of the PGP-Repository (https://doi.ipk-gatersleben.de/report) This screenshot shows the registered accesses and downloads of some comprehensive research datasets associated with the publication of whole-genome draft sequence of rye (Secale cereale L.) from Bauer et al. (Plant J 2017, http://dx.doi.org/10.1111/tpj.13436). All records were worldwide accessed by already around 700 users, which shows the high visibility of the repository as well as the need of the scientific community for retrieving such kind of research data.

of the rye genome, including 27,784 rye gene models. We combined this resource with the re-sequencing data of 10 inbred lines and a wild progenitor *S. vavilovii* to construct a large genotyping assay (RYE600k) that was used to characterize 264 diverse rye lines. The complete sequence resource was released to the research community as data publication in the PGP repository (http://dx.doi.org/10.5447/IPK/2016/56 and see Fig. 25) and is integrated for comparative sequence analysis in our IPK Rye Blast Server (http://webblast.ipk-gatersleben.de/ryeselect/).

Together with RG *CSF* we constructed in the DFG funded project *Origin, function and regulation of B-chromosome located gene fragments in the species Aegilops speltoides* a first draft of a WGS assembly totaling 1 Gbp. A comparative approach of the constructed WGS assembly revealed 27,000 candidate sequences assigned to the B-chromosome. In addition, we used high-throughput sequencing of microdissected B-chromosomes which will be used to further validate these sequence regions.

The research group is partner of the *German Network for Bioinformatics Infrastructure* – de.NBI and Uwe Scholz coordinates the service unit GCBN - *German Crop BioGreenformatics Network* (http://www.denbi.de/gcbn).

Embedding in Departmental and IPK Research Strategy

The research in the area of Breeding Informatics is of fundamental importance to reach to goals of the department of *Breeding Research.* With our research activities, we are contributing to the IPK research themes *Concepts for the Valorization of Plant Genetic Resources* and *Genome Diversity and Evolution*. With applications like PGP and e!DAL and with our further developments for data management we are supporting the IPK strategy to develop the institute to a biological and digital resource center. Besides the research activities the group is providing bioinformatics service in the field of sequence analysis. We are hosting a GALAXY workflow infrastructure, which enables scientists at the IPK to perform e.g. sequence analysis without deeper knowledge of Linux command line tools. Furthermore, internal resources (e.g. genomes, blast databases or annotation) are provided via the GALAXY system. Currently, more than five complex workflows and several custom tools are available, such as RNASeq analysis workflow or a pipeline to identify putative promotor sequences. In total, we have more than 40 registered wet lab researchers.

Plans, Opportunities and Challenges

In the near future, we will create a web-based information system to access and browse the diversity of plant genetic resources. We are partner in various resequencing projects which will produce diversity data sets for barley, wheat as well as phaseolus.

Peer Reviewed Papers

2016

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BEIER, S., A. HIMMELBACH, T. SCHMUTZER, M. FELDER, S. TAUDIEN, K.F.X. MAYER, M. PLATZER, N. STEIN, U. SCHOLZ & M. MASCHER: Multiplex sequencing of bacterial artificial chromosomes for assembling complex plant genomes. Plant Biotechnol. J. 14 (2016) 1511-1522.

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BEIER, S., A. HIMMELBACH, C. COLMSEE, X.-Q. ZHANG, R.A. BARRERO, Q. ZHANG, L. LI, M. BAYER, D. BOLSER, S. TAUDIEN, M. GROTH, M. FELDER, A. HASTIE, H. ŠIMKOVÁ, H. STAŇKOVÁ, J. VRÁNA, S. CHAN, M. MUÑOZ-AMATRIAÍN, R. OUNIT, S. WANAMAKER, T. SCHMUTZER, L. ALIYEVA-SCHNORR, S. GRASSO, J. TANSKANEN, D. SAMPATH, D. HEAVENS, S. CAO, B. CHAPMAN, F. DAI, Y. HAN, H. LI, X. LI, C. LIN, J.K. MCCOOKE, C. TAN, S. WANG, S. YIN, G. ZHOU, J.A. POLAND, M.I. BELLGARD, A. HOUBEN, J. DOLEŽEL, S. AYLING, S. LONARDI, P. LANGRIDGE, G.J. MUEHLBAUER, P. KERSEY, M.D. CLARK, M. CACCAMO, A.H. SCHULMAN, M. PLATZER, T.J. CLOSE, M. HANSSON, G. ZHANG, I. BRAUMANN, C. LI, R. WAUGH, U. SCHOLZ, N. STEIN & M. MASCHER: Construction of a map-based reference genome sequence for barley, *Hordeum vulgare* L. Scientific Data 4 (2017) 170044.

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ULPINNIS, C.: Entwicklung einer Pipeline für eine verbesserte Genvorhersage durch die Verknüpfung von Assemblierungsdaten mittels RNA-seq Daten. (Master Thesis) Martin-Luther-Universität Halle-Wittenberg, Institut für Informatik der Naturwissenschaftlichen Fakultät III, Halle/S. (2017) 124 pp.

Research Group: Chromosome Structure and Function (CSF)

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Keywords

Centromere
Chromatin Organization
Chromosome Segregation
CENH3
Haploidization
Mitosis
Meiosis

Highlights

The publication, Sandmann et al., 2017: Targeting of *A. thaliana* KNL2 to centromeres depends on the conserved CENPC-k motif of its C-terminus, was featured by Plant Cell in a mini-review.

The first CRISPR-imaging in plants has been developed and published in 2017 in Plant Journal.

A review on haploidization via chromosome elimination was prepared and published 2016 by Annual Review Plant Biology.

Development of a single pollen analysis tool to determine recombination events.

Start of the BMBF-funded project 'HaploTools' with Andreas Houben as coordinator.

Three students awarded the PhD degree.

Funding

BMBF, DFG, DAAD, EU-funded Marie Curie ITN, BMGF (USA) sub-award from CSIRO (Australia), Industry (Bayer).

The research group deciphers the regulation, organization, segregation and evolution of mitotic, meiotic and interphase chromosomes with the aim to unravel basic mechanisms of chromosome biology in model, wild, and crop species. The gained knowledge will be translated to accelerate and optimize the breeding process of crop plants. Therefore, a combination of different DNA-, RNA- and protein-based methods in combination with bioinformatics, optical and transgenic tools are employed.

Research Statement and Major Achievements

The generation of haploids is one of the most powerful means to accelerate the plant breeding process. To establish a genome elimination-based method for the generation of haploid sorghum and cowpea plants we characterized the CENH3 genes of both species for subsequent gene editing and identified centromeric repeats. Phylogenetic analysis revealed a CENH3 duplication event during the speciation of cowpea. Both CENH3 variants localize at different centromeric subdomains and differ in the expression dynamics.

To develop alternative strategies of uniparental genome elimination we focused on deciphering the mechanism of centromere assembly via the identification of CENH3 interactors like KNL2 in *A. thaliana*. Our study revealed a CENH3 nucleosome-binding CENPC-k motif at the C-terminus of KNL2 that is required for the centromeric localization of KNL2. It can be functionally replaced by the CENPC motif of CENP-C. KNL2 binds DNA sequence-independently *in vitro*, but *in vivo* it preferentially associates with centromeric repeats. In addition, the Aurora3 kinase activating domain of INCENP was characterized. INCENP showed a high specificity in the activation of Aurora3, but not of Aurora1. In addition an activation of Aurora1 by TPX proteins was found. However, the strongest activation revealed TPXL3. Additionally, epigenetic mutants are undergoing analysis as potential haploidy inducers in *A. thaliana*. In *Aegilops speltoides* a centromere-independent mechanism of chromosome elimination has been found. Supernumerary B chromosomes of this species undergo complete elimination

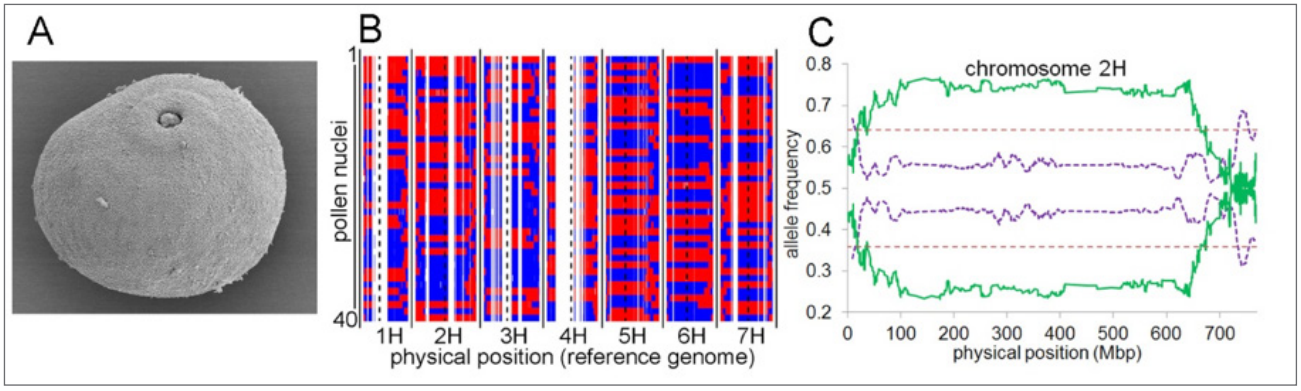

Fig. 26 Sequencing of single pollen nuclei reveals meiotic recombination events at megabase resolution and avoids segregation distortion caused by postmeiotic processes. (A) Single pollen. (B) Graphical genotypes of individual pollen nuclei revealed by single-cell genome sequencing. The two parental barley genotypes are shown in red ('Morex') and blue ('Barke'). Consensus genotypes were mapped to the physical reference genome of barley at 1 Mbp resolution. Centromere positions are indicated by dashed black lines. White gaps which consistently occur in all samples are regions where no genetic polymorphisms exist between 'Morex' and 'Barke'. (C) Segregation distortion is almost absent if measured in pollen but abundant in double haploid (DH) plants. Allele frequencies for 'Morex' and 'Barke' measured in pollen (dashed line in purple) and DH plants (straight line in green) are shown as 10 Mbp moving averages for chromosome 2H. Dashed red lines represent the significance threshold of distorted segregation ratios (χ^2-test, $P<0.05$) (S. Dreissig, J. Fuchs, A. Himmelbach, M. Mascher and A. Houben).

in roots during early embryogenesis (in cooperation with the RGs *ME*, *PRB*, *SZB*, *BIT* and external cooperation partners).

Meiotic recombination is a fundamental mechanism to generate novel allelic combinations which can be used by breeders to achieve crop improvement. A novel approach to directly investigate recombination at the DNA sequence level by combining flow-sorting of haploid pollen nuclei of barley with single-cell genome sequencing has been developed (Fig. 26). We confirm the skewed distribution of recombination events towards distal chromosomal regions and show that segregation distortion is almost absent if directly measured in pollen. The bimodal distribution of inter-crossover distances supports the existence of two classes of crossovers which are sensitive or insensitive to physical interference (in cooperation with the RGs *DG*, *GGR*).

Members of *Structural Maintenance of Chromosome* (SMC) complexes are cohesins, condensins and SMC5/6 complexes. The Arabidopsis CAP-D2 and CAP-D3 condensin subunits (confirmed by mass spectrometry analysis) are required for the arrangement of centromeric and 45S rDNA interphase chromatin. Comparative RNAseq analysis of cap-d3 mutants and wild-type plants demonstrated only minor alteration of the entire transcriptome. The Arabidopsis NSE4 components of the SMC5/6 complexes are involved in mitosis and meiosis to ensure plant viability and fertility (in cooperation with the RGs *SZB*, *NAM* and external cooperation partners).

The carnivorous genus Genlisea is characterized by an 25-fold genome size difference and an extreme genome plasticity. The 19 chromosome pairs of *G. margaretae* (184 Mbp/1C), could be distinguished individually by an approach combining optimized probe pooling and consecutive rounds of multicolor FISH with BACs selected for repeat-free inserts. The assigned BACs provide a tool for future investigations of karyotype evolution in the genus *Genlisea*. (in cooperation with the RGs *QG*, *GP* and external cooperation partners).

Holocentric chromosomes possess centromeres along the entire poleward chromatid surfaces. To test whether the organisation and regulation of mono- and holocentric chromosomes differ we characterised the distribution of alpha-kleisin, CENH3, histone marks and sister chromatid exchanges. While centromeric repeats reveal line-like signals at both chromatids, non-centromeric satellite DNAs form distinct clusters along the chromosomes. Thus, holocentricity influences the chromosomal organisation of centromeric and non-centromeric satDNA (in cooperation with the RGs *BIT*, *PAK* and external cooperation partners).

A novel imaging technique based on the CRISPR/Cas9 system has been developed for plants (see highlights). In addition, fluorescent labelling of in situ hybridisation probes through the copper-catalysed azide-alkyne cycloaddition reaction ('click-chemistry') was established (in cooperation with the RGs *SZB*, *BA* and external cooperation partners).

Embedding in Departmental and IPK Research Strategy

The projects of the research group *CSF* are part of the IPK research themes *Mechanisms of Plant Reproduction* and *Genome Diversity and Evolution*.

Plans, Opportunities and Challenges

The future application of light sheet microscopy will enable live imaging of chromatin dynamics in a tissue-specific context.

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Articles in Compilations

2016

SANDMANN, M., J. FUCHS & I. LERMONTOVA: Immunolabeling of nuclei/chromosomes in *Arabidopsis thaliana*. In: CAILLAUD, M.-C. (Ed.): Plant cell division: methods and protocols. (Series: Methods in Molecular Biology, Vol. 1370) New York [u.a.]: Humana Press (2016) 127-135.

2017

BADAEVA, E., A.S. RUBAN, L. ALIYEVA-SCHNORR, C. MUNICIO, S. HESSE & A. HOUBEN: In situ hybridisation to plant chromosomes. In: LIEHR, T. (Ed.): Fluorescence In Situ Hybridization (FISH): Application Guide, 2nd edition. Berlin Heidelberg: Springer (2017) 477-494.

ISHII, T.: Wide hybridization between oat and pearl millet. In: GASPARIS, S. (Ed.): Oat: methods and protocols. (Series: Methods in Molecular Biology, Vol. 1536) New York [u.a.]: Humana Press (2017) 31-42.

Other Papers

2016

SCHUBERT, V. & T. ISHII: *Hordeum vulgare*. (Calendar page). In: INAGA, S., M. NAKATA & K. TANIGUCHI (Eds.): Chromosome Calendar 2017. Japan: The Society of Chromosome Research (2016) 1.

2017

HESSE, S., M. ZELKOWSKI, T. ISHII, A. HOUBEN & V. SCHUBERT: *Secale cereale*. (Calendar page). In: INAGA, S., M. NAKATA & K. TANIGUCHI (Eds.): Chromosome Calendar 2018. Japan: The Society of Chromosome Research (2017) 1.

Theses

2016

ALIYEVA-SCHNORR, L.: Cytogenetic mapping of BAC contigs assigned to barley chromosome 3H and comparative subchromosomal analysis within the genus *Hordeum*. (PhD Thesis) Martin-Luther-Universität Halle-Wittenberg, Institut für Agrar- und Ernährungs-wissenschaften der Naturwissenschaftlichen Fakultät III, Halle/S. (2016) 65 pp.

JANKOWSKA, M.: Functional consequences of chromosome holocentricity. (PhD Thesis) Martin-Luther-Universität Halle-Wittenberg, Institut für Agrar- und Ernährungs-wissenschaften der Naturwissenschaftlichen Fakultät III, Halle/S. (2016) 120 pp.

VOGT, M.: Characterization of the centromere specific histone variant CENH3 in cowpea (*Vigna unguiculata* L.) and sorghum (*Sorghum bicolor* L.). (Master Thesis) Martin-Luther-Universität Halle-Wittenberg, Institut für Agrar- und Ernährungswissenschaften der Naturwissenschaftlichen Fakultät III, Halle/S. (2016) 67 pp.

2017

MA, W.: Analysis of two exceptional chromosome-types in plants. (PhD Thesis) Martin-Luther-Universität Halle-Wittenberg, Institut für Agrar- und Ernährungswissenschaften der Naturwissenschaftlichen Fakultät III, Halle/S. (2017) 93 pp.

MESSMER, G.: Charakterisierung der Condensine in *Arabidopsis thaliana* und *Nicotiana benthamiana*. (Bachelor Thesis) Universität Regensburg, Fakultät für Biologie und Vorklinische Medizin, Lehrstuhl für Zellbiologie und Pflanzenbiochemie, Regensburg (2017) 58 pp.

PTOSKOVA, K.: Regulation of Aurora kinase 1 by members of TPX2 family in *Arabidopsis thaliana*. (Master Thesis) Palacký University Olomouc, Faculty of Science Departament of Cell Biology and Genetics, Olomouc, Czech Republic (2017) 68 pp.

Patents

2016

HOUBEN, A., R. KARIMI ASHTIYANI, T. ISHII, N. STEIN & J. KUMLEHN: Generation of haploid plants. (Industrieanmeldung), Veröffentlichung: 03.03.2016, IPK-Nr. 2014/01. EP 14182719.6 (2016).

2017

LERMONTOVA, I.: Generation of haploid plants based on KNL 2. (IPK-Anmeldung), Veröffentlichung: 27.04.2017, IPK-Nr. 2015/01. WO2017/067714 (2017).

Research Group: Apomixis (APM)

Head: Prof. Dr. Jochen C. Reif (temp. until 31.05.2017)

Scientists

Dr. Jonathan Brassac

Stefanie Hilpert

Dr. Martin Mau

Dr. Lars-Gernot Otto

Dr. Paride Rizzo

Prof. Dr. Timothy f. Sharbel

Keywords

APOLLO

Apomixis

Muller´s Ratchet

UPGRADE-2

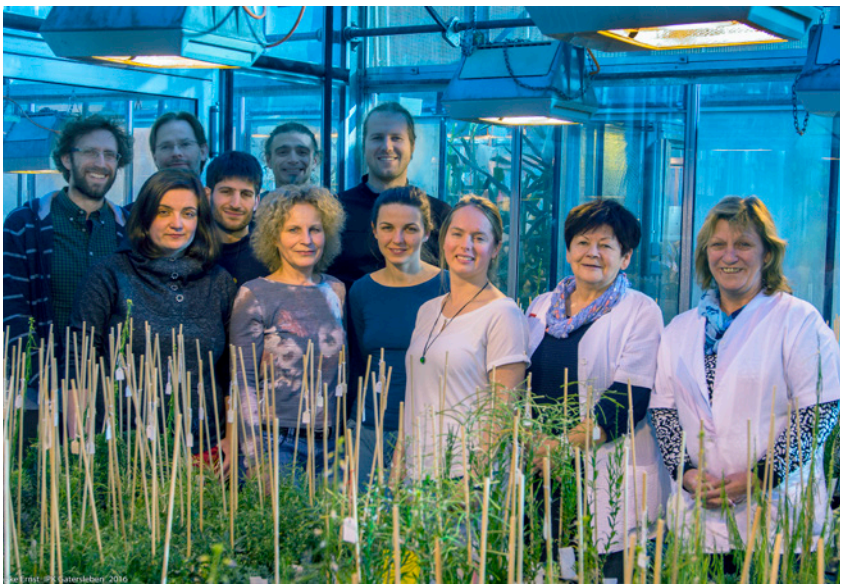
Ploidy Variation

Highlights

Molecular study in Boechera revealed that asexual individuals harbor many more DNA mutations than sexual individuals, which is an explanation why sexual reproduction dominate among multicellular organisms (PLoS Genet. 13 (2017) e1006550).

Funding

DFG, Industry (Virgin Plants International), BMEL/FNR



***Boechera*, *Hypericum perforatum*, the *Ranunculus auricomus* complex, and *Poa pratensis* are all characterised by naturally occurring sexual and apomictic members. Based on comparisons of expression profiles of reproductive tissues between sexual and apomictic plants, we identified the candidate apomixis factors APOLLO and UPGRADE2. Both genes are currently functionally characterised in Boechera, Arabidopsis, Brassica and maize.**

Research Statement and Major Achievements

The focus of the *Apomixis* research group is the evolution of naturally occurring asexual seed production in plants (apomixis), and the group specializes in population genetics and evolution, high-throughput phenotyping, various *omics* methods (NGS, microarray expression profiling, CGH, miRNA analyses), and functional genetics. Asexual plants are naturally occurring and are typically hybrid and polyploid; thus, our research includes the cause and effect aspects of these phenomena on asexuality. The relative success of sexual versus asexual reproduction reflects an evolutionary puzzle which has long challenged biologists, and our applied work on apomixis has enabled us to delve relatively deeply into some of these evolutionary hypotheses, both in wild populations and in the lab.

Apomixis is often associated with polyploidy, hybridization and genomic instability. Therefore, we also investigate these phenomenons. Dealing frequently with questions of ploidy variation and (male) sterility, the methodological pipeline from our apomixis research was applied to generate the prerequisites for the development of a sterile chamomile variety (*Matricaria recutita* L.). Similar to sterile triploid fruit and ornamental crops, seeds are neither needed nor – due to contamination with the soil for many years – desired in chamomile cultivation. The genetic diversity within cultivated chamomile was analysed with Genotyping-by-Sequencing as basis for our future work (Fig. 27). Several approaches to manipulate plant reproduction are investigated (i.e. genic male sterility, cytoplasmic male sterility, self-incompatibility), such that selfing is inhibited and outcrossing is propagated.

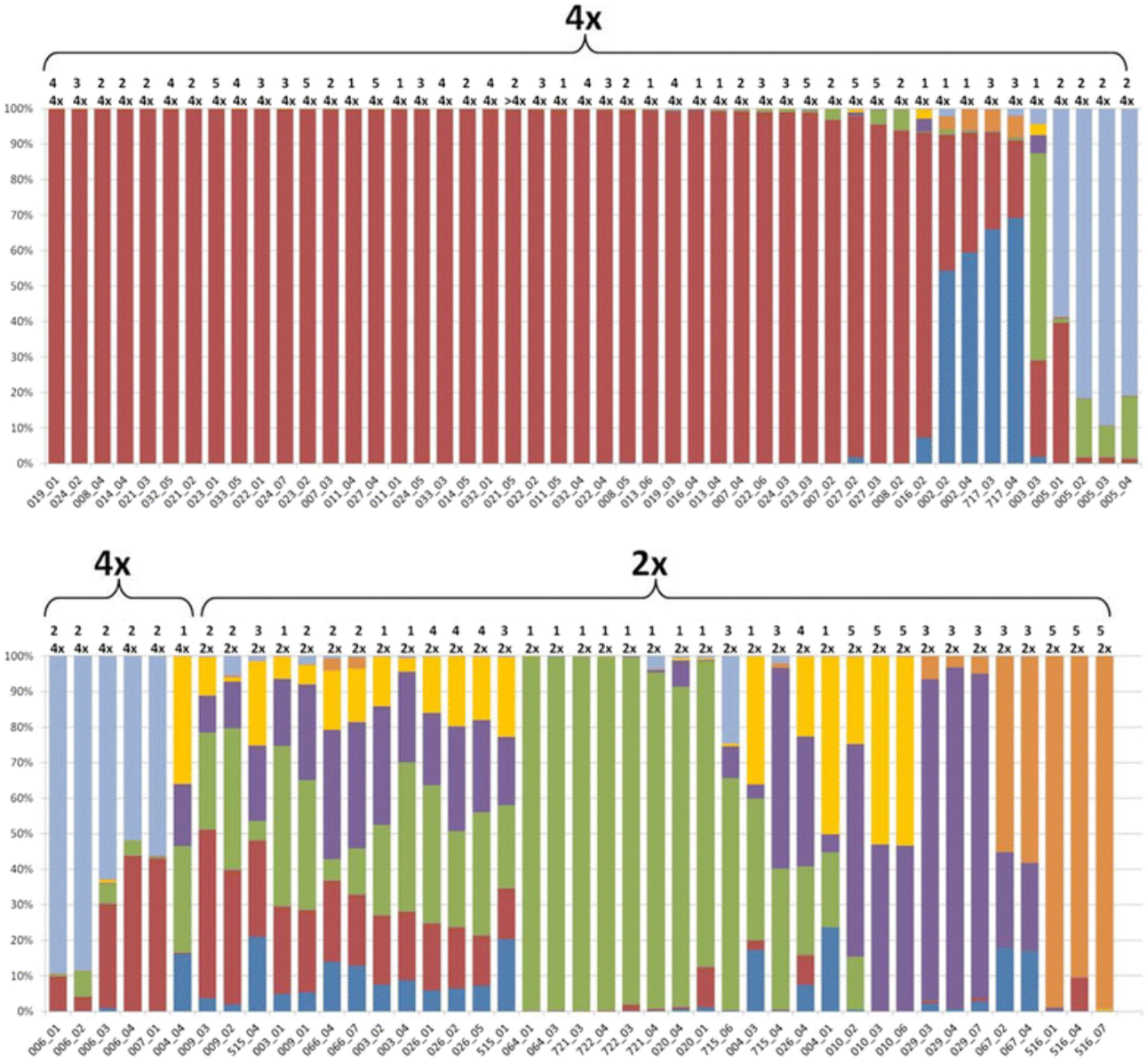


Fig. 27 STRUCTURE analysis (k = 7) for *Matricaria recutita* L., with data for geographic origin and ploidy (both upper rows). The barplot is organized according to the ploidy. The genotypes are represented by the vertical bars, whereas the different colours indicate the seven genetic clusters.

Asexual plants should be less adapted than sexual plants, as apomictic (*i.e.* asexual) reproduction should be accompanied by a gradual accumulation of mutations, some of which would be deleterious to the plant. We have designed a sequence capture experiment whereby approx. 500 KB of sequence around the candidate apomixis APOLLO gene are being captured and sequenced using long sequencing methods (e.g. 11 KB reads). This region will be compared between many populations of *Boechera*, and closely related species. Much as an analysis of copy number variation in candidate cancer factors, this project will enable us to identify the "absolute minimal requirement" of *Boechera* genome which is required to induce apomixis.

Embedding in Departmental and IPK Research Strategy

The Apomixis group integrates itself in the research of the department and of the IPK by unraveling the differences between sexual and apomictic reproduction, i.e. investigating the mechanism of plant reproduction. Moreover, the aspects of genome-diversity and evolution leading to the different pathways of plant reproduction are examined.

Plans, Opportunities and Challenges

The group of Apomixis has been closed down since June 2017.

Peer Reviewed Papers

2016

RÓIS, A.S., F. SADIO, O.S. PAULO, G. TEIXEIRA, A.P. PAES, D. ESPÍRITO-SANTO, T.F. SHARBEL & A.D. CAPERTA: Phylogeography and modes of reproduction in diploid and tetraploid halophytes of *Limonium* species (Plumbaginaceae): evidence for a pattern of geographical parthenogenesis. Ann. Bot. 117 (2016) 37-50.

VALVERDE, J., J.M. GOMEZ, C. GARCIA, T.F. SHARBEL, M.N. JIMENEZ & F. PERFECTTI: Inter-annual maintenance of the fine-scale genetic structure in a biennial plant. Sci. Rep. 6 (2016) 37712.

2017

GALLA, G., S. ZENONI, L. AVESANI, L. ALTSCHMIED, P. RIZZO, T.F. SHARBEL & G. BARCACCIA: Pistil transcriptome analysis to disclose genes and gene products related to Aposporous apomixis in *Hypericum perforatum* L. Front. Plant Sci. 8 (2017) 79.

LOVELL, J.T., R.J. WILLIAMSON, S.I. WRIGHT, J.K. MCKAY & T.F. SHARBEL: Mutation accumulation in an asexual relative of Arabidopsis. PLoS Genet. 13 (2017) e1006550.

NAVARRO-DOMÍNGUEZ, B., F.J. RUIZ-RUANO, J. CABRERO, J.M. CORRAL, M.D. LÓPEZ-LEÓN, T.F. SHARBEL & J.P. CAMACHO: Protein-coding genes in B chromosomes of the grasshopper *Eyprepocnemis plorans*. Sci. Rep. 7 (2017) 45200.

OTTO, L.-G., P. MONDAL, J. BRASSAC, S. PREISS, J. DEGENHARDT, S. HE, J.C. REIF & T.F. SHARBEL: Use of GBS to determine the genetic structure in the medicinal plant chamomile, and to identify flowering time and alpha-bisabolol associated SNP-loci by GWAS. BMC Genomics 18 (2017) 599.

ŠARHANOVÁ, P., T.F. SHARBEL, M. SOCHOR, R.J. VAŠUT, M. DANČÁK & B. TRÁVNÍČEK: Hybridization drives evolution of apomicts in *Rubus* subgenus *Rubus* - evidence from microsatellite markers. Ann. Bot. 120 (2017) 317-328.

SCHERIAU, C.L., N.M. NUERK, T.F. SHARBEL & M.A. KOCH: Cryptic gene pools in the *Hypericum perforatum-H. maculatum* complex: diploid persistence versus trapped polyploid melting. Ann. Bot. 120 (2017) 955-966.

TEDESCHI, F., P. RIZZO, T. RUTTEN, L. ALTSCHMIED & H. BÄUMLEIN: RWP-RK domain-containing transcription factors control cell differentiation during female gametophyte development in Arabidopsis. New Phytol. 213 (2017) 1909-1924.

Theses

2016

RIZZO, P.: Novel insights on female gametophyte development in the apomictic model species *Boechera* spp. and *Hypericum* spp. (PhD Thesis) Martin-Luther-Universität Halle-Wittenberg, Naturwissenschaftliche Fakultät I Biowissenschaften, Halle/S. (2016) 182 pp.

2017

MILKER, S.: Untersuchung von männlicher Sterilität und Selbstinkompatibilität bei *Matricaria chamomilla* L. zur Bestäubungslenkung. (Bachelor Thesis) Ernst-Abbe-Hochschule Jena, Fachbereich Medizintechnik und Biotechnologie, Studiengang Biotechnologie, Jena (2017) 56 pp.

Research Group: Pathogen Stress Genomics (PSG)

Head: Dr. habil. Patrick Schweizer

Scientists

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Dr. Daniela Nowara

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Hassan Razzak

Karolina Slominska

Keywords

Plant-Pathogen Interactions

Durable Crop-Plant Resistance

Nonhost Resistance

Resistance-Associated Gene Haplotypes

Resistance Engineering

Highlights

BMBF funds research on exploiting wheat genetic resources: PSG contributes with precision phenotyping of disease resistance by using the DPPN-PATHO pipeline.

New candidate genes for disease resistance in barley and wheat validated (New Phytologist 212: 421-433; Frontiers in Plant Science 7: article 1836).

Extended range of potential application of RNA-mediated plant defense to Fusarium sp. attacking wheat (J. Exp. Botany 67: 4979-4991).

Funding

BMBF, DFG, EU (H2020: Marie S. Curie)

The research of the group focuses on functional genomics approaches for durable resistance of barley and wheat against important fungal pathogens. By using precise disease phenotyping, (high-throughput) *gene silencing*, transcript profiling, and allele mining gene discovery is achieved, followed by validation via transient allele expression and allele-introgression by backcrossing.

Research Statement and Major Achievements

Two projects are aiming at the identification of genes in barley with significant association of single nucleotide polymorphisms (SNP) or gene haplotypes to the degree of quantitative resistance against the powdery mildew (PM) fungus *Blumeria graminis*. For this, PM infection was quantified in a detached leaf assay, and adjusted entry means were used for association-genetic analysis of SNP and indel data from Exome Capture re-sequencing of diverse populations of barley. This was done in parallel in a European barley collection (ClimBar project) as well as in a worldwide legacy collection of barley (project WHEALBI). The genome-wide association scans (GWAS) were performed in close collaboration with RG *QG*. A number of resistance QTL were identified containing all together more than 1,000 significantly associated markers. Of special interest are prominent QTL (GWAS peaks) on chromosomes 2H and 5H. From these peaks a number of candidate genes were identified, and allele mining as well as gene-haplotype association with the trait “PM resistance” is being performed. Potentially superior alleles will be cloned from corresponding genotypes and used for transient expression experiments, comparing two or more alleles per candidate gene.

Another project is aiming at a better understanding and eventually utilizing RNA-based defense of wheat and barley against the fungal pathogens *B. graminis* and *Fusarium culmorum/graminearum*. There is accumulating evidence that the phenomenon known as Host-Induced Gene Silencing (HIGS) is reflecting a natural defense mechanism, which may be based on miRNA genes. Transient silencing by the barley stripe mosaic virus BSMV of putative target genes of naturally accumulating small RNAs

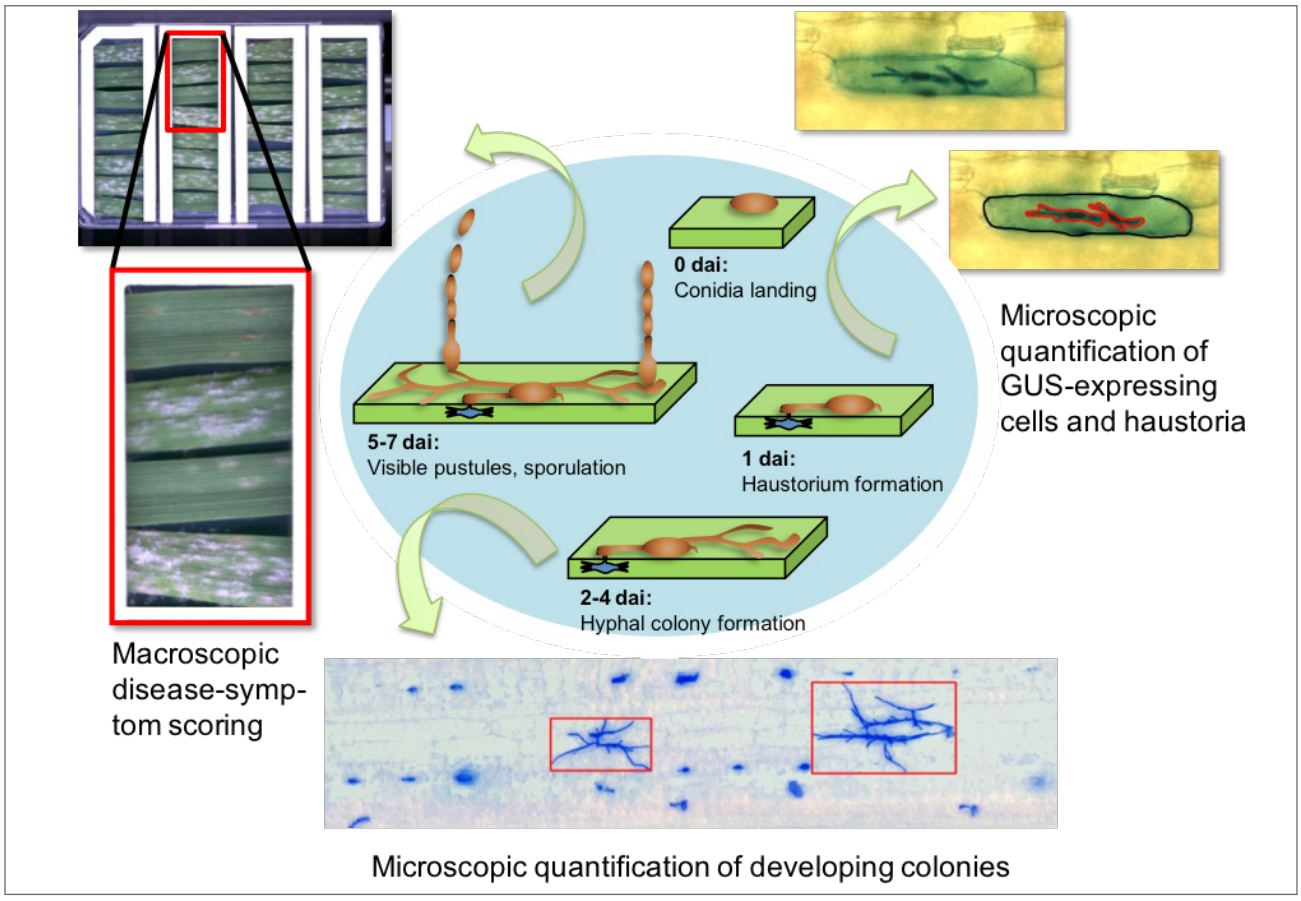

Fig. 28 Micro- and macrophenomics platform and BluVision analysis of cereal-pathogen interactions at the example of the powdery mildew fungus *Blumeria graminis*.
To assess early interactions, initial haustorium (feeding cell) formation in transformed GUS-expressing epidermal cells of barley or wheat is quantified 1 day after inoculation (dai) under the microscope. For the characterization of intermediate stages of infection, the numbers and microscopic sizes of early developing colonies are determined at 2-3 dai. Final disease- and stress symptoms are scored automatically 5-7 dai and expressed as percentage of pustule- or spot-covered leaf area.

of wheat are in progress and revealed trends for enhanced resistance against *F. culmorum*.

By using BSMV-mediated silencing we also functionally address a number of candidate genes that are transcriptionally regulated by the major QTL for *Fusarium sp.* resistance in wheat on chromosome 3BS (*Fhb1*). At least two candidates revealed a phenotypic effect, which is currently under validation by using more specific RNAi constructs that have no potential off-targets in homeologs or close paralogs.

Finally a large-scale phenotying project has started (as part of project Genebank 2.0), which is utilizing the phenomics pipeline developed in the *German Plant Phenotyping Network* (DPPN). Here the main focus lies on assessment of *Fusarium* head-blight resistance in winter wheat accessions. To allow the required throughput and reproducibility for the screen, a plate based bioassay with germinating wheat seed was developed, but still needs more extensive testing for comparability to spike-infection data and for reproducibility.

Activities related to software development for phenotying of plant-pathogen interactions resulted in a prototype platform BluVision for PM (Fig. 28). Provided the automated segmentation of PM haustoria will finally also be implemented, we could provide a fully automated platform for all relevant stages of the interaction of PM with cereal hosts.

Embedding in Departmental and IPK Research Strategy

The identification of genes and alleles for traits of moderate complexity such as quantitative disease resistance is a central objective of the *Breeding Research* department. The research of the RG *PSG* contributes mainly to the Research theme 5 *Mechanisms of Resistance and Stress Tolerance*.

Plans, Opportunities and Challenges

We plan to further validate genes in barley, which contribute to disease resistance, with a major emphasis on superior alleles of host susceptibility factors. We also aim at a better understanding of the function of antifungal, double-stranded RNAs in host-plant engineering and in natural resistance.

Peer Reviewed Papers

2016

CHEN, W., C. KASTNER, D. NOWARA, E. OLIVEIRA-GARCIA, T. RUTTEN, Y. ZHAO, H.B. DEISING, J. KUMLEHN & P. SCHWEIZER: Host-induced silencing of *Fusarium culmorum* genes protects wheat from infection. J. Exp. Bot. 67 (2016) 4979-4991.

CHOWDHURY, J., M.S. SCHOBER, N.J. SHIRLEY, R.R. SINGH, A.K. JACOBS, D. DOUCHKOV, P. SCHWEIZER, G.B. FINCHER, R.A. BURTON & A. LITTLE: Down-regulation of the *glucan synthase-like 6 gene* (*HvGsl6*) in barley leads to decreased callose accumulation and increased cell wall penetration by *Blumeria graminis* f. sp. *hordei*. New Phytol. 212 (2016) 434-443.

DOUCHKOV, D., S. LUECK, G. HENSEL, J. KUMLEHN, J. RAJARAMAN, A. JOHRDE, M.S. DOBLIN, C.T. BEAHAN, M. KOPISCHKE, R. FUCHS, V. LIPKA, R.E. NIKS, V. BULONE, J. CHOWDHURY, A. LITTLE, R.A. BURTON, A. BACIC, G.B. FINCHER & P. SCHWEIZER: The barley (*Hordeum vulgare*) cellulose synthase-like D2 gene (*HvCslD2*) mediates penetration resistance to host-adapted and nonhost isolates of the powdery mildew fungus. New Phytol. 212 (2016) 421-433.

GE, X., W. DENG, Z.Z. LEE, F.J. LOPEZ-RUIZ, P. SCHWEIZER & S.R. ELLWOOD: Tempered *mlo* broad-spectrum resistance to barley powdery mildew in an Ethiopian landrace. Sci. Rep. 6 (2016) 29558.

GHAFFARI, M.R., M. GHABOOLI, B. KHATABI, M.-R. HAJIREZAEI, P. SCHWEIZER & G.H. SALEKDEH: Metabolic and transcriptional response of central metabolism affected by root endophytic fungus *Piriformospora indica* under salinity in barley. Plant Mol. Biol. 90 (2016) 699-717.

RAJARAMAN, J., D. DOUCHKOV, G. HENSEL, F. STEFANATO, A. GORDON, N. EREFUL, O. CALDARARU, A.-J. PETRESCU, J. KUMLEHN, L. BOYD & P. SCHWEIZER: An LRR/malectin receptor-like kinase mediates resistance to non-adapted and adapted powdery mildew fungi in barley and wheat. Front. Plant Sci. 7 (2016) 1836.

2017

CHOWDHURY, J., S. LÜCK, J. RAJARAMAN, D. DOUCHKOV, N.J. SHIRLEY, J.G. SCHWERDT, P. SCHWEIZER, G.B. FINCHER, R.A. BURTON & A. LITTLE: Altered expression of genes implicated in xylan biosynthesis affects penetration resistance against powdery mildew. Front. Plant Sci. 8 (2017) 445.

DELVENTHAL, R.*, J. RAJARAMAN*, F.L. STEFANATO, S. REHMAN, R. AGHNOUM, G.R.D. MCGRANN, M. BOLGER, B. USADEL, P.E. HEDLEY, L. BOYD, R.E. NIKS, P. SCHWEIZER & U. SCHAFFRATH: A comparative analysis of nonhost resistance across the two *Triticeae* crop species wheat and barley. BMC Plant Biol. 17 (2017) 232. (*joint first authorship)

Other Papers

2016

SCHWEIZER, P.: Die Waffen der Pflanzen. Ackerbautag Frankfurter Landw. Verein e.V. 42 (2016) 26-29.

Theses

2016

RAJARAMAN, J.: Discovery and validation of genes for quantitative host- and nonhost-resistance in barley and wheat to powdery mildew attack. (PhD Thesis) Martin-Luther-Universität Halle-Wittenberg, Institut für Agrar- und Ernährungswissenschaften der Naturwissenschaftlichen Fakultät III, Halle/S. (2016) 193 pp.

Research Group: Gene and Genome Mapping (GGK)

Head: Dr. Marion S. Röder

Scientists

Dalia Alomari

Quddoos ul Haq Muqaddasi

Dr. Christine Zanke

Keywords

Genome-Wide Association Mapping

Validation of Quantitative Trait Loci

Linking Genetic with Physical Map

Identification of Candidate Genes

Highlights

Collaboration with Bayer for the map-based cloning of a gene controlling thousand-grain weight in wheat including the licensing of near isogenic wheat lines.

Disentangling pleiotropic and close linkage for yield and yield components in wheat (Journal of Experimental Botany 68:4089-4101).

Genome-wide analysis in genetic resources of wheat revealed complex genetic architecture of anther extrusion (Frontiers Plant Sci 8:754).

Candidate gene identified for eyespot resistance in wheat (Theor Appl Genet 130:505-514).

GABI WHEAT and VALID populations are successfully used in trans-departmental collaboration projects (New Phytologist 214:257-270).

Funding

BMBF, DAAD, Industry (Bayer Crop Science)

The general goal is the exploitation of the natural genetic diversity in plants for the identification, genetic mapping and cloning of genes for agronomically important traits in cereals. The current project phase mainly served to establish the relationship between various agronomic traits and a new generation of molecular markers. The marker-trait associations will be used for knowledge-based improvement of wheat varieties but also to identify underlying causal genes.

Research Statement and Major Achievements

Genetic analysis of anther extrusion in wheat: Anther extrusion is an important trait for the male parent during hybrid seed production in wheat. We started to investigate this trait in various variety panels of spring and winter wheat consisting of genetic resources from the gene bank (in collaboration with the RG *RGR*) and elite germplasm. Initial analysis of marker-trait associations confirmed the presence of several QTL loci for anther extrusion. The link to the genome zipper and preliminary genome sequence of wheat allowed the identification of genomic regions harbouring potential genes for this trait. Moreover, in collaboration with the RG *QG* a select-and-backcross method is implemented in order to identify major genes for anther extrusion using a large panel of wheat genetic resources.

Genetic analysis of eyespot resistance in wheat: Genome-wide analysis of eyespot, a fungal disease of wheat, confirmed gene Pch1 as major resistance source. This gene was introduced to wheat by a translocation from the wild species *Triticum ventricosum*. By applying a high density chip of novel molecular SNP-markers we were able to define recombination events in the original translocated genome segment of *T. ventricosum* in various varieties (Fig. 29) which allowed a fine mapping of the gene. The link to the genome zipper and preliminary genome sequence of wheat yielded a defined genomic region with a potential candidate gene for *Pch1*.

Marker		Lynx	Intérêt	Musketeer	Manager	Bueno	Format	Renan	Tritis	Piko	PR 22 R 28	Sankara	Limes	Azimut	Allister	Oratorio	Zobel	Hermann	Intense	Kosack	Consort
AX-94810080	35K	A	A	A	A	A	A	A	A	-	-	G	G	G	G	G	G	G	G	G	G
D_GBUVHFX02F4VT5_101	90K	T	T	T	T	T	T	T	T	-	-	C	C	C	C	C	C	C	C	C	C
Kukri_rep_c82239_85	90K	A	A	A	A	A	A	A	A	A	-	G	G	G	G	G	G	G	G	G	G
AX-94484239	35K	G	G	G	G	G	G	G	G	G	-	A	A	A	A	A	A	A	A	A	A
GENE-4717_482	90K	G	G	G	G	G	G	G	G	G	-	T	T	T	T	T	T	T	T	T	T
D_contig18045_60	90K	G	G	G	G	G	G	G	G	G	G	A	A	A	A	A	A	A	A	A	A
GENE-4288_261	90K	G	G	G	G	G	G	G	G	G	-	G	G	A	A	A	A	A	A	A	A
AX-94625988	35K	G	G	G	G	G	G	G	G	G	G	G	G	C	C	C	C	C	C	C	C
AX-158521727	135K	C	C	C	-	C	C	C	C	C	C	C	C	C	C	C	C	A	A	A	A
AX-158568141	135K	C	C	C	-	C	C	C	C	C	C	C	C	C	C	C	C	A	A	A	A
AX-158594018	135K	A	A	A	-	A	A	A	A	A	A	A	A	A	A	A	A	G	G	G	G
AX-94622337	35K	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	T	T	T	T
BobWhite_rep_c52163_55	90K	C	C	C	C	C	C	C	C	-	C	C	C	C	C	C	C	T	T	T	T
Ep-D1b-7D (resistant)	cand	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	0	0	0	0
BS00096025_51*	90K	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	T	T	C
BS00096024_51*	90K	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	T	T	C
BS00079734_51*	90K	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	T	T	C
BS00021745_51*	90K	G	G	G	G	G	G	G	G	G	G	G	G	G	G	G	G	G	A	A	G
Kukri_rep_c105287_311*	90K	C	C	C	C	C	C	C	C	C	C	C	C	-	C	C	C	T	T	T	C
AX-94663462*	35K	G	G	G	G	G	G	G	G	G	G	G	G	G	G	G	G	G	A	A	G
AX-95024837*	35K	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	T	T	C
AX-94816466	35K	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	T	T	T
AX-94799158	35K	C	C	C	C	C	C	C	C	C	-	C	C	C	C	C	C	C	A	A	A
AX-94428861	35K	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	G	G	G
AX-158593991	135K	A	A	A	-	-	A	A	A	A	-	-	-	A	A	A	A	A	G	G	G
AX-158601616	135K	-	T	T	-	T	-	T	T	T	T	T	T	T	T	T	T	T	G	G	G
AX-158554596	135K	T	T	T	-	T	T	T	T	T	T	T	T	T	T	-	T	C	C	C	C
AX-158593993	135K	-	A	A	-	A	A	A	-	A	A	A	A	A	A	A	A	G	G	G	G
AX-158553795	135K	-	G	G	-	G	G	G	-	G	G	G	G	G	G	G	G	A	A	A	A
AX-158620130	135K	T	T	T	-	T	-	T	-	T	T	T	T	T	-	T	T	G	G	G	G
AX-95076896	135K	C	C	C	-	C	C	C	C	-	C	C	-	C	C	C	C	T	T	T	T
AX-158568137	135K	T	T	-	-	T	T	T	T	T	T	T	T	T	T	T	T	C	C	C	C
AX-158554604	135K	A	A	-	-	A	A	A	A	A	A	A	A	A	A	A	A	C	C	C	C
AX-158590121	135K	G	G	G	-	G	-	G	G	G	G	G	G	G	G	G	G	A	-	A	A
AX-158568140	135K	T	T	T	-	T	-	T	T	T	T	T	T	T	T	T	T	G	G	G	G
AX-158541394	135K	G	G	G	-	-	G	G	G	G	G	G	G	G	G	G	G	T	T	T	T
AX-158594021	135K	A	A	A	-	A	A	A	-	A	A	A	A	A	A	A	A	G	G	G	G
AX-158554718	135K	A	A	A	-	A	A	A	A	A	A	A	A	A	A	A	A	G	G	G	G
AX-158594056	135K	T	T	T	-	T	T	T	-	T	T	T	T	T	T	T	T	C	C	C	C
AX-158578004	135K	C	C	C	-	C	C	C	C	C	C	C	C	C	C	C	C	A	A	A	A
AX-158554602	135K	T	T	T	-	T	T	T	T	T	T	T	T	T	T	T	T	C	C	C	C
AX-158589622	135K	C	C	C	-	C	C	C	C	C	C	C	C	C	C	C	C	T	T	T	T
AX-158554605	135K	T	T	T	-	T	T	T	T	T	T	T	T	T	T	T	T	G	G	G	G
AX-158554616	135K	A	A	A	-	A	A	A	A	A	A	A	A	A	A	A	A	C	C	C	C
AX-94638691	35K	C	C	C	C	C	C	C	C	C	-	C	C	C	C	C	C	T	T	T	T
AX-94405923	35K	A	A	A	A	A	A	A	A	A	-	A	A	A	A	A	A	G	G	G	G
AX-109506502	135K	-	G	-	-	G	-	G	G	G	G	G	G	G	G	G	G	-	G	T	T
AX-158593989	135K	C	C	C	-	C	C	C	-	C	-	-	C	C	-	C	C	-	C	T	-
AX-109521244	135K	T	T	-	-	T	T	-	-	-	T	T	T	T	T	T	T	-	T	C	C
AX-158544274	135K	G	G	-	-	G	G	G	G	G	G	G	G	G	G	G	G	G	G	T	T
AX-158554588	135K	C	C	-	-	C	C	C	C	C	C	C	C	C	C	C	C	C	C	T	T
AX-158554568	135K	-	G	G	-	G	G	G	G	G	G	G	G	G	G	G	G	G	G	-	A
AX-158554614	135K	-	A	A	-	A	A	A	A	A	A	A	A	A	A	A	A	A	A	C	C
AX-158624950	135K	T	T	T	-	T	T	T	T	T	T	T	T	T	T	-	T	T	T	C	-
AX-158577385	135K	G	G	G	-	G	G	G	G	G	G	G	G	G	G	-	G	G	G	A	A
AX-158554577	135K	T	T	-	-	T	T	T	T	T	T	T	T	T	T	T	T	T	T	G	G
AX-158594050	135K	T	T	T	-	T	T	T	T	T	T	T	T	T	T	T	T	T	T	G	G
AX-158532241	135K	G	G	G	-	G	G	G	G	G	G	G	G	G	G	G	G	G	G	T	T
AX-158594017	135K	A	A	A	-	A	A	A	A	A	A	A	A	A	A	A	A	A	A	G	G
AX-158594118	135K	C	C	C	-	C	C	C	C	C	C	C	C	C	C	C	C	C	C	T	T
AX-158568139	135K	G	G	G	-	G	G	G	G	G	G	G	G	G	G	G	G	G	G	A	A
AX-158544191	135K	A	A	A	-	A	A	A	A	A	A	A	A	A	A	A	A	A	A	G	G
AX-94707847*	35K	G	G	G	G	G	G	G	G	G	G	G	G	G	G	G	G	G	G	C	C
AX-95247409*	35K	C	C	C	-	C	C	C	C	C	-	C	C	C	C	C	C	C	C	T	T
AX-94505889	35K	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	G	G
AX-94813468	35K	A	A	A	A	A	A	-	A	A	A	A	A	A	G	A	A	A	A	G	G
AX-95099642	35K	G	G	G	G	G	G	G	G	G	G	G	G	G	G	G	G	G	G	A	A
AX-94525717	35K	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	G	G
WMS4526_null	SSR	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	0	0
orw6_167bp	cand	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	0	0
orw1_183bp	cand	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	0	0
EY_BLUEs		2	2	2	2	2	2	2	3	2	2	2	2	1	2	2	2	2	2	3	4

Fig. 29 Genotypes with the *Triticum ventricosum*-introgression on chromosome 7DL (in dark green). The genotypes are sorted according to the length of the *Triticum ventricosum* –introgression (marked in ocker). Markers co-segregating with Pch1 are marked in yellow.

Genetic analysis of mineral content of wheat grains: In collaboration with the RG *MPE* we started to analyse the contents of micro- and macronutrients in wheat grains of a panel of winter wheat varieties. Genome-wide association mapping focused on Fe, Zn and Ca contents and yielded a number of stable QTL. By linking to the genome zipper and preliminary wheat sequence we were able to define the respective genomic regions and identify potential candidate genes.

Embedding in Departmental and IPK Research Strategy

The studies on the genetic architecture of important agronomic traits are central for the research strategy of the department of *Breeding Research*. The studies on anther extrusion and mineral element content of wheat grains contributed to Research theme 1 *Concepts for the Valorization of Plant Genetic Resources*.

Plans, Opportunities and Challenges

The goal is to (1) validate QTL mentioned in this report and from previous activities, to (2) apply the further improved genomic tools (i.e. genomic wheat sequence) to identify physical genomic regions with the ultimate goal to (3) identify candidate genes for the traits of interest. The challenge will be to verify the identified candidate genes.

Peer Reviewed Papers

2016

KUMAR, S., M.S. RÖDER, R.P. SINGH, S. KUMAR, R. CHAND, A.K. JOSHI & U. KUMAR: Mapping of spot blotch disease resistance using NDVI as a substitute to visual observation in wheat (*Triticum aestivum* L.). Mol. Breed. 36 (2016) 95.

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MUQADDASI, Q.H., U. LOHWASSER, M. NAGEL, A. BÖRNER, K. PILLEN & M.S. RÖDER: Genome-wide association mapping of anther extrusion in hexaploid spring wheat. PLoS One 11 (2016) e0155494.

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JIANG, Y., A.W. SCHULTHESS, B. RODEMANN, J. LING, J. PLIESKE, S. KOLLERS, E. EBMEYER, V. KORZUN, O. ARGILLIER, G. STIEWE, M.W. GANAL, M.S. RÖDER & J.C. REIF: Validating the prediction accuracies of marker-assisted and genomic selection of Fusarium head blight resistance in wheat using an independent sample. Theor. Appl. Genet. 130 (2017) 471-482.

MUQADDASI, Q.H., J. BRASSAC, A. BÖRNER, K. PILLEN & M.S. RÖDER: Genetic architecture of anther extrusion in spring and winter wheat. Front. Plant Sci. 8 (2017) 754.

MUQADDASI, Q.H., K. PILLEN, J. PLIESKE, M.W. GANAL & M.S. RÖDER: Genetic and physical mapping of anther extrusion in elite European winter wheat. PLoS One 12 (2017) e0187744.

MUQADDASI, Q.H., J.C. REIF, Z. LI, B.R. BASNET, S. DREISIGACKER & M.S. RÖDER: Genome-wide association mapping and genome-wide prediction of anther extrusion in CIMMYT spring wheat. Euphytica 213 (2017) 73.

SCHULTHESS, A.W., J.C. REIF, J. LING, J. PLIESKE, S. KOLLERS, E. EBMEYER, V. KORZUN, O. ARGILLIER, G. STIEWE, M.W. GANAL, M.S. RÖDER & Y. JIANG: The roles of pleiotropy and close linkage as revealed by association mapping of yield and correlated traits of wheat (*Triticum aestivum* L.). J. Exp. Bot. 68 (2017) 4089-4101.

ZANKE, C.D., B. RODEMANN, J. LING, Q.H. MUQADDASI, J. PLIESKE, A. POLLEY, S. KOLLERS, E. EBMEYER, V. KORZUN, O. ARGILLIER, G. STIEWE, T. ZSCHÄCKEL, M.W. GANAL & M.S. RÖDER: Genome-wide association mapping of resistance to eyespot disease (*Pseudocercosporella herpotrichoides*) in European winter wheat (*Triticum aestivum* L.) and fine-mapping of *Pch1*. Theor. Appl. Genet. 130 (2017) 505-514.

Articles in Compilations

2016

BÖRNER, A., A.J. WORLAND, C.N. LAW, V. KORZUN, E.K. KHLESTKINA, T.A. PSHENICHNIKOVA, S. CHEBOTAR, S. LANDJEVA, B. KOBILJSKI, E. PESTSOVA, S.V. OSIPOVA, A.F. BALINT, A. GIURA, K. KOWALCZYK, M. AGACKA-MOLDOCH, M.R. SIMON, A.M. CASTRO, Y. CHESNOKOV, N. TIKHENKO, M.A. REHMAN ARIF, M. NAGEL, K. NEUMANN, S. NAVAKODE, U. LOHWASSER & M.S. RÖDER: EWAC – the past 25 years (1991-2015). In: BÖRNER, A. & K. KOWALCZYK (Eds.): Proceedings of the 16th International EWAC Conference, 24 - 29 May 2015, Lublin, Poland. (Series: European Wheat Aneuploid Co-operative newsletter, Vol. 16) Gatersleben: Leibniz-Institut für Pflanzengenetik und Kulturpflanzenforschung (2016) 15-26.

2017

ZANKE, C., J. LING, J. PLIESKE, S. KOLLERS, E. EBMEYER, O. ARGILLIER, G. STIEWE, M. HINZE, S. BEIER, M.W. GANAL & M.S. RÖDER: Genetic architecture of main effect QTL for heading date in European winter wheat. In: JUNG, C., K. PILLEN, D. STAIGER, G. COUPLAND & M. VON KORFF (Eds.): Recent Advances in Flowering Time Control. (ebook: doi: 10.3389/978-2-88945-115-9). Lausanne: Frontiers Media (2017) 209-220.

Other Papers

2016

BÖRNER, A., M. AGACKA-MOŁDOCH, G.I. BATALOVA, D.R. CÁRDENAS, T. CASTELLANOS, A.M. CASTRO, Y.V. CHESNOKOV, A.M. DELL, J.L. DIAZ DE LEON, A.V. DOROSHKOV, G.S. GERARD, D. GIMENEZ, P. KOURIA, J. LING, U. LOHWASSER, G. LORI, Q.H. MUQADDASI, M. NAGEL, S.V. OSIPOVA, L. PERELLO, A.V. PERMYAKOV, M.D. PERMYAKOVA, F. PINTO, T.A. PSHENICHNIKOVA, C.O. QUALSET, M.A. REHMAN ARIF, M.E. RICCI, M.S. RÖDER, A. ROJAS-HERNANDEZ, E.G. RUDIKOVSKAYA, A.V. RUDIKOVSKY, A.A. SHISHPARENOK, M.R. SIMÓN, V.V. VERCHOTUROV, C. ZANKE & K. ZAYNALI NEZHAD: Items from Germany. Ann. Wheat Newsl. 62 (2016) 5-11.

2017

BÖRNER, A., M. AGACKA-MOŁDOCH, D.Z. ALOMARI, M.G. CARDELLI, A.M. CASTRO, Y.V. CHESNOKOV, A.K. CHISTYAKOVA, M. DELL' ARCIPRETE, J.I. DIETZ, K. EGGERT, G.S. GERARD, D. GIMÉNEZ, K. JOŃCZYK, U. LOHWASSER, G. LORI, I. MALBRÁN, E.V. MOROZOVA, Q.H. MUQADDASI, M. NAGEL, S.V. OSIPOVA, H.M. PARDI, A.E. PERELLÓ, L. PERELLO, A.V. PERMYAKOV, M.D. PERMYAKOVA, T.A. PSHENICHNIKOVA, M.A. REHMAN ARIF, M.S. RÖDER, S.V. RUDAKOV, A.S. RUDAKOVA, E.G. RUDIKOVSKAYA, A.V. RUDIKOVSKY, L. SALDÚA, M. SCHIERENBECK, U. SKOMRA, L.V. SHCHUKINA, S. SHOKAT, M.R. SIMÓN, A.V. SIMONOV, R. TARAWNEH, J.P. URANGA, M.E. VICENTE, N. VON WIRÉN, M. YANNICCARI & C.D. ZANKE: Items from Germany. Ann. Wheat Newsl. 63 (2017) 8-16.

Research Group: Genome Plasticity (GP)

Head: Dr. habil. Renate Schmidt (until 31.07.2017)

Scientists

Phuong Dung Le

Keywords

Allellic Diversity

Expression QTL

Post-Transcriptional Gene Silencing

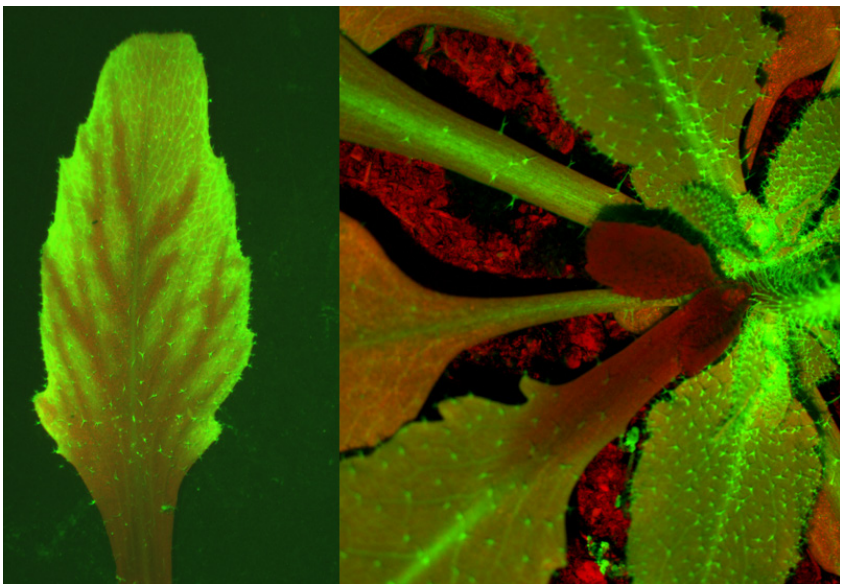
Seed Yield QTL

Highlights

Identification of regions in *Arabidopsis thaliana* accession genomes carrying modulators of post-transcriptional gene silencing.

A sequence-based approach was developed to tailor high-density oligonucleotide arrays for the analysis of transcript profiles of different *Arabidopsis thaliana* accessions. Plant Cell Rep. 36 (2017) 1323-1332.

A method was established to extract genotype information of *Arabidopsis thaliana* recombinant inbred lines from genome-wide transcript profiles established with high-density oligonucleotide arrays. Plant Cell Rep. 36 (2017) 1871-1881.



The focus was on projects which entailed molecular genetic analyses in *Arabidopsis thaliana*. The impact that genetic diversity may have on the process of post-transcriptional gene silencing was studied. Quantitative genetic approaches were used to analyse traits of importance for seed yield. Genetical genomics studies of developing seeds complemented this work to allow a more detailed understanding of the genes underlying seed yield-related traits of interest.

Research Statement and Major Achievements

Modulators of post-transcriptional gene silencing (PTGS): High and stable expression of transgenes is a prerequisite for the use of transgenic plants in research and plant breeding, yet highly expressed transgenes may be readily subjected to PTGS. The PTGS pathway has been elucidated at large, but knowledge on the role of natural variation in this process is scant. A survey involving 25 *A. thaliana* accessions revealed for several genes of the PTGS pathway alleles with particularly high sequence divergence when compared to reference accession Col-0. Individual plants of an isogenic population differ regarding the onset and spread of silencing, thus a transgenic system that allows fast and precise recording of silencing for populations of plants at different stages of development was chosen for the functional analysis of diverged alleles. Selected alleles were introgressed into Col-0 transgenic lines harbouring PTGS-prone *GFP* transgenes and silencing behaviour of the established introgression lines was compared to that of Col-0 transgenic lines. Several introgression lines with significantly altered silencing behaviour were identified; for example, two lines carrying Gie-0 introgressions showed less silencing than Col-0 lines. In several introgression lines significantly more silencing was seen. The establishment of independent lines for each of the introgressed alleles together with a detailed characterisation of the lines with respect to number, position and size of introgressions enabled to delimit those regions of the accession genomes carrying PTGS modulators. Intriguingly, in several cases the introgressed regions correlating with enhanced *GFP* silencing did not coincide with the region carrying the introgressed allele of interest. Fine-mapping narrowed down the regions harbouring the PTGS modulators (Fig. 30).

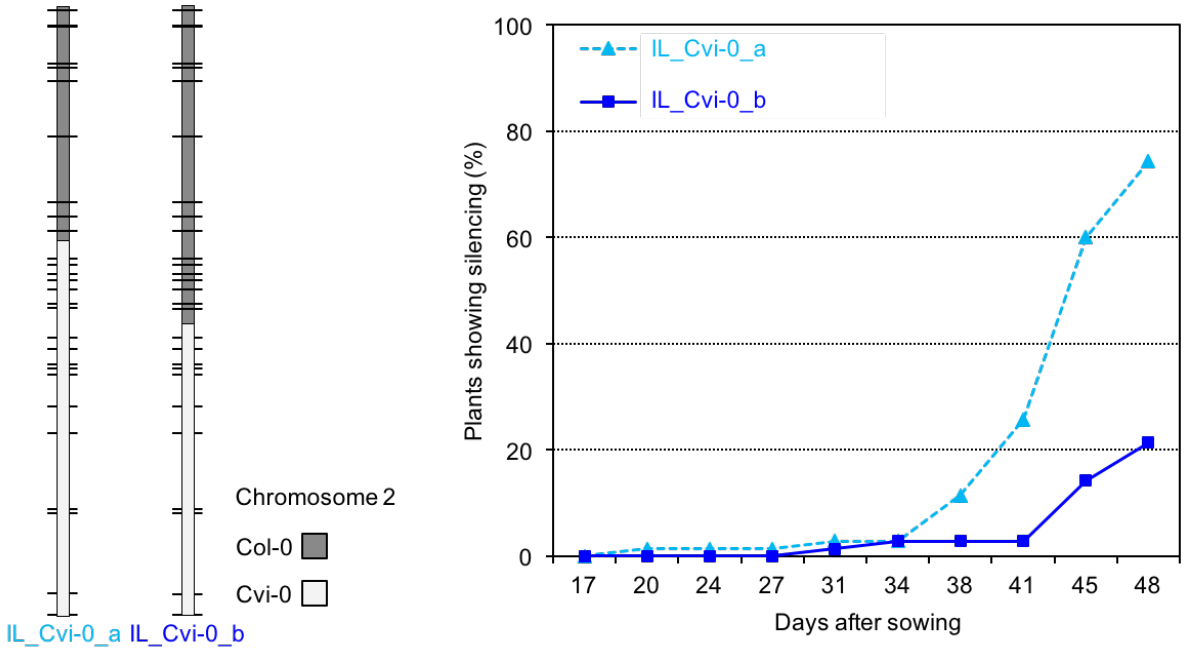


Fig. 30 Introgression lines with contrasting genotypes in a region of *Arabidopsis thaliana* chromosome 2 show differences with respect to gene silencing. On the left the position and extent of Cvi-0 introgression segments are shown for two introgression lines. On the right the occurrence of silencing in plant populations of these two lines is displayed for different stages of development.

Genetical genomics of *Arabidopsis thaliana* seeds: Genome-wide transcript profiles were established for a defined stage of seed development with Affymetrix ATH1 arrays for recombinant inbred lines (RILs) derived from accessions Col-0 and C24. The analysis was restricted to array features perfectly matching gene sequences in both parental accessions, approximately 20,000 genes were evaluated. Extraction of genotype information from the expression profiles of the lines permitted the generation of a dense genetic map, a prerequisite for composite interval mapping of expression traits. For the majority of analysed transcripts at least one significant expression QTL (eQTL) was found, whereas only few hundred differentially expressed genes had been identified for this stage of seed development in Col-0 and C24. Several regions showing significant overrepresentation of eQTL were observed. The implementation of genomic selection approaches permitted to study the genetic architecture of the expression traits in detail; the relative proportions to which eQTL that colocalised with the map position of their corresponding gene, eQTL in *cis*, and those that did not, eQTL in *trans*, explained the transcript variance were of particular interest (in collaboration with RG *QG*). The results of the eQTL study in the RIL population were exploited for genetical genomics approaches, QTL for polar primary metabolites in seeds were studied in collaboration with RG *HET*. QTL for seed yield and seed yield-related traits were also assessed and revealed a seed yield QTL that colocalised with several QTL for seed yield-related traits. The analysis of those phenotypes in near isogenic lines corroborated the results.

Embedding in Departmental and IPK Research Strategy

The characterisation of a locus influencing seed yield contributed to one aim of the department of *Breeding Research*; the molecular identification of genes for agronomically important traits. The studies were also in line with the goal of research theme 4; the identification and characterisation of regulators affecting plant performance.

Peer Reviewed Papers

2017

BOUDICHEVSKAIA, A., H.X. CAO & R. SCHMIDT: Tailoring high-density oligonucleotide arrays for transcript profiling of different *Arabidopsis thaliana* accessions using a sequence-based approach. Plant Cell Rep. 36 (2017) 1323-1332.

JIANG, Y., R.H. SCHMIDT, Y. ZHAO & J.C. REIF: A quantitative genetic framework highlights the role of epistatic effects for grain-yield heterosis in bread wheat. Nat. Genet. 49 (2017) 1741-1746.

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TRAN, T.D., H. ŠIMKOVÁ, R. SCHMIDT, J. DOLEŽEL, I. SCHUBERT & J. FUCHS: Chromosome identification for the carnivorous plant *Genlisea margaretae*. Chromosoma 126 (2017) 389-397.

Theses

2017

LE, P.D.: Analysis of sense transgene-induced gene silencing in introgression lines reveals the presence of silencing modulators in *Arabidopsis thaliana* accession genomes. (PhD Thesis) Martin-Luther-Universität Halle-Wittenberg, Naturwissenschaftliche Fakultät I Biowissenschaften, Halle/S. (2017) 168 pp.

Abteilung Molekulare Genetik ▪ Department of Molecular Genetics

Leiter ▪ Head:
Prof. Dr. Thomas Altmann

Allgemeine Forschungsziele

Die Forschungsarbeiten der Abteilung *Molekulare Genetik* (MOG) richten sich auf die Untersuchung und Modulation molekularer Mechanismen der pflanzlichen Produktivität. Im Fokus stehen die Dynamik des vegetativen Sprosswachstums und seines Stoffwechsels sowie die Prozesse der Entwicklung und der Füllung von Samen. Wesentliche Ziele sind die molekulargenetische Identifizierung und Charakterisierung leistungsbestimmender Faktoren, die Aufklärung der verantwortlichen molekularen Prozessketten und die Nutzung der gewonnenen Informationen für die Entwicklung von Lösungsansätzen zur Verbesserung von Kulturpflanzen.

Stand der Forschungsarbeiten und wichtige Ergebnisse

Die zentralen Forschungsziele der Abteilung *Molekulare Genetik* liegen in der Aufklärung molekularer Mechanismen, die wesentlichen produktivitätsbestimmenden Prozessen bei Kulturpflanzen zugrunde liegen. Die gewonnenen Kenntnisse sollen genutzt werden, um Wege für die zielgerichtete Optimierung der Leistungsfähigkeit von Kulturpflanzen auszuarbeiten. Um diese Ziele erreichen und wesentliche Aufgaben der Abteilung *MOG* erfüllen zu können, ist mit Beginn des Jahres 2016 ein entscheidender Transformationsprozess mit einer personellen Erneuerung auf Ag-Leitungsebene und mit einer thematischen Fokussierung eingeleitet worden. Dieser beinhaltete in 2016 die Etablierung der neuen experimentellen Ag *Assimilat-Allokation und NMR* (AAN) und die Wiedereinsetzung der bioinformatischen Ags *Netzwerkanalyse und Modellierung* (NAM) sowie *Bildanalyse* (BA). In 2017 erfolgten die Wiederbesetzung der Leitungsstelle der thematisch neu ausgerichteten Ag *Samenentwicklung* (SE) und die Neueinrichtung der Ag *Akklimierungsdynamik und Phänotypisierung* (ADP). Diese Veränderungen sind auf die Etablierung von drei eng miteinander verknüpften Forschungsbereichen innerhalb der Abteilung *MOG* ausgerichtet, die aus bereits zuvor intensiv bearbeiteten Themenfeldern hervorgehen:

- Wachstumsdynamik des Sprosses während der vegetativen Entwicklung,
- Samenbiologie: Entwicklungs- und Stoffwechselprozesse in Samen,
- Systemgenetik zugrundeliegender genetischer Mechanismen und Verbesserungsstrategien.

General Research Goals

The research efforts of the *Molecular Genetics* department (MOG) are focused on the investigation and modulation of molecular mechanisms that govern plant productivity. The dynamics of vegetative shoot growth and metabolism and the processes of seed development and filling are in the main focus. Major goals are the molecular-genetic identification and characterization of factors determining plant performance, the elucidation of the involved molecular process chains, and the use of the acquired knowledge for the development of solutions for crop improvement.

Research Statement and Major Achievements

The central research goals of the *Molecular Genetics* department are the elucidation of molecular processes that underlie major processes determining crop plant productivity. The acquired knowledge will be used to provide means for targeted improvement of the crop performance potential. To enable the achievement of these goals and to carry out major tasks of the *MOG* department, in the beginning of 2016 a pivotal transformation process was initiated that concerns personnel turnover at the research group (RG) leader level and a thematic focusing. In 2016 it included the creation of the new experimental RG *Assimilate Allocation and NMR* (AAN) and the re-installation of the bioinformatics groups *Network Analysis and Modelling* (NAM) and *Image Analysis* (BA). In 2017 refilling of the leader position of the thematically re-focused *Seed Development* (SE) RG and installation of the new RG *Acclimation Dynamics and Phenotyping* (ADP) was achieved. These changes are oriented towards the establishment of three tightly interlinked research areas within the *MOG* department, which emerge from certain previously addressed fields of research:

- Growth Dynamics during vegetative shoot development,
- Seed Biology, addressing developmental and metabolic processes in seeds,
- and Systems Genetics of underlying genetic mechanisms and improvement strategies.

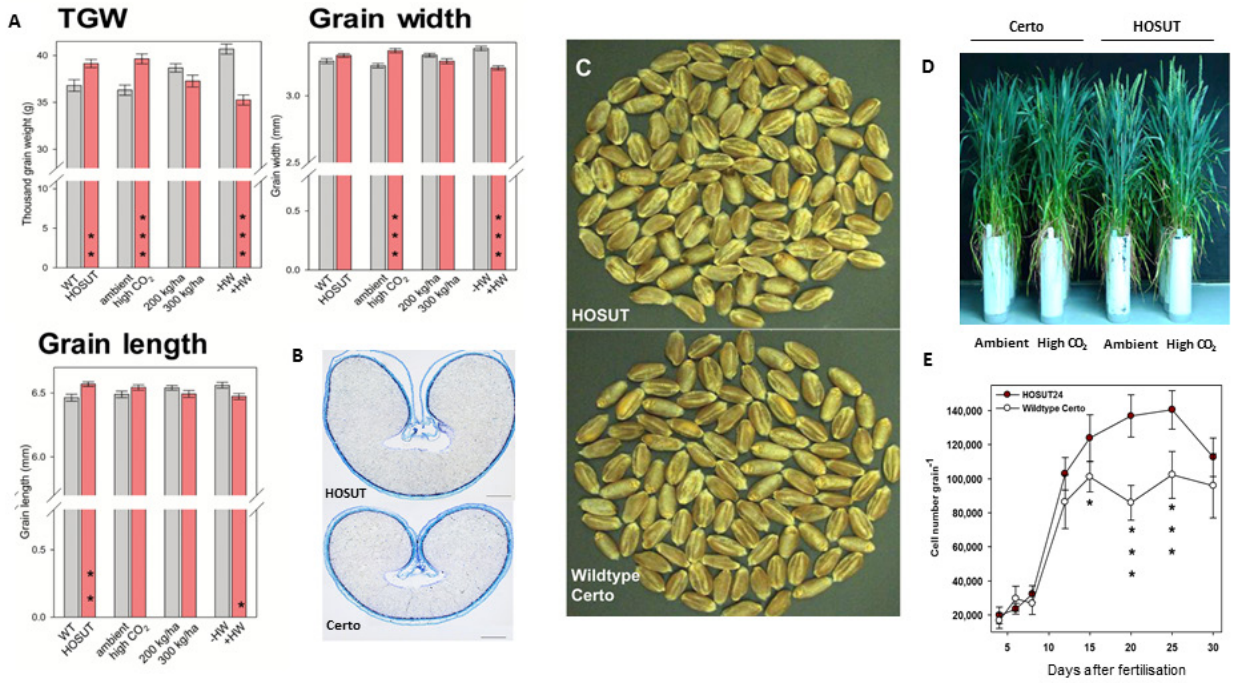

Fig. 31 Pflanzenphänotyp und Samengrößeneigenschaften von Weizenpflanzen, die einen Saccharosetransporter aus Gerste überexprimieren (HOSUT24). (A) Balkendiagramme: die Faktoren Linie; CO2, N-Düngung und Hitze beeinflussen die Korngröße; das Tausendkorngewicht (TGW), Kornbreite und Kornlänge; die Balken zeigen Mittelwerte +-SE, n=48, *p<0,05, ** p<0.01, ***p<0,001. (B) Querschnitte durch die Mitte eines HOSUT24 (oben) und eines Certo (unten) Kornes, Balken = 500 µm. (C) Reife Körner von HOSUT24 und Certo. (D) Weizenpflanzen der Linien HOSUT und Certo zum Blütezeitpunkt nach Wachstum in Klimakammern. (E) Endosperm-Zellzahl pro Korn für HOSUT24 und Certo. Mittwelwerte +-SD, n=6 *p<0,05, ***p<0.001. ▪ Plant Phenotype and grain size characteristics of wheat expressing a barley sucrose transporter (HOSUT24). (A) Bar charts: the factors line, CO2, N fertilization, and heat wave influencing grain dimensions, thousand grain weight (TGW), grain width and grain length; bars are means ±SE, n=48, *P<0.05; **P<0.01, ***P<0.001. (B) Mid-section of a HOSUT24 (top) and Certo (bottom) grain, bar = 500 µm. (C) Mature grains of HOSUT and Certo. (D) Wheat plants of Certo and HOSUT around the flowering stage as grown in the climate chambers. (E) Endosperm cell number per grain for HOSUT24 and Certo. Data are means ±SD, n=6, *P<0.05, ***P<0.001.

Die Abteilung *MOG* leistet mit der Bearbeitung dieser Bereiche zentrale Beiträge zu den IPK-Forschungsschwerpunkten 4 *Wachstum und Stoffwechsel* und 5 *Mechanismen der Resistenz und Stresstoleranz* und sie ist in begrenzterem Umfang in die Forschungsschwerpunkte 1, 2 und 3 involviert. In 2016–2017 besonders hervorzuhebende wissenschaftliche Erfolge der Abteilung *MOG* betreffen den Nachweis der molekularen Wirkkette des *FUM2*-Gens von Arabidopsis und seiner Assoziation mit der Biomasseproduktion und die Identifizierung Entwicklungsphasen-spezifischer Wachstums-QTL bei Mais. Die Umweltabhängigkeit der Wirkung der Saccharosetransporter-Überexpression auf die Samengröße bei Weizen wurde belegt (Fig. 31) und es wurde eine hohe Plastizität der ABA-Phytohormonwirkung in Gerstensamen und die Verknüpfung der Zuckersignalwirkung mit der Auxinproduktion in Erbsensamen gezeigt, sowie die Rollen des vakuolären Prozessierungsenzyms (VPE-4) in Gerstensamen und der RKD-Transkriptionsfaktoren während der weiblichen Gametophytenentwicklung aufgeklärt. Die Stabilität samenspezifisch exprimierter Spinnenseidenprotein-Multimere und die Immunogenität oligomerisierte Hämagglutinine des Vogelgrippevirus wurde nachgewiesen und eine neue Strategie zum gezielten Proteinabbau in Pflanzenzellen entwickelt (Fig. 32). Ferner wurden neue Kenntnisse zur Evolution der CAM- und C4-Typen der Photosynthese gewonnen sowie ein Beitrag

By working in these areas, the MOG department contributes profoundly to the IPK research themes 4 *Growth and Metabolism* and 5 *Mechanisms of Resistance and Stress Tolerance* and to lesser extents to the IPK research themes 1, 2, and 3. In 2016-2017 major scientific *MOG* achievements concerned the elucidation of the molecular reaction cascade of the Arabidopsis *FUM2* gene and its association with biomass production and the identification of developmental phase-specific growth QTL in maize. The environment-dependency of the sucrose transporter overexpression effect on seed size in wheat was shown (Fig. 31) and the plasticity in the phytohormone action of ABA in barley seeds and links between sugar signaling and auxin production in pea seeds were demonstrated. The roles of the vacuolar processing enzyme (VPE-4) in barley seeds and of RKD transcription factors during female gametophyte development were clarified. The stability of seed-specifically expressed spider silk multimers and the immunogenicity of avian flu hemagglutinin oligomers were verified and a new strategy for targented protein degradation in plant cells was developed (Fig. 32). Furthermore, new knowledge on the evolution of the CAM and C4 types of photosynthesis was gained and a contribution towards visualization of telomere movements in living cells was made.

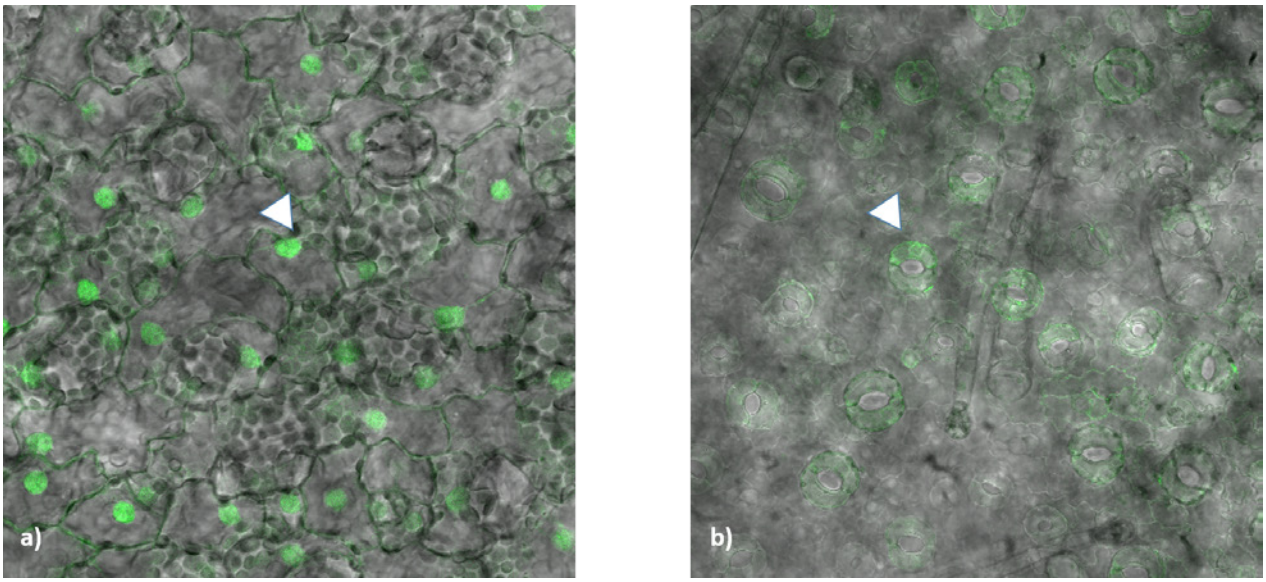

Fig. 32 Fluoreszenz mikroskopische Aufnahme der Blattunterseite transgener *N. tabacum* Pflanzen: a) Transgen: Sap11-GFP (kernlokalisiertes grün fluoreszierendes Fusionsprotein). b) Transgen: Sap11-GFP übertransformiert mit BTB-VHHGFP4 (Fusionsprotein zum GFP-Abbau, deutliche Reduzierung der Gesamtfluoreszenz durch potentiellen Abbau des Fusionsproteins). ▪ Fluorescence microscopy image of lower leaf surfaces of transgenic tobacco (*N. tabacum*) plants: a) Transgene: Sap11-GFP (nuclear localized green fluorescent fusion protein). B) Transgene: Sap11-GFP supertransformed with BTB-VHHGFP4 (fusion protein for GFP degradation, significant reduction of overall fluorescence as the result of potential degradation of the fusion protein).

zur Visualisierung von Telomerbewegungen in lebenden Zellen geleistet.

Perspektiven und Herausforderungen

Der Transformationsprozess der Abteilung *MOG* soll bis zum Jahreswechsel 2019/2020 intensiv weitergeführt werden und nach der Einrichtung der neuen Ag *Metabolische Diversität* (MD) sollen sieben Abteilungsinterne Ags und eine weitere neue Abteilungs-assoziierte unabhängige Nachwuchsgruppe (Ag *Synthetische Biologie und Systemengineering*, SBS) etabliert sein. Damit wird der inhaltliche und organisatorische Abteilungsumbau mit der Einrichtung und Verknüpfung der für die Bearbeitung der drei o.g. *MOG*-Forschungsbereiche nötigen komplementären Expertise abgeschlossen. Mit den beiden Ags *NAM* und *BA* werden zudem entscheidende institutsweite Aufgaben der Bioinformatik wahrgenommen. Darüber hinaus etablieren und stellen *MOG*-AGs entscheidende Forschungsinfrastrukturen und –verfahren bereit: U.a. Mikroprobennahme und –analyse, NMR-basierte Visualisierung von Strukturen und Inhaltsstofflokalisierung und –quantifizierung, GC-MS- und LC-MS-basierte Metabolitanalytik, Mikrosensorik, immunologische Verfahren, sowie Plattformen und Verfahren für die automatisierte nicht-invasive Phänotypisierung. Hier übernimmt die Abteilung *MOG* eine IPK-weite leitende Funktion, besonders hinsichtlich der Einbindung in das BMBF-geförderte *Deutsche Pflanzen-Phänotypisierungs-Netzwerk* (DPPN; http://www.dppn.de). Neben dem Ausbau und der Nutzung der komplexen *LemnaTec*-basierten Hochdurchsatzanlagen für die automatisierte Analyse ganzer Pflanzen standen beson-

Plans, Opportunities and Challenges

The transformation process of the *MOG* department will be continued until the turn of the years 2019/20. After installation of the new research group *Metabolic Diversity* (MD), seven *MOG*-internal research groups and one associated independent junior research group (*Synthetic Biology and Systems Engineering*, SBS) will be established. This will mark the completion of the topical and organizational reconstruction of the department with the establishment and interconnection of the complementary expertise required to execute the three research areas mentioned above. With the two RGs *NAM* and *BA*, essential institute-wide bioinformatics tasks are carried out. Furthermore, *MOG* RGs establish and provide important research infrastructures and methods: These include microsampling and analysis, NMR-based visualization of structures and localization and quantification of substance contents, GC-MS and LC-MS-based metabolite profiling, microsensorics, immunological techniques, as well as platforms and procedures for automated non-invasive phenotyping. In the latter area, the *MOG* department takes an IPK-wide leading role, in particular with respect to the integration into the BMBF-funded German Plant Phenotyping Network (*DPPN*; http://www.dppn.de). In addition to the upgrade and use of the complex *LemnaTec*-based high-throughput installations for automated analyses of entire plants, the installation of a 3D imaging NMR system (by RG *AAN*) and the completion of the plant cultivation hall (PKH) were in the main focus (Fig. 33). The existing and the planned plant phenotyping installations are the key com-

Fig. 33 Feierliche Eröffnung der Pflanzenkulturhalle des IPK (28.08.2017) in Gegenwart des Ministerpräsidenten des Landes Sachsen-Anhalt, Dr. Reiner Haseloff, der Bundesministerin für Bildung und Forschung, Prof. Dr. Johanna Wanka und des Präsidenten der Leibniz-Gemeinschaft, Prof. Dr. Matthias Kleiner (Foto: Markus Scholz). ▪ Opening of the Plant Cultivation Hall of IPK (28.08.2017) in the presence of the Prime Minister of the Federal State of Saxony-Anhalt, Dr. Reiner Haseloff, of the Federal Minister of Education and Research Prof. Dr. Johanna Wanka, and the President of the Leibniz Association, Prof. Dr. Matthias Kleiner (Foto: Markus Scholz).

ders die Installation und Inbetriebnahme eines 3D bildgebenden NMR-Systems (durch die Ag *AAN*) und die Fertigstellung der neuen Pflanzenkulturhalle (PKH) im Vordergrund (Fig. 33). Die bestehenden und neu zu installierenden Anlagen bilden die entscheidende Grundlage für die Beteiligung des IPK an nationalen (*DPPN*, s.o.), europäischen (*EPPN2020*; http://www.plant-phenotyping-network.eu; *ESFRI*-Projekt *EMPHASIS*) und internationalen (*IPPN*; http://www.plant-phenotyping.org/) Netzwerken. Der effiziente und nachhaltige Betrieb dieser Anlagen und ihre Nutzung für eigene und in Kooperation bearbeitete Forschungsarbeiten der *MOG*-Fokusbereiche eröffnet dabei (weltweit) einzigartige Chancen und stellt gleichermaßen eine besondere Herausforderung dar.

ponents of IPK's participation in national (DPPN, s. above), European (*EPPN2020*, http://www.plant-phenotyping-network.eu; *ESFRI*-project *EMPHASIS*) and international (*IPPN*, http://www.plant-phenotyping.org/) networks. The efficient and sustainable operation of these installations constitutes both, a unique opportunity for the conductance of own and collaborative research projects on the *MOG* focus areas and a particular challenge.

Research Group: Heterosis (HET)

Head: Prof. Dr. Thomas Altmann

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Dr. Kathleen Weigelt-Fischer
Hongwen Wang
Janine Wiebach

Keywords

Vegetative Growth Dynamics
Plant Metabolism and Performance Relations
Molecular/Genetic Mechanisms of Heterosis
High-Throughput Plant Phenotyping

Highlights

Identification of developmental phase-specific growth and growth dynamics-determining QTL in maize (Muraya et al., 2017).
Major technical upgrades of high-throughput plant phenotyping facilities.
Establishment of plant (oxy-)lipidome analytics (Riewe et al., 2017).
Start of the EPPN2020 project (2017).
Start of ScienceCampus Halle IDRIB project (2017).
Completion of the IPK Plant Cultivation Hall construction (2017).

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Major aims of the research group *Heterosis* are the identification and characterization of factors controlling vegetative plant growth performance and metabolism, and the elucidation of the affected molecular and physiological mechanisms. Molecular genetic/genomic approaches are followed to detect controlling genes with emphasis on loci contributing to heterosis (in Arabidopsis, maize, and oilseed rape). A broad range of molecular biologic, biochemical, and high-throughput non-invasive phenotyping techniques applied to plants cultivated in sophisticated controlled environment facilities are established and used.

Research Statement and Major Achievements

In 2016-2017, important advances were made in the identification of genes / QTL controlling vegetative plant growth and metabolism performance and the affected molecular/physiological processes: The Arabidopsis *FUM2*-gene was shown to carry two major naturally occurring promoter InDel polymorphisms (Riewe et al., 2016). The alternative alleles confer large variation of mRNA expression and corresponding changes in fumarase enzyme activity and in leaf fumarate and malate levels. A population-wide association of the promoter polymorphism with plant growth supports a role of *FUM2* in diurnal carbon storage and points to a growth advantage of accessions carrying the Col-0 allele. Using the automated non-invasive IPK plant phenotyping facility for large plants, the genetics of growth dynamics were assessed by monitoring 252 diverse maize inbreds (Muraya et al., 2017). Combining 50k SNP data and image-derived size estimates at 11 time points detected 12 main-effect QTL and 6 pairs of epistatic interactions with very prominent patterns of expression changes during developmental progression (Fig. 34). Non-parametric functional and multivariate mapping approaches identified four further loci affecting growth dynamics. The results highlight the need of time-resolved systems analyses to uncover the action of the responsible genes and the affected molecular processes. Evidence of mQTL hotspots and a master regulator of seed metabolism was gained by QTL analysis using GC-MS-based metabolite profiles of seeds of *A. thaliana* recombinant

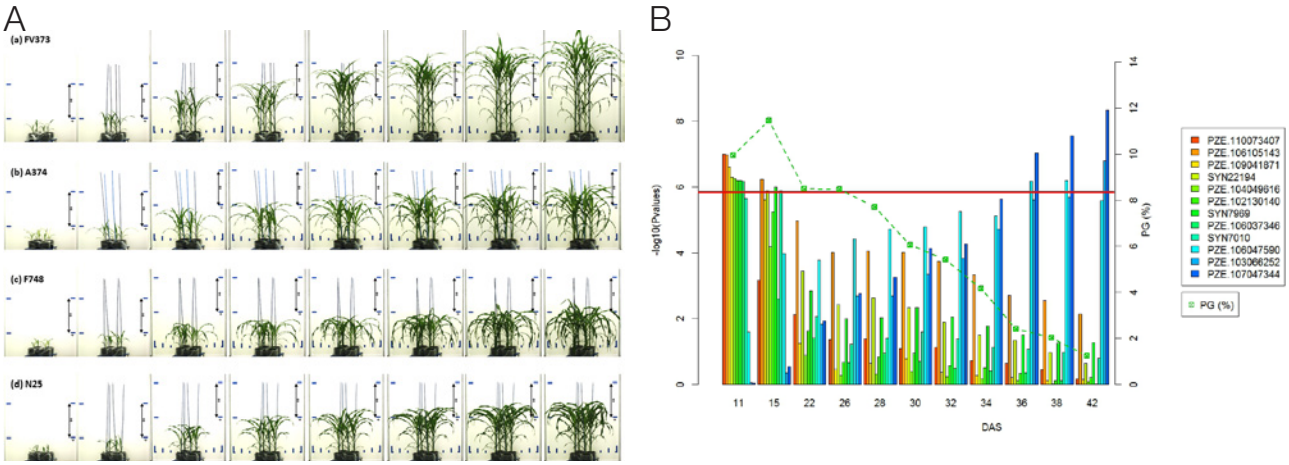

Fig. 34 Assessment of maize growth dynamics through automated high-throughput plant phenotyping and identification of developmental phase-specific QTL of estimated plant biomass (Muraya et al., 2017).
A) Plant images of four different maize inbred lines cultivated and phenotyped for whole plant traits using the IPK phenotyping platform for large plants. Pictures were taken sequentially at 8 different days throughout the period from 11 days after sowing (DAS) until 42 DAS.
B) Effects (displayed as p-values) of 12 QTL detected as SNP marker-trait associations at 11 different time points. Colors indicate marker effect (p-value) trends, either decreasing (red to green) or increasing (light to dark blue) highlighting two opposing patterns of changes.

inbred lines (Knoch et al., 2017). Unequal distribution of 786 detected (m)QTL and a QTL of the first PC of metabolite variation indicated the presence of a higher order metabolism control locus.

Major technical advances were achieved in upgrading the HTP whole plant phenotyping platforms with installations for kinetic chlorophyll fluorescence imaging (Tschiersch et al., 2017) and environmental sensor networks. A procedure for plant lipidome analysis was established using high-resolution LC-MS/MS (Riewe at al., 2017). This approach enables multiparallel quantitative detection of 516 lipids of known acyl composition in wheat seeds, and lead to the observation of increased lipid oxidation and hydrolysis during long-term storage.

Embedding in Departmental and IPK Research Strategy

Of the *MOG* departments main research areas, the *HET* RG predominantly addresses *Growth Dynamics* during vegetative shoot development. It aims at the identification of genes and alleles, and the elucidation of molecular mechanisms that determine (vegetative) plant growth performance. In particular, the interactions between growth and metabolism controlling factors, their genetic variation and their impact in response to specific environmental conditions reflect a major line of research in the *MOG* department. The *HET* RG's major focus is on experimental work, using molecular/genetic (*omics*) analyses including genome-wide genotyping (GBS), transcript and metabolite profiling in combination with HTP whole plant phenotyping. It closely collaborates with other groups in the *MOG* department (e.g. *BA*, *NAM*) as well as IPK-wide (e.g. *GP*, *BIT*, *QG*, *RGR*, *GGR*, *DG*). The *HET* RG also works towards identification of loci/genes and molecular/genetic mechanisms contributing to heterosis. In collaboration with *SE* and *AAN*, the *HET* RG provides methodological expertise and capacity to the second research area of *MOG*, *Seed Biology*. These lines of research are centrally embedded in the IPK research themes 4 *Growth and Metabolism* and 5 *Mechanisms of Resistance and Stress Tolerance*. Further contributions are made to the research theme 1 *Concepts for Valorization of Genetic Resources*. IPK-wide, the *HET* RG co-ordinates the plant phenotyping efforts and it has the lead in building/advancing the corresponding research infrastructure.

Plans, Opportunities and Challenges

Based on its fundamental research results on Arabidopsis, maize, rapeseed, and barley and on its unique research infrastructures, the *HET* RG will in future focus on (i) candidate genes and gene networks involved in variation and heterosis of vegetative growth and related physiological parameters, (ii) analysis of epigenetic effects on heterosis and stress tolerance, (iii) time-resolved systems analyses of growth dynamics in inbreds and hybrids, (iv) systems mapping of hybrid-performance related processes under dynamically changing environmental conditions. Acclimation and performance response to changing temperature and light, metabolism-growth relations, and viability feature analyses will be followed up by the new *MOG* RGs *ADP* and *MD*. They will also take over parts of the corresponding research infrastructure responsibilities. The opportunities to increase the scientific impact by sharpening the *HET* RG's scientific focus also impose the challenges to organize the interaction with related groups and to co-ordinate the shared responsibilities on the research infrastructures.

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Other Papers

2016

CHEN, D., R. SHI, J.-M. PAPE & C. KLUKAS: Predicting plant biomass accumulation from image-derived parameters. bioRxiv (2016).

HASHEMIPETROUDI, S.H., G. NEMATZADEH, G. AHMADIAN, A. YAMCHI & M. KUHLMANN: Expression analysis of salt stress related expressed sequence tags (ESTs) from *Aeluropus littoralis* by quantitative real-time PCR. Biosci. Biotech. Res. Comm. 9 (2016) 445-456.

Theses

2016

WIEBACH, J.: Prädiktion der Keimfähigkeit von Weizen und Gerste durch metabole Signaturen. (Diploma Thesis) Technische Universität Berlin, Institut für Biotechnologie, Berlin (2016) 80 pp.

2017

BLOSSEI, J.: Untersuchung zum Einfluss der Überexpression von ERI auf die Zunahme der frühen Biomasse. (Bachelor Thesis) Hochschule Bremen, Internationaler Studiengang Technische und Angewandte Biologie, Fakultät 5, Bremen (2017) 42 pp.

CHEN, D.: Dissecting and modeling the ohenotypic components of plant growth and drought responses based on high-throughput image analysis. (PhD Thesis) Martin-Luther-Universität Halle-Wittenberg, Naturwissenschaftliche Fakultät I Biowissenschaften, Halle/S. (2017) 185 pp.

VENKATASUBBU, T.: Dosage of duplicated and antifunctionalized homeobox proteins influences leaf and spikelet development in barley (*Hordeum vulgare* L.). (PhD Thesis) Martin-Luther-Universität Halle-Wittenberg, Naturwissenschaftliche Fakultät I - Biowissenschaften, Halle/S. (2017) 165 pp.

WANG, H.: Genetic manipulation of the cross-talk between abscisic acid and strigolactones and their biosynthetic link during late tittelring in barley. (PhD Thesis) Martin-Luther-Universität Halle-Wittenberg, Naturwissenschaftliche Fakultät I Biowissenschaften, Halle/S. (2017) 114 pp.

Research Group: Seed Development (SE)

Head: Dr. Hans Weber (temp. until 30.09.2017), Dr. Bruno Müller (since 01.10.2017)

Scientists

Yemisrach Melkie Abebaw

Dr. Maria Isabel Mora

Dr. Ruslana Radchuk

Van Tran Thi Thuy

Dr. Johannes Thiel

Dr. Winfriede Weschke

Keywords

Cereal Grain Development

Endosperm Transfer Cell Development

Hormone-Transcriptional Interactions of Grain Growth

Sink-Source Interactions

Highlights

Hormone-mediated control mechanisms of cell/tissue differentiation and growth dynamics during seed development.

Research transfer into agricultural application in cooperation with breeding companies.

Field testing of performance of transgenic wheat.

Funding

DFG, Leibniz Association, Industry (Bayer Crop Science), Government of Vietnam (fellowships)

The general goal is to understand molecular control mechanisms of cell specification, tissue differentiation and growth in cereal grains with the long-term aim to improve seed yield and quality. Hormone physiology, metabolic networks and functional genomics are integrated towards identification of key genes and regulators of yield-related developmental parameters of grain shape and size. Sink-induced metabolite transfer and remobilisation have been investigated to identify bottlenecks for grain formation. New wheat lines with altered sucrose transport and partitioning are explored under field conditions.

Research Statement and Major Achievements

We aim to understand how cell specification, tissue differentiation and growth of the developing seed are controlled and coordinated at the molecular level. A better understanding will reveal key regulatory points and allow targeted manipulations to improve seed yield and quality of crop plants. Following this strategy, the RG has investigated hormone signal transduction components and sink-induced metabolite transfer as potential bottlenecks for grain formation. Based on high-resolution transcriptome profiling experiments done in barley (Thiel et al. 2012, Thiel 2014.), a function for Two Component Signaling (TCS) in early endosperm differentiation is predicted. Knockdown of the TCS element *histidine kinase 1* (*HvHK1*) produces smaller grains with reduced starch (Fig. 35), confirming its key functional role (J. Thiel, ongoing DFG project). Interactions between TCS and other hormone signal pathways, such as ABA and ethylene, have been uncovered. In addition, the profiling data revealed potential roles for assimilate and sugar transport. New wheat lines with potentially improved metabolite transport and partitioning were constructed and are currently explored under field conditions. Abscisic acid accumulates in seeds at the filling phase and triggers maturation. Surprisingly, immunomodulation of the ABA status in barley grains yields mature grains with nearly unchanged dry weight and composition, probably due to compensatory changes in physiological metabolic ABA-enzymes (Staroske et al. 2016). Overlapping expression of *HvSUT1* and *HvSUT2* sucrose transporters in the barley endosperm suggested concerted functions. *HvSUT1/2*-deficient seeds

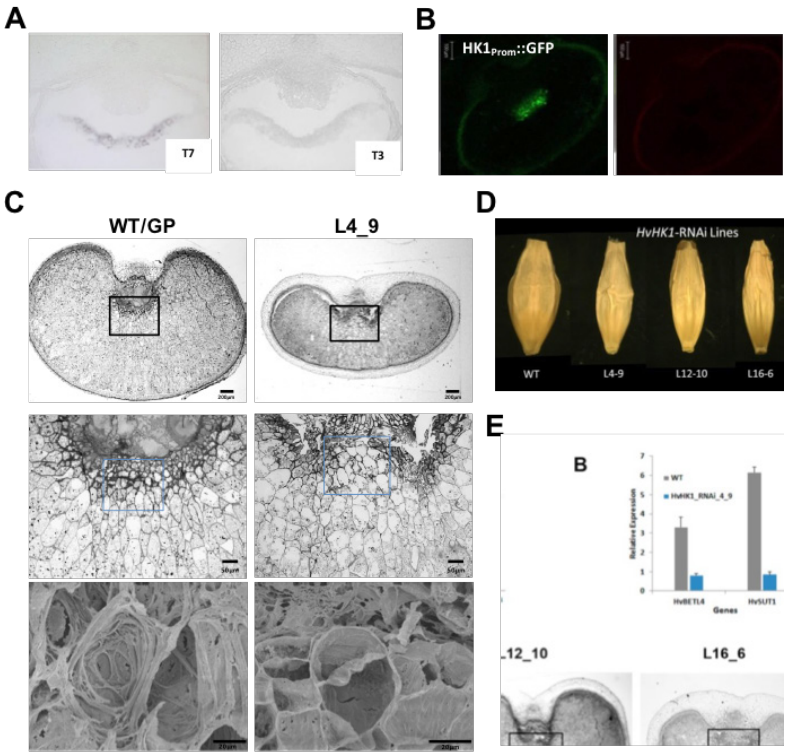

Fig. 35 Reduction of *HvHK1* expression by RNAi results in aberrant endosperm development and smaller grains. (A) *In situ* hybridization of *HvHK1* specifies expression in the ETC region of the cellularizing endosperm (2/3 DAF). (B) *HvHK1*-promoter fused to a GFP reporter gives a strong signal in the central cellularizing ETC region corresponding to *in situ* hybridization. (C) Histological analysis of WT and homozygous transgenic grains of *HvHK1*-RNAi plants (line 4_9) at 12 DAF. Squared regions are enlarged in light microscopic images below and scanning electron microscopy pictures at the bottom. Light microscopic images show differences in endosperm shape and size. Magnification of the central ETC region depicted disturbed ETC differentiation in transgenic grains. Scanning electron microscopy indicates differences in cell shape and cell wall architecture of ETCs from WT and L4_9 grains. (D) Ripe grains of transgenic lines show a shrunken phenotype and display a reduced grain width compared to the wildtype Golden Promise. (E) Thousand grain weight and starch content are reduced in mature grains of RNAi-lines.

accumulated less starch and dry weight, due to sugar starvation responses that were triggered by reduced cytoplasmic sugar content (Radchuk et al. 2017). Winter wheat lines (HOSUT) expressing a barley sucrose transporter exhibited increased grain yield compared to the non-transformed control (Saalbach et al. 2014, Fig. 31). Field trials were performed 2016/2017 to analyse performance of transgenic lines together with *AgROSCOPE* (Zürich). Specific N transporters are currently validated by knock-down approaches in barley. Preliminary results confirm a role in remobilisation and N transport during grain filling.

Embedding in Departmental and IPK Research Strategy

Special emphasis will be given to communication between maternal and filial seed tissues, and its impact on seed development. The elucidation of signaling pathways in seeds of model organisms and cereals will provide unique opportunities to functionally evaluate the roles of these pathways for crop productivity. To resolve the dynamics of development, we will follow the manipulations spatiotemporally and analyze the resulting phenotypes using non-invasive imaging technologies. The developed models will be available for integrative approaches, which comprise non-invasive metabolic and phenotypic analyses by NMR and FTIR-spectroscopy and omics analysis for modeling of transcriptional and metabolic networks. This will be done in tight cooperation with other RGs of the *MOG* department, the *AAN* RG (led by Ljudmilla Borisjuk) and the Network and Modeling (*NAM*) RG and will help to make progress in a systems-orientated view on seed development.

Plans, Opportunities, and Future Challenges

Our finding that cytokinin transport mediated by Arabidopsis PURINE PERMEASE 14 (PUP14) controls the TCS responses (Zürcher et al. 2016) offers additional possibilities for manipulations of the TCS signaling landscape during seed development. Based on the high-resolution transcriptome data in barley, we aim to identify PUP transporters in addition to cytokinin homeostasis genes, TCS genes, and other strikingly localized genes, and evaluate their cellular functions in transient expression experiments using Arabidopsis and barley protoplasts. *In planta* functional studies will be performed in Arabidopsis, and transferred to barley and wheat. Challenges are to establish a functional barley protoplast system, and whether obtained working model will sustain the tests *in planta*. Our data will be incorporated into an *in silico* model of seed development and will help to provide keys for knowledge-based improvement of yield potential.

Peer Reviewed Papers

2016

CÁPAL, P., T.R. ENDO, J. VRÁNA, M. KUBALÁKOVÁ, M. KARAFIÁTOVÁ, E. KOMÍNKOVÁ, I. MORA-RAMÍREZ, W. WESCHKE & J. DOLEŽEL: The utility of flow sorting to identify chromosomes carrying a single copy transgene in wheat. Plant Methods 12 (2016) 24.

KASPAR-SCHOENEFELD, S., K. MERX, A.M. JOZEFOWICZ, A. HARTMANN, U. SEIFFERT, W. WESCHKE, A. MATROS & H.-P. MOCK: Label-free proteome profiling reveals developmental-dependent patterns in young barley grains. J. Proteomics 143 (2016) 106-121.

PEUKERT, M., J. THIEL, H.-P. MOCK, D. MARKO, W. WESCHKE & A. MATROS: Spatiotemporal dynamics of oligofructan metabolism and suggested functions in developing cereal grains. Front. Plant Sci. 6 (2016) 1245.

STAROSKE, N., U. CONRAD, J. KUMLEHN, G. HENSEL, R. RADCHUK, A. ERBAN, J. KOPKA, W. WESCHKE & H. WEBER: Increasing abscisic acid levels by immunomodulation in barley grains induces precocious maturation without changing grain composition. J. Exp. Bot. 67 (2016) 2675-2687.

2017

RADCHUK, V., D. RIEWE, M. PEUKERT, A. MATROS, M. STRICKERT, R. RADCHUK, D. WEIER, H.-H. STEINBIß, N. SREENIVASULU, W. WESCHKE & H. WEBER: Down-regulated sucrose transporters HvSUT1, HvSUT2 affects sucrose homeostasis along its delivery path in barley grains. J. Exp. Bot. 68 (2017) 4595-4612.

WEICHERT, H., P. HÖGY, I. MORA-RAMIREZ, J. FUCHS, K. EGGERT, P. KOEHLER, W. WESCHKE, A. FANGMEIER, H. WEBER & G. REBETZKE: Grain yield and quality responses of wheat expressing a barley sucrose transporter to combined climate change factors. J. Exp. Bot. 68 (2017) 5511-5525.

Theses

2016

AMMANN, M.K.: Analyse der Ertragsparameter und molekularen Grundlagen der RNAi-vermittelten Suppression der ABA-8'Hydroxylase-Aktivität in Gerste. (Bachelor Thesis) Friedrich-Schiller-Universität Jena, Biologisch-Pharmazeutische Fakultät, Institut für Ernährungswissenschaften, Jena (2016) 46 pp.

BOHRA, U.: Phenotypic variation of the trait grain yield distribution along the spike in a winter wheat population of elite lines and genetic resources. (Master Thesis) Technische Universität München, Biotechnologie gartenbaulicher Kulturen Weihenstephan, Department Pflanzenwissenschaften, München (2016) 43 pp.

MORA RAMIREZ, M.I.: Transgenic winter wheat – increased sucrose uptake capacity accelerates plant development and enhances grain yield. (PhD Thesis) Martin-Luther-Universität Halle-Wittenberg, Naturwissenschaftliche Fakultät I Biowissenschaften, Halle/S. (2016) 89 pp.

2017

ABEBAW, Y.M.: Ectopic expression of a *Vicia faba* amino acid permease (*VfAAP1*) improves grain yield and stimulates seedling root growth in wheat (*Triticum aestivum*). (PhD Thesis) Martin-Luther-Universität Halle-Wittenberg, Naturwissenschaftliche Fakultät I Biowissenschaften, Halle/S. (2017) 127 pp.

TRAN THI THUY, V.: The role of vacuolar processing enzymes in programmed cell death in maternal tissues of the developing barley grain. (PhD Thesis) Martin-Luther-Universität Halle-Wittenberg, Naturwissenschaftliche Fakultät I Biowissenschaften, Halle/S. (2017) 106 pp.

Research Group: Gene Regulation (GR)

Head: Dr. habil. Helmut Bäumlein (until 17.04.2017), Prof. Dr. Thomas Altmann (temp.)

Scientists

Dr. Paride Rizzo

Dr. Francesca Tedeschi

Keywords

Apospory Marker Locus

Gametophytic Cell Differentiation

Transcription Regulators

Epigenetic Regulators

DNA Methylation

CRISPR-CAS Mutants

Highlights

Tedeschi F, et al. RWP-RK domain-containing transcription factors control cell differentiation during female gametophyte development in Arabidopsis. New Phytol. 213 (2017) 1909-1924.

Funding

DFG

The research group deals with the molecular dissection of genetic and epigenetic pathways that control sexual and asexual plant reproduction. We characterize a genetic locus co-segregating with apospory, a component of apomixis. We identify regulatory networks that control gametophytic development including gene regulators of the RKD class. We analyze ET factors as novel epigenetic gene regulators involved in the control of DNA-methylation with effects on cell differentiation and development during plant reproduction.

Research Statement and Major Achievements

The RG deals with the molecular dissection of genetic and epigenetic pathways that control sexual and asexual plant reproduction.

In *Hypericum*, we further characterize the HAPPY locus which co-segregates with apospory, an important component of apomixis (in cooperation with RG *HET*). The apo-linked allele contains destroyed genes, is extended by the insertion of copia-like transposons, and is composed of three contributing sexual loci. To improve assembly and annotation, two overlapping BACs (in total 0.6 Mb) of the aposporous allele have been reanalyzed by mate paired sequencing (in cooperation with RG *HET*). Deep RNA sequencing has been performed on carefully characterized reproductive organs at different developmental stages with the aim of identifying candidate genes of critical importance for the occurrence of aposporic events (Fig. 36). Candidate gene transcripts have been mapped on HAPPY and a model of the aposporous developmental pathway combining morphological and molecular data has been proposed (in cooperation with RG *HET*).

Another approach concerns the identification of regulatory networks that control gametophytic development. Based on egg cell specific genes of wheat, we continue to characterize a class of gametophytic transcription regulators, the RKD factors, of Arabidopsis. The plant-specific occurrence, egg-cell specific expression, the mis-expression phenotype and evolutionary conservation identify RKD factors as key re-

Fig. 36 Ovule of *Hypericum perforatum* carrying a mature female gametophyte; two synergids cells (highlighted in green), one egg cell (highlighted in cyan), two polar nuclei (highlighted in pink), gametophytic domain (highlighted in blue).

gulators of female gamete identity. Ectopic expression of RKD genes causes the reprogramming of sporophytic cells to adopt aspects of egg cell identity. In total we have isolated and characterized 12 T-DNA insertion alleles and one TILLING allele of all five RKD genes. An approach to isolate additional alleles using the TALEN technique failed and is currently replaced by the CRISPR/Cas9 approach with first observations being promising. Due to functional redundancy we have used selected alleles to generate various double mutant combinations. Interestingly, these mutants exhibit heterochronic shifts in gametophyte developmental as well as arrest at the stage of the functional megaspore. The mutants are analyzed based on gametophytic marker lines specifying the functional megaspore, central cell, synergids and egg cell. In addition to the previously used markers we currently apply more advanced constructs with nuclei-located reporters (Tedeschi et al., 2017).

We have progressed in the functional characterization of the EFFECTOR OF TRANSCRIPTION (ET) gene family. ET factors function as novel gene regulators and participate in the control of cell differentiation, including processes during plant reproduction. We have isolated and analyzed in total 5 T-DNA insertion alleles as well as double mutants for the three genes in the Arabidopsis genome. Mutant analyses of the Arabidopsis *ET* gene family revealed pleiotropic developmental effects including failure in polar nuclei fusion required for double fertilization and endosperm development. Mutants exhibit a conspicuous homoeotic transformation of flower organs with anthers transformed into carpel-like structures. The endosperm nuclei of the mutants exhibit unusually large nucleoli probably indicating a high synthetic activity. The mutants germinate precociously with the cotyledons and not the root tip penetrating the seed coat first. Comparative molecular analyses including deep RNA sequencing and genome-wide methylation studies have been performed and reveal a strong ET1-specific induction of Athila transposon expression. The results suggest that ETs act as novel epigenetic regulators of genomic DNA methylation and are required for normal plant development (in cooperation with RG *HET*). For putative further studies novel CRISPR/Cas9 generated mutants (two alleles both for *ET1* and *ET2*) have been isolated and partially characterized.

Embedding in Departmental and IPK Research Strategy

The research of the group contributes to the *MOG* research area *Seed Biology* and the IPK research theme 3 *Mechanism of Plant Reproduction*.

Plans, Opportunities and Challenges

The group leader retired by April 2017 and all other scientific group members or associated scientists were relocated to other RGs or to new positions in science or industry until the end of 2017. Currently we heavily pursue the publication of the ET- and Hypericum data. Further utilization of the groups research resources as for instance *rkd*- and *et*- mutants, gametophyte cell- specific marker lines, transcriptome and methylome data etc. are under discussion.

Peer Reviewed Papers

2016

SHAH, J.N., O. KIRIOUKHOVA, P. PAWAR, M. TAYYAB, J.L. MATEO & A.J. JOHNSTON: Depletion of key meiotic genes and transcriptome-wide abiotic stress reprogramming mark early preparatory events ahead of apomeiotic transition. Front. Plant Sci. 7 (2016) 1539.

2017

TEDESCHI, F., P. RIZZO, T. RUTTEN, L. ALTSCHMIED & H. BÄUMLEIN: RWP-RK domain-containing transcription factors control cell differentiation during female gametophyte development in Arabidopsis. New Phytol. 213 (2017) 1909-1924.

Theses

2016

RIZZO, P.: Novel insights on female gametophyte development in the apomictic model species *Boechera* spp. and *Hypericum* spp. (PhD Thesis) Martin-Luther-Universität Halle-Wittenberg, Naturwissenschaftliche Fakultät I Biowissenschaften, Halle/S. (2016) 182 pp.

Research Group: Phytoantibodies (PAK)

Head: Prof. Dr. Udo Conrad

Scientists

Dr. Trong Hoang Phan

Eberhard Sorge

Dr. Nicola Weichert

Keywords

Molecular Farming

Plant-based Vaccines

Directed Protein Degradation

Recombinant Antibodies

Highlights

Phan, HT, et al.: Neutralizing immune responses induced by oligomeric H5N1-hemagglutinins from plants. Veterinary Research, in press (S-Tag-S-protein interaction).

Funding and start of the Multifluvac project: Neutralisierende Immunantworten gegen Vogelgrippeviren durch oligomere H5-Vogelgrippevirushämagglutinine aus Pflanzen. WIPANO-Wissens- und Technologietransfer durch Patente und Normen. The project will help to strengthen the S-Tag-S-protein patent application.

Funding

FNR, BMBF

The main objectives of the research group *Phytoantibodies* are the production of recombinant vaccines and recombinant fiber proteins in plants, and directed proteolysis of proteins in transgenic plants.

Research Statement and Major Achievements

Molecular Farming experiments were performed with recombinant spider silk proteins to develop new materials for technical and medical purposes in plants. Methods to purify and desalt multimeric recombinant spider silk proteins from leaves and seeds have been further developed. Nanofleeces have been produced from these materials and were characterized. The use of these fleeces as scaffolds for cell cultures is under study (in cooperation with Tobias Kürbitz *IWM* Halle, Sarah Strauß *Transplantationsmedizin Hannover*).

Two further new strategies to oligomerize hemagglutinin have been developed using streptactin-strep-tag interaction and S-protein–S-Tag interaction. In combination with trimerization oligomers of large size have been produced in *N. benthamiana* (Fig. 37). The oligomers have been tested by an hemagglutination assay and multimers showing higher degrees of hemagglutination induction have been selected and purified by imnunoaffinity chromatography. The immunological characterization by injection in mice and measurement of hemagglutination inhibition capacity showed high neutralizing capacity for both strategies. This has also been shown for crude extracts. The streptactin-strep-tag oligomers can be formed *in vitro* and could be kept stable for at least 6 weeks at 4°C. Oligomers induced by trimerization and tailpiece sequences, trimerization and antiparallel peptides as well as trimerization and homodimer proteins have been tested as purified oligomers as well as crude extracts by injection in mice and measurement of hemagglutination inhibition capacity and show in all cases enhanced neutralizing capacity. Purified oligomers from these constructs as well as trimers have been succesfully tested in a challenge experiment in chicken (in cooperation with *FLI* Riems).

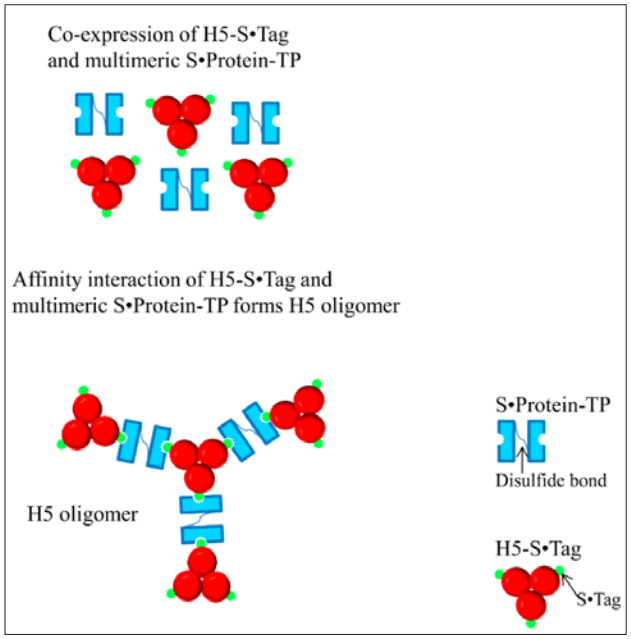

Fig. 37 Model of H5 oligomer formation by co-expression of H5-S•-Tag and multimeric S•Protein-TP oligomerized by disulfide bonds.

The degradation of proteins by the 26S proteasome after polyubiquitinylation is one significant pathway of intracellular degradation of proteins. The interaction with F-box proteins as well as with BTB is a presumption for the transport of the proteins to the proteasome. A specific nanobody against a methyltransferase from *Plasmodiophora brassicae* has been selected by Phage Display and characterized. This nanobody is under study to allow destruction of the pathogen methyltransferases. Anti GFP nanobody – BTB fusions have been shown to cause GFP depletion especially in nuclei of GFP expressing transgenic plants. This result is a precedence of targeted proteolysis of proteins like transcription factors in the nucleus.

Embedding in Departmental and IPK Research Strategy

The studies to allow destruction of a pathogen methyltransferases by nanobody-directed degradation fit into Research Theme 5 *Mechanisms of Resistance and Stress Tolerance*.

We cooperate with the RG *Chromosome Structure and Function* to induce haploidization via proteasome mediated degradation of CENH3 (Research Theme 3: *Mechanisms of Plant Reproduction*).

Plans, Opportunities and Challenges

The directed degradation of functional proteins will be used to selectively degrade key factors of regulation in hormone-dependent and other regulatory pathways. This will contribute to Research Themes 4 (*Growth and Metabolism*) and 3 (*Mechanisms of Plant Reproduction*). The Molecular Farming projects (Spider silk protein multimers from plants, Avian flu vaccines from plants) will be further developed in the next two years and planned to be continued in labs of cooperation partners (*Institut für Transplantationsmedizin* Hannover, *IBT* Hanoi, *AIPlanta* Neustadt).

Peer Reviewed Papers

2016

HEPPNER, R., N. WEICHERT, A. SCHIERHORN, U. CONRAD & M. PIETZSCH: Low-tech, pilot scale purification of a recombinant spider silk protein analog from tobacco leaves. Int. J. Mol. Sci. 17 (2016) 1687.

HOFBAUER, A., S. MELNIK, M. TSCHOFEN, E. ARCALIS, H.T. PHAN, U. GRESCH, J. LAMPEL, U. CONRAD & E. STOGER: The encapsulation of hemagglutinin in protein bodies achieves a stronger immune response in mice than the soluble antigen. Front. Plant Sci. 7 (2016) 142.

MA, W., V. SCHUBERT, M.M. MARTIS, G. HAUSE, Z. LIU, Y. SHEN, U. CONRAD, W. SHI, U. SCHOLZ, S. TAUDIEN, Z. CHENG & A. HOUBEN: The distribution of alpha-kleisin during meiosis in the holocentromeric plant *Luzula elegans*. Chromosome Res. 24 (2016) 393-405.

STAROSKE, N., U. CONRAD, J. KUMLEHN, G. HENSEL, R. RADCHUK, A. ERBAN, J. KOPKA, W. WESCHKE & H. WEBER: Increasing abscisic acid levels by immunomodulation in barley grains induces precocious maturation without changing grain composition. J. Exp. Bot. 67 (2016) 2675-2687.

TOPP, E., R. IRWIN, T. MCALLISTER, M. LESSARD, J.J. JOENSUU, I. KOLOTILIN, U. CONRAD, E. STÖGER, T. MOR, H. WARZECHA, J.C. HALL, M.D. MCLEAN, E. COX, B. DEVRIENDT, A. POTTER, A. DEPICKER, V. VIRDI, L. HOLBROOK, K. DOSHI, M. DUSSAULT, R. FRIENDSHIP, O. YAROSH, H.S. YOO, J. MACDONALD & R. MENASSA: The case for plant-made veterinary immunotherapeutics. Biotechnol. Adv. 34 (2016) 597-604.

WEICHERT, N., V. HAUPTMANN, C. HELMOLD & U. CONRAD: Seed-specific expression of spider silk protein multimers causes long-term stability. Front. Plant Sci. 7 (2016) 6.

2017

PHAM, N.B., T.T. HO, G.T. NGUYEN, T.T. LE, N.T. LE, H.C. CHANG, M.D. PHAM, U. CONRAD & H.H. CHU: Nanodiamond enhances immune responses in mice against recombinant HA/H7N9 protein. J. Nanobiotechnol. 15 (2017) 69.

PHAN, H.T., T.T. HO, H.H. CHU, T.H. VU, U. GRESCH & U. CONRAD: Neutralizing immune responses induced by oligomeric H5N1-hemagglutinins from plants. Vet. Res. 48 (2017) 53.

SANDMANN, M., P. TALBERT, D. DEMIDOV, M. KUHLMANN, T. RUTTEN, U. CONRAD & I. LERMONTOVA: Targeting of *A. thaliana* KNL_2 to centromeres depends on the conserved CENPC-k motif in its C-terminus. Plant Cell 29 (2017) 144-155.

Articles in Compilations

2016

PHAN, H.T. & U. CONRAD: Plant-based vaccine antigen production. In: BRUN, A. (Ed.): Vaccine technologies for veterinary viral diseases. Methods and protocols. (Series: Methods in molecular biology, Vol. 1349) New York: Springer (2016) 35-47.

Theses

2016

HO, T.T.: Oligomeric avian flu hemagglutinins from plants based on S tag–S protein interaction induce potentially neutralizing immune responses in mice. (Master Thesis) University of Science and Technology of Hanoi, Bio-Pharmacology, Hanoi, Vietnam (2016) 49 pp.

SORGE, E.: Analysen zur Interaktion von ASK-Proteinvarianten mit F-Box-Proteinen. (Master Thesis) Martin-Luther-Universität Halle-Wittenberg, Naturwissenschaftliche Fakultät I Biowissenschaften, Halle/S. (2016) 41 pp.

WESELEK, A.: Multimerisierung von Nanobodies durch Intein-vermitteltes trans-splicing in Pflanzen. (Master Thesis) Martin-Luther-Universität Halle-Wittenberg, Naturwissenschaftliche Fakultät III, Institut für Agrar- und Ernährungswissenschaften, Halle/S. (2016) 56 pp.

2017

BRÜNNER, B.: Expression von *Shiga-like* Toxoiden in Pflanzen. (Bachelor Thesis) Martin-Luther-Universität Halle-Wittenberg, Naturwissenschaftliche Fakultät I Biowissenschaften, Halle/S. (2017) 48 pp.

Research Group: Assimilate Allocation and NMR (AAN)

Head: PD Dr. Ljudmilla Borisjuk

Scientists

Dipl.-Ing. Andre Gündel
Dr. Nicolas Heinzel
Dipl.-Ing. Peter Keil
Dipl. Biol. Christina König
Dr. Christiane Matthess
Dipl. Biol. Tobias Meitzel
Dipl. Phys. Eberhard Munz
Dipl. Biol. Aleksandra Muszynska
Dipl.-Ing. Stefan Ortleb
Dr. Volodymyr Radchuk
Dr. Paride Rizzo
Dr. habil. Hardy Rolletschek
Dr. Diana Weier

Keywords

Seed Metabolism
Metabolic Architecture
NMR
In vivo Monitoring
Assimilate Delivery
Functional Imaging

Highlights

Dynamic visualization of transport tissue and *in vivo* monitoring of glandular secretion in plants (Dissertation E. Munz; PNAS 114/2017).

SWEET´s - genes involved in sugar transport to developing barley seeds (Nature 544/2017).

Functional imaging of seed germination (New Phytologist, 10.1111/nph.14736) and molecular-physiological characterization of oilseed rape seeds (Dissertation C. König, 2017).

Novel link between seed filling and the phytohormone auxin was discovered (Dissertation Meitzel; McAdam et al., New Phytol. 2017).

Mechanisms controlling seed size: TaHDZipI-2 (New Phytol, 211/2016), VPE -4(New Phytologist, 10.1111/nph.14729).

New imaging methods for metabolites and phytohormones based on FTIR microscopy, spatial and temporal mapping of lipid species using MRI and MALDI-MSI in seeds (Biochemistry 139/2016; Plant Physiology 173/2017).

Funding

Leibniz, PhytoAD, EU, BMBF (DPPN), DFG, Industry-funded projects

Our overreaching goal is an understanding of the mechanisms of seed performance. We investigate the architecture and the metabolism of seeds during filling and germination. We develop topographical, *in vivo* approaches to identify key factors determining the uptake and transport of assimilates in the developing seed and their partitioning into starch, lipids and storage proteins. Preferred plant models are cereals and oil crops. Our approaches crucially rely on novel, non-destructive and imaging procedures, based on nuclear magnetic resonance (NMR), infrared spectroscopy and optical sensors.

Research Statement and Major Achievements

Assimilate allocation from the maternal plant into the developing seed is essential for seed growth and filling, and has been in the focus of our work for a long time. We recently demonstrated that expansions and specifications in SWEET and Vacuolar Processing Enzyme (VPE) gene families are related to the specific function of the nucellar projection as a predominant tissue for assimilate delivery into barley grains. Both SWEET11a/b genes are active in maternal seed tissue but differed in the distribution of expression domains (Mascher et al., 2017). Further we have demonstrated that the vacuolar Sucrose Transporter 2 (SUT2) acts coordinately with the plasma membrane-localized SUT1 to maintain sucrose homeostasis along the grains sucrose delivery route (Radchuk et al., 2017). Studies on their relation to morphological and physiological features of grain will be continued in current DFG and industry funded projects.

By analyzing metabolite delivery, metabolic and hormone status in garden pea and its wrinkled seed mutants, a novel link between seed filling and the phytohormone auxin was discovered. This demonstrates that specific auxins can be key factors for the control of seed size and starch accumulation (McAdam et al., 2017). We further demonstrated that VPE4 executes PCD in maternal seed tissues and contributes to maternal control of grain size in barley (Radchuk et al., 2017). Novel NMR-based tools

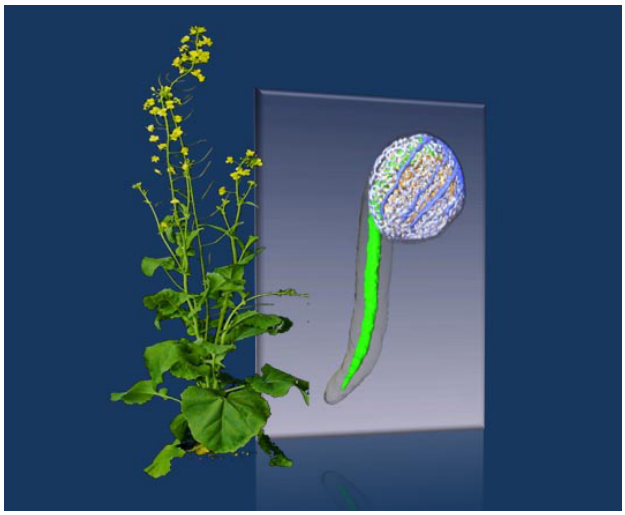

Fig. 38 Noninvasive visualization of germinating seed (*Brassica napus*) and its vasculature, which gives rise to the vascular system of the mature plant. Recent NMR-based studies uncovered how seed architecture predetermines the pattern of water intake and sets the stage for the orchestrated restart of life (Image by S. Ortleb and S. Herrmann).

for *in vivo* analytic on plants support our scientific work and co-operations (PNAS 114/2017; Biochem. 139/2016; Plant Physiol. 173/2017).

Germination, the process whereby a dormant seed springs to life, was investigated in *Brassica napus*. A holistic *in vivo* approach was designed to characterize the structural changes occurring during germination, the entry and redistribution of water, as well as carbon and energy metabolism. Functional NMR-imaging visualizes how imbibition is governed by the seed's architecture and the embryo's vasculature (Fig. 38). For the first time the spatiotemporal sequence of the awakening process in seed has been demonstrated (Munz et al., 2017).

Embedding in Departmental and IPK Research Strategy

We contribute centrally to the *MOG* research area *Seed Biology* by addressing critical processes of uptake, distribution, and conversion of assimilates and their accumulation into storage compounds in relation to the 3D architecture of seeds. We collaborate closely with the *MOG* RGs *SE* (in particular with respect to growth and differentiation of seed tissues), *NAM*, and *HET* and further IPK RGs such as *ABC*, *CSF*, and *PRB* e.g. by investigations of the role of VPEs and sucrose transporters in barley grains (joint publications Radchuk et al., 2017; Radchuk et al., 2017). Our work is mainly integrated into the IPK research theme 4 *Growth and Metabolism* and we contribute to theme 1 *Concepts for Valorization of Generic Resources*, theme 2 *Genome Diversity and Evolution*, and theme 5 *Mechanism of Resistance and Stress Tolerance*. Studies on SWEETs led to cooperation with the *GB* and *BR* departments (Mascher et al., 2017). We develop new technology approaches, which are open to other users aiming at investigation of seed performance and crop biodiversity.

Plans, Opportunities and Challenges

Our plans involve: 1) Identifying new seed traits and quantifying seed diversity (non-invasive imaging and high-throughput screening). 2) Spatially and temporally resolved assimilate delivery toward reproductive structures. 3) Assimilate uptake and redistribution within seed organs (e.g. role of SWEET´s, maternal-filial exchange, Jekyll and PCD). 4) Architecture of storage metabolism in seeds. 5) Assimilate conversion in central metabolism. 6) Developmental determinants of seed germination, vigour and, seed quality markers. 7) Development of new technologies (based on NMR and FT IR) for spatial analysis of metabolites, marker free assessment of physiological parameters and seed growth. 8) Development of new Orbitrap-technology (LC/MS) for ultra-sensitive detection of metabolic signatures. 9) Establishing a strong collaboration with the maize scientific community toward dissemination of our new technology and scientific exchange in the field of seed metabolism.

Installation of the novel NMR-instrumentation (Avance III HD 400 WB Spectrometer and Cryo-Probehead MIC 400) for high resolution structural and metabolic imaging of seeds relies on cooperation with specialists from *Bruker GmbH*, *University of Würzburg* and *Pennsylvania State University* (USA) and will open new perspectives for *in vivo* analytics at IPK. Our RG thanks Steffen Wagner for excellent technical support and teamworking. Establishment of new labs was largely supported by the *Administration and Central Services* Department.

Peer Reviewed Papers

2016

KOVALCHUK, N., W. CHEW, P. SORNARAJ, N. BORISJUK, N. YANG, R. SINGH, N. BAZANOVA, Y. SHAVRUKOV, A. GUENDEL, E. MUNZ, L. BORISJUK, P. LANGRIDGE, M. HRMOVA & S. LOPATO: The homeodomain transcription factor TaHDZipI-2 from wheat regulates frost tolerance, flowering time and spike development in transgenic barley. New Phytol. 211 (2016) 671-687.

MUNZ, E., P.M. JAKOB & L. BORISJUK: The potential of nuclear magnetic resonance to track lipids in planta. Biochimie 130 (2016) 97-108.

2017

MASCHER, M., H. GUNDLACH, A. HIMMELBACH, S. BEIER, S.O. TWARDZIOK, T. WICKER, V. RADCHUK, C. DOCKTER, P.E. HEDLEY, J. RUSSELL, M. BAYER, L. RAMSAY, H. LIU, G. HABERER, X.-Q. ZHANG, Q. ZHANG, R.A. BARRERO, L. LI, S. TAUDIEN, M. GROTH, M. FELDER, A. HASTIE, H. ŠIMKOVÁ, H. STAŇKOVÁ, J. VRÁNA, S. CHAN, M. MUÑOZ-AMATRIAÍN, R. OUNIT, S. WANAMAKER, D. BOLSER, C. COLMSEE, T. SCHMUTZER, L. ALIYEVA-SCHNORR, S. GRASSO, J. TANSKANEN, A. CHAILYAN, D. SAMPATH, D. HEAVENS, L. CLISSOLD, S. CAO, B. CHAPMAN, F. DAI, Y. HAN, H. LI, X. LI, C. LIN, J.K. MCCOOKE, C. TAN, P. WANG, S. WANG, S. YIN, G. ZHOU, J.A. POLAND, M.I. BELLGARD, L. BORISJUK, A. HOUBEN, J. DOLEŽEL, S. AYLING, S. LONARDI, P. KERSEY, P. LANGRIDGE, G.J. MUEHLBAUER, M.D. CLARK, M. CACCAMO, A.H. SCHULMAN, K.F.X. MAYER, M. PLATZER, T.J. CLOSE, U. SCHOLZ, M. HANSSON, G. ZHANG, I. BRAUMANN, M. SPANNAGL, C. LI, R. WAUGH & N. STEIN: A chromosome conformation capture ordered sequence of the barley genome. Nature 544 (2017) 427-433.

MCADAM, E.L.*, T. MEITZEL*, L.J. QUITTENDEN, S.E. DAVIDSON, M. DALMAIS, A.I. BENDAHMANE, R. THOMPSON, J.J. SMITH, D.S. NICHOLS, S. URQUHART, A. GÉLINAS-MARION, G. AUBERT & J.J. ROSS: Evidence that auxin is required for normal seed size and starch synthesis in pea. New Phytol. 216 (2017) 193-204. (*joint first authorship)

MUNZ, E., H. ROLLETSCHEK, S. OELTZE-JAFRA, J. FUCHS, A. GUENDEL, T. NEUBERGER, S. ORTLEB, P.M. JAKOB & L. BORISJUK: A functional imaging study of germinating oilseed rape seed. New Phytol. 216 (2017) 1181-1190.

RADCHUK, V., D. RIEWE, M. PEUKERT, A. MATROS, M. STRICKERT, R. RADCHUK, D. WEIER, H.-H. STEINBIß, N. SREENIVASULU, W. WESCHKE & H. WEBER: Down-regulated sucrose transporters HvSUT1, HvSUT2 affects sucrose homeostasis along its delivery path in barley grains. J. Exp. Bot. 68 (2017) 4595-4612.

SCHERZER, S., L. SHABALA, B. HEDRICH, J. FROMM, H. BAUER, E. MUNZ, P. JAKOB, K.A.S. AL-RASCHEID, I. KREUZER, D. BECKER, M. EIBLMEIER, H. RENNENBERG, S. SHABALA, M. BENNETT, E. NEHER & R. HEDRICH: Insect haptoelectrical stimulation of Venus flytrap triggers exocytosis in gland cells. Proc. Natl. Acad. Sci. U. S. A. 114 (2017) 4822-4827.

WOODFIELD, H.K., D. STURTEVANT, L. BORISJUK, E. MUNZ, I.A. GUSCHINA, K.D. CHAPMAN & J.L. HARWOOD: Spatial and temporal mapping of key lipid species in *Brassica napus* seeds. Plant Physiol. 173 (2017) 1998-2009.

Articles in Compilations

2016

KELLER, E.R.J., M. GRÜBE, M.-R. HAJIREZAEI, M. MELZER, H.-P. MOCK, H. ROLLETSCHEK, A. SENULA & K. SUBBARAYAN: Experience in large-scale cryopreservation and links to applied research for safe storage of plant germplasm. In: LAMBARDI, M. & S. HAMILL (Eds.): Proceedings of the XXIX IHC - Int. Symp. on Micropropagation and In Vitro Techniques, Brisbane, Australia, August 17-22, 2014. (Series: Acta Horticulturae, Vol. 1113) Leuven: ISHS (2016) 239-249.

2017

KEIL, P., G. LIEBSCH, L. BORISJUK & H. ROLLETSCHEK: MultiSense: a multimodal sensor tool enabling the high throughput analysis of respiration. In: KAPUGANTI, J.G. (Ed.): Plant respiration and internal oxygen. Methods and protocols. (Series: Methods in molecular biology, Vol. 1670) New York, NY [u.a.]: Humana Press (2017) 47-56.

REICHELT, W.N., M. BRILLMANN, P. THURROLD, P. KEIL, J. FRICKE & C. HERWIG: Physiological capacities decline during induced bioprocesses leading to substrate accumulation. In: FERREIRA, G.N.M. & J. GLASSEY (Eds.): Biotechnol. J. (Special Issue: European Symposium on Biochemical Engineering Science, Dublin 2016). (Vol. 7): WILEY-VCH Verlag (2017) 1600547.

ROLLETSCHEK, H., L. BORISJUK, T.A. HENNEN-BIERWAGEN & A.M. MYERS: Central metabolism and its spatial heterogeneity in maize endosperm. In: LARKINS, B.A. (Ed.): Maize Kernel Development. Boston, MA: CABI (2017) 134-148.

ROLLETSCHEK, H. & G. LIEBSCH: A method for imaging oxygen distribution and respiration at a microscopic level of resolution. In: KAPUGANTI, J.G. (Ed.): Plant respiration and internal oxygen. Methods and protocols. (Series: Methods in molecular biology, Vol. 1670) New York, NY [u.a.]: Humana Press (2017) 31-38.

Theses

2017

BORISJUK, L.: The inner life of seed: from seeing to understanding. (Habilitation Thesis) Leibniz Universität Hannover, Naturwissenschaftliche Fakultät, Hannover (2017) 402 pp.

KÖNIG, C.: Molecular and metabolic characterization of assimilate uptake and storage product synthesis in *Brassica napus.* (PhD Thesis) Leibniz Universität Hannover, Naturwissenschaftliche Fakultät, Hannover (2017) 119 pp.

Research Group: Image Analysis (BA)

Head: Dr. Evgeny Gladilin (since 01.11.2016)

Scientists

Dr. Michael Henke

Jean-Michel Pape

Keywords

Automated image analysis

Shoot/root segmentation

Multimodal image fusion

Quantitative plant traits

Virtual plant modeling

Highlights

Establishment of RG BA (incl. new personal and infrastructure).

Publication a joint paper together with RG CSF (Dressig et al., Plant J. 2017).

Participation on PLANT 2030 Status Seminar 2017, Potsdam.

Funding

DPPN

The research group *Image Analysis* (BA) focuses on development of algorithms and an integrative software environment for quantitative characterization (phenotyping) of morphological, developmental and physiological plant traits from multimodal and multidimensional data such as visible light, fluorescence, near-infrared, 3D or microscopic images. The tasks of image analysis include image enhancement, segmentation, registration, recognition, classification, virtual modelling and phenotypic description of relevant plant structures (e.g., shoots, roots, seeds, cells).

Research Statement and Major Achievements

In November 2016, the position of the reserach group leader *BA* was taken by Dr. E. Gladilin and the group is still in its building-up phase (Postdoc, Dr. M. Henke, since 15. April 2017, technician A. Chelamalashetty, since 1. July 2017). As a part of *Dept. Molecular Genetics* (MOG), the RG *BA* focuses on development of advanced algorithmic solutions and an integrative software environment for quantitative description (phenotyping) of morphological, developmental and physiological plant traits on the basis of multimodal and multidimensional image data from different camera systems, including visible light, fluorescence and near-infrared, and 3D image data. The research foci of the group include development of methods for

- enhancement and segmentation of high-throughput plant images, Fig. 39 (A,B),
- registration of multimodal images and image time-series, Fig. 39 (C,D),
- statistical modeling of plant and background structures,
- integrative software environment including efficient algorithms and GUI interfaces,
- physiological modeling of plant light interception,
- derivation of advanced traits of plant morphology, development and function.

In 2016-2017, the focus of R&D activities of the group was on investigation of advanced techniques for automated registration and segmentation of shoot/root images.

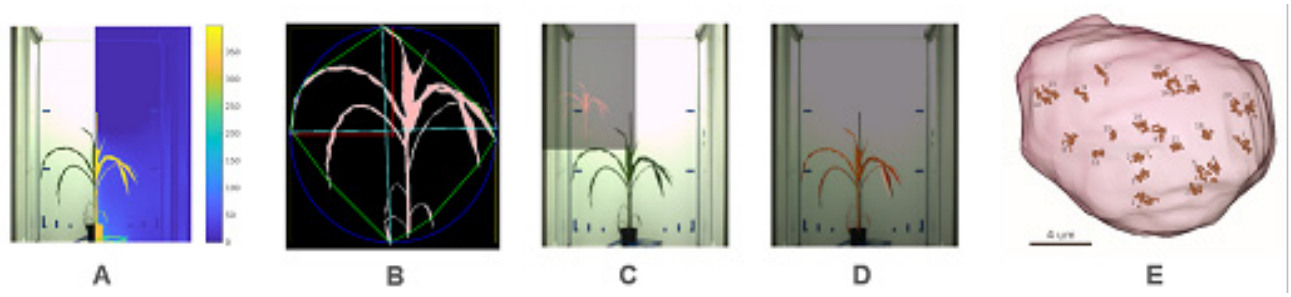

Fig. 39 Examples of plant image analysis. A. Segmentation of visible light image of a maize shoot by means of background-distance clustering. B. Segmented image of a maize shoot including measurements of some morphological features. C-D. Overlay of visible light and fluorescence images of a maize shoot before (C) and after affine image registration (D). E. 3D model of a plant cell nucleus and telomeres generated from time-series of CLSM images (Dreissig et al., Plant J. 2017).

Contacts to different groups and departments of IPK and external technology providers (i.a., Fa. *LemnaTec*, Fa. *Phenospex*) were established. Existing infrastructure for image acquisition and analysis was assessed and upgraded.

Embedding in Departmental and IPK Research Strategy

The RG *BA* is closely cooperating with several research groups at IPK. Within the scope of the *DPPN* (Deutsches Pflanzen Phänotypisierungsnetzwerk, BMBF) project, the RG *BA* develops and evaluates novel methods for macroscopic shoot/root phenotyping using image data from high-throughput experiments carried out by the RGs *HET*, *GED*, *MPE*. The results of image analysis, in turn, serve as an input for integrative bioinformatics models developed in the RG *NAM*. Concepts of unified data-base interfaces for different data modalities are elaborated together with the RG *BIT*. Furthermore, the RG *BA* contributes to analysis of microscopic images in the RGs *ABC*, *PSG*, *CSF*, Fig. 39 (E).

Plans, Opportunities and Challenges

Due to a number of natural and technical reasons, the optical appearance of plants undergoes considerable variations in color, shape and location. Furthermore, plant images are overlaid with statistical and structural noise which makes generalization and full automation of image analysis a challenging task. Consequently, previously developed algorithms often require a time-consuming manual adjustment for every new dataset. In order to process a large amount of heterogeneous image data in an unsupervised manner, advanced algorithmic solutions are required. Experimental and theoretical investigations of supervised and unsupervised methods for image segmentation and registration carried out this year provide a basis for further development of approaches to automated image analysis. Publication of R&D works is currently in preparation.

Phenotyping of plant roots growing in an opaque environment represents a great challenge for image analysis. Scarce structural information, low image contrast and high level of noise make application of conventional methods of image segmentation ineffective. Consequently, root image analysis is typically performed using manual or semi-automated approaches. To cope with the complexity of root images, novel algorithmic solutions are required. Investigations of structural enhancement and machine learning techniques started this year and will be continued in the future.

Development and maintenance of complex scientific code for analysis of large amount of heterogeneous image data requires sustainable human resources. The RG *BA* plans acquisition of third party funding's and actively participates in establishment of funding consortia together with IPK and external cooperation partners.

Peer Reviewed Papers

2016

AREND, D., M. LANGE, J.-M. PAPE, K. WEIGELT-FISCHER, F. ARANA-CEBALLOS, I. MÜCKE, C. KLUKAS, T. ALTMANN, U. SCHOLZ & A. JUNKER: Quantitative monitoring of *Arabidopsis thaliana* growth and development using high-throughput plant phenotyping. Scientific Data 3 (2016) 160055.

ĆWIEK-KUPCZYŃSKA, H., T. ALTMANN, D. AREND, E. ARNAUD, D. CHEN, G. CORNUT, F. FIORANI, W. FROHMBERG, A. JUNKER, C. KLUKAS, M. LANGE, C. MAZUREK, A. NAFISSI, P. NEVEU, J. VAN OEVEREN, C. POMMIER, H. POORTER, P. ROCCA-SERRA, S.-A. SANSONE, U. SCHOLZ, M. VAN SCHRIEK, Ü. SEREN, B. USADEL, S. WEISE, P. KERSEY & P. KRAJEWSKI: Measures for interoperability of phenotypic data: minimum information requirements and formatting. Plant Methods 12 (2016) 44.

SCHARR, H., M. MINERVINI, A.P. FRENCH, C. KLUKAS, D.M. KRAMER, X. LIU, I. LUENGO, J.-M. PAPE, G. POLDER, D. VUKADINOVIC, X. YIN & S.A. TSAFTARIS: Leaf segmentation in plant phenotyping: a collation study. Mach. Vision Appl. 27 (2016) 585-606.

2017

DREISSIG, S., S. SCHIML, P. SCHINDELE, O. WEISS, T. RUTTEN, V. SCHUBERT, E. GLADILIN, M.F. METTE, H. PUCHTA & A. HOUBEN: Live cell CRISPR-imaging in plants reveals dynamic telomere movements. Plant J. 91 (2017) 565-573.

GLADILIN, E.: Graph-theoretical model of global human interactome reveals enhanced long-range communicability in cancer networks. PLoS One 12 (2017) e0170953.

GONZÁLEZ-AVALOS, P., M. MÜRNSEER, J. DEEG, A. BACHMANN, J. SPATZ, S. DOOLEY, R. EILS & E. GLADILIN: Quantification of substrate and cellular strains in stretchable 3D cell cultures: an experimental and computational framework. J. Microsc. 266 (2017) 115-125.

GUO, Z., D. CHEN, A.M. ALQUDAH, M.S. RÖDER, M.W. GANAL & T. SCHNURBUSCH: Genome-wide association analyses of 54 traits identified multiple loci for the determination of floret fertility in wheat. New Phytol. 214 (2017) 257-270.

HENKE, M. & G.H. BUCK-SORLIN: Using a full spectral raytracer for the modelling of light microclimate in a functional-structural plant model. Comput. Inform. 36 (2017) 1492-1522.

MESSICA, Y., A. LASER-AZOGUI, T. VOLBERG, Y. ELISHA, K. LYSAKOVSKAIA, R. EILS, E. GLADILIN, B. GEIGER & R. BECK: The role of vimentin in regulating cell invasive migration in dense cultures of breast carcinoma cells. Nano Lett. 17 (2017) 6941-6948.

MURAYA, M.M., J. CHU, Y. ZHAO, A. JUNKER, C. KLUKAS, J.C. REIF & T. ALTMANN: Genetic variation of growth dynamics in maize (*Zea mays* L.) revealed through automated non-invasive phenotyping. Plant J. 89 (2017) 366-380.

Other Papers

2016

CHEN, D., R. SHI, J.-M. PAPE & C. KLUKAS: Predicting plant biomass accumulation from image-derived parameters. bioRxiv (2016).

Theses

2016

PAPE, J.-M.: Ein Klassifikationssystem zur quantitativen Analyse von Krankheitssymptomen im Kontext der Hochdurchsatz-Phänotypisierung von Pflanzen. (Master Thesis) Fakultät für Informatik, Otto-von-Guericke-Universität, Magdeburg (2016) 84 pp.

Research Group: Network Analysis and Modelling (NAM)

Head: Dr. Andrea Bräutigam (until 30.09.2017), Prof. Dr. Thomas Altmann (temp.)

Scientists

Dr. Mary-Ann Blätke

Stephan Erbe

Florian Schilling

Keywords

Transcriptomics

Photosynthesis

Stoichiometric and Kinetic Models

Regulatory Networks

Highlights

Professorship offer: W2 university of Bielefeld „Computational Biology", accepted.

Seven publications in 2017 including the conceptual model of CAM evolution.

Seven publications in 2016 including a summary on the evolution of C4 photosynthesis.

The research group *Network Analysis and Modeling* describes and models metabolic and regulatory networks focused on but not limited to photosynthesis (regulation, limitations, add-ons such as CAM and C4, associated pathways like photorespiration). Transcriptomics datasets are used to understand complex traits, to elucidate responses to mutations and to stimuli, and to reconstruct regulatory networks underlying complex traits.

Research Statement and Major Achievements

Since starting at the IPK in January 2016, research with a photosynthetic focus has resulted in publications about CAM evolution, the characteristics of C3-C4 intermediate plants and a summary of C4 evolution with particular focus on the role of photorespiration, see Fig. 40 for a brief comparison of C3 and C4 plant characteristics.. Publications concerning the development of photosynthetic leaves were published for de-etiolation of maize, for tissue specific transcriptomes in maize leaves and for barley leaf development. Studies about photorespiration were published dealing with transcriptome responses of mutants, expression specificity in C4 plants, and algal responses to limited CO_2. The *NAM* RG delivered all or parts of the transcriptomic analyses for the transcriptome based publications and the models for the publications about evolution. At the same time, transcriptome analyses for existing and new datasets were started in collaboration with the groups of *GGR* and *CSB* in Genbank, with *BIT* and *CSF* in *Breeding Research*, with *HET* and *SE* in *Molecular Genetics*, with *ABC* in *Physiology and Cell Biology* and with the independent research groups *PBP* and *MT*. Stoichiometric modeling of photosynthetic tissue has resulted in predictions confirmed through literature (unpublished) and are currently extended to include variations in inputs and possible variations in outputs with regard to the photosynthetic type. A kinetic model of C4 photosynthesis has revealed mechanistic explanations for long-known but unexplained features of C4 plants (manuscript prepared), see also Fig. 40.

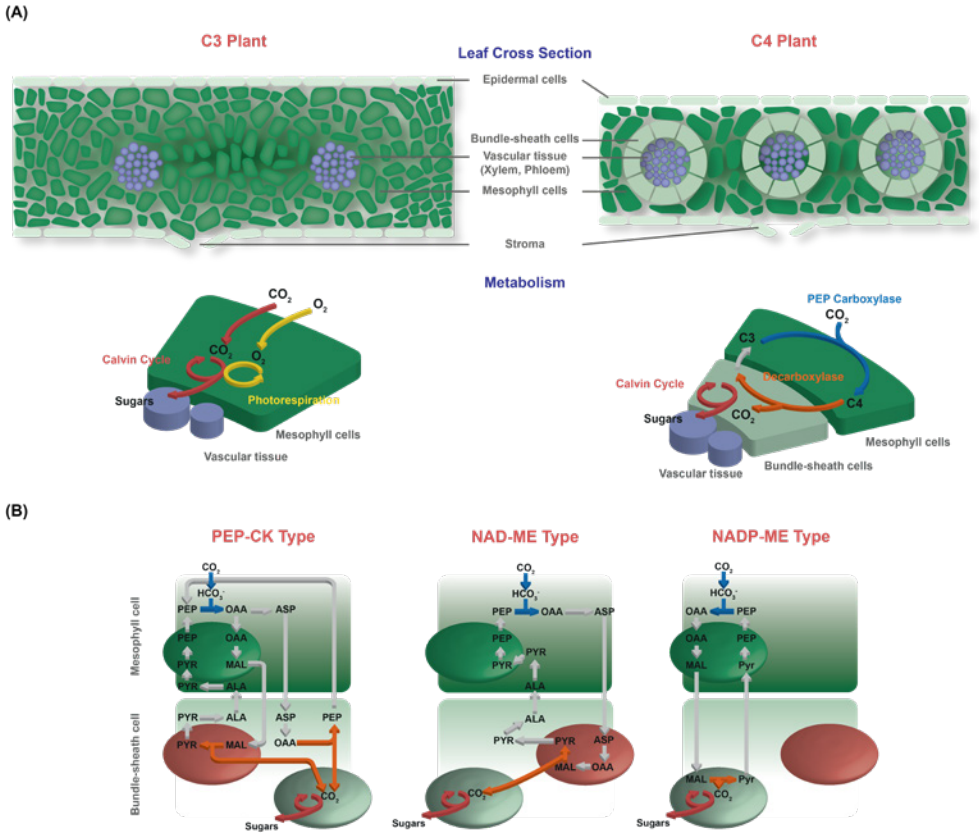

Fig. 40 (A) Comparison of C3 and C4 plants based on leaf cross section and metabolism. The distinct anatomical leaf traits of C4 plants, in particular the Kranz anatomy, facilitate the development of CO_2 concentration mechanisms, which outperforms C3 metabolism in hot and arid climates. The concentration of CO_2 around Rubisco by the C4 cycle drastically reduces photorespiration.
(B) Comparison of C4 cycle modes. In the bundle sheath cells, the release of CO_2 from the C4 acids can be catalysed by the enzyme PEP-CK (cytosol) or by the malic enzymes NADP-ME (chloroplast) and NAD-ME (mitochondria).

Embedding in Departmental and IPK Research Strategy

The RG of *NAM* interacts with interested parties from all departments concerning transcriptome analyses without considering the particular research focus. The research focus of *NAM* is directed to the phenotypic analyses and questions raised in *MOG/HET* (primary metabolism as one determinant for hybrid vigour), *MOG/SE*, and *AAN*, as well as *PBP* (primary metabolism as the source for seeds) which makes *NAM* a member of IPK research theme 4 *Growth and Metabolism*. Currently *NAM* investigates a spike developmental dataset generated by *PBP* and a developmental datasets for different phenotyped maize lines generated by *HET*.

Plans, Opportunities and Challenges

The research of *NAM* was grounded in the past focus of its leader, Andrea Bräutigam, and therefore in primary metabolism in leaves. For the present and the future, the extension of the existing approaches and models to seed development and filling is planned. Indeed, seed developmental RNA-seq datasets from *PBP* and *SE* are currently under investigation to develop regulatory networks of seed development. A seed filling model project is planned to be started in 2017, and it will extend the current models of leaf metabolism towards the seed. The major challenge of *NAM* will be the transition to a new group leader while maintaining the existing level of cooperation (i.e. bioinformatics consulting, bioinformatics courses for the institute) and the projects which were started. The postdoc, Mary-Ann Blätke, will extend the existing leaf models to the seed (until 08/2019) and will be co-mentored by the group leaders of *AAN* and *HET* for biological data and by Andrea Bräutigam for modelling and analytical questions. Two master students currently acquire the skillset for large-scale data analysis of transcriptome data only and of disparate data types including transcriptome and phenome data. Both can serve as a bridge until the position is filled. Andrea Bräutigam has agreed to mentor all *NAM* members long-distance until they finish their contracts at IPK or until a new group leader takes over. This set-up will ensure that the necessary skill sets with regard to modeling, RNA-seq analyses, and network analyses are available for current research projects.

A major future challenge to be picked up and addressed by the *NAM* RG in close collaboration with the RGs *SE*, *AAN*, *HET*, *BA*, and *BIT* and external partners will be the development and implementation of novel *in silico* tools for the display and exploration of the accumulated multidimensional and highly complex morphogenetic, physiologic, biochemical, and molecular data. With focus on the formation of seeds, models of the developmental and physiological processes are to be generated that display the *omics* data and the derived process networks in the form of a virtual and interactive 4D system.

Peer Reviewed Papers

2016

BRÄUTIGAM, A. & U. GOWIK: Photorespiration connects C_3 and C_4 photosynthesis. J. Exp. Bot. 67 (2016) 2953-2962.

DÖRING, F., M. STREUBEL, A. BRÄUTIGAM & U. GOWIK: Most photorespiratory genes are preferentially expressed in the bundle sheath cells of the C_4 grass *Sorghum bicolor.* J. Exp. Bot. 67 (2016) 3053-3064.

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XU, J., A. BRÄUTIGAM, Y. LI, A.P.M. WEBER & X.-G. ZHU: Systems analysis of *cis*-regulatory motifs in C_4 photosynthesis genes using maize and rice leaf transcriptomic data during a process of de-etiolation. J. Exp. Bot. 67 (2016) 5105-5117.

2017

BRÄUTIGAM, A., M. EISENHUT, U. SCHLÜTER & U. GOWIK: On the evolutionary origin of CAM photosynthesis. Plant Physiol. 174 (2017) 473-477.

BROUWER, P., A. BRÄUTIGAM, V.A. BUIJS, A.O.E. TAZELAAR, A. VAN DER WERF, U. SCHLÜTER, G.J. REICHART, A. BOLGER, B. USADEL, A.P.M. WEBER & H. SCHLUEPMANN: Metabolic adaptation, a specialized leaf organ structure and vascular responses to diurnal N_2 fixation by *Nostoc azollae* sustain the astonishing productivity of *Azolla* ferns without nitrogen fertilizer. Front. Plant Sci. 8 (2017) 442.

DENTON, A.K., J. MASS, C. KULAHOGLU, M.J. LERCHER, A. BRÄUTIGAM & A.P. WEBER: Freeze-quenched maize mesophyll and bundle sheath separation uncovers bias in previous tissue-specific RNA-Seq data. J. Exp. Bot. 68 (2017) 147-160.

EISENHUT, M., A. BRÄUTIGAM, S. TIMM, A. FLORIAN, T. TOHGE, A.R. FERNIE, H. BAUWE & A.P.M. WEBER: Photorespiration is crucial for dynamic response of photosynthetic metabolism and stomatal movement to altered CO_2 availability. Mol. Plant 10 (2017) 47-61.

KÖNIG, S., M. EISENHUT, A. BRÄUTIGAM, S. KURZ, A.P.M. WEBER & C. BÜCHEL: The influence of a cryptochrome on the gene expression profile in the diatom *Phaeodactylum tricornutum* under blue light and in darkness. Plant Cell Physiol. 58 (2017) 1914-1923.

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Abteilung Physiologie & Zellbiologie ▪ Department of Physiology & Cell Biology

Leiter ▪ Head:
Prof. Dr. Nicolaus von Wirén

Allgemeine Forschungsziele

Die Forschungsschwerpunkte der Abteilung *Physiologie & Zellbiologie* (PZB) liegen in der Aufklärung von Transport-, Stoffwechsel- und Entwicklungsprozessen in Pflanzen und Hefezellen, die ihre Stresstoleranz, Nährstoffeffizienz und Anpassung an landwirtschaftliche oder biotechnologische Produktionssysteme verbessern.

Stand der Forschungsarbeiten und wichtige Ergebnisse

Die Arbeitsgruppen *Molekulare Pflanzenernährung* (MPE), *Metalloid-Transport* (MT, als eigenständige aber assoziierte Ag) und *Angewandte Biochemie* (ABC) verfolgen einen biochemisch-physiologischen Ansatz mit dem Ziel, Faktoren der Stresstoleranz und Nährstoffeffizienz in Pflanzen zu erforschen. In Arabidopsis und Kulturpflanzen werden physiologische und morphologische Reaktionen und Anpassungsstrategien an definierte Stress- oder Produktionsbedingungen untersucht, um Gene oder Prozesse zu identifizieren, die Leistungs- und Qualitätsmerkmale verbessern. So wurden in einem Ag-übergreifenden Ansatz Proteine gesucht, die Salztoleranz in Gerste vermitteln. Dazu wurden die beiden Gerstensorten Morex (salztolerant) und Steptoe (salzsensitiv; Fig. 41 A) hydroponisch unter Salzstress angezogen und das Proteom von Plasmamembranen der Wurzel über Massenspektrometrie bestimmt (Fig. 41 B). Unter 182 sortenspezifischen oder salzstress-induzierten Proteinen wurde MSBP (Membrane Steroid Binding Protein) identifiziert, das nach Expression in Hefezellen deren Salztoleranz erhöht (Fig. 41 C). Diese Ergebnisse deuten auf einen neuen, Membran-assoziierten Mechanismus der Salztoleranz in Pflanzen hin (unveröffentlicht). Des Weiteren wurde in der Ag *ABC* ein transkriptioneller Regulator der Flavonoidsynthese identifiziert, der zur Kältetoleranz beiträgt (Petridis et al., 2016, New Phytol.). Flavonoide schützen Pflanzen vor Kältestress, indem sie Photonen absorbieren und reaktive Sauerstoffspezies aus der Photosynthese inaktivieren.

Die Ag *MPE* hat die physiologische Funktion des Membranproteins AMT2;1 aufgeklärt, das Ammonium in Form von Ammoniak über die Plasmamembran von Wurzelzellen transportieren

General Research Goals

Research in the department *Physiology & Cell Biology* (PZB) focusses on transport, metabolic and developmental processes in plants and yeast cells, which improve their stress tolerance, nutrient efficiency or their adaptation to agricultural or biotechnological production systems.

Research Statement and Major Achievements

The groups *Molecular Plant Nutrition* (MPE), *Metalloid Transport* (MT, independent but associated) and *Applied Biochemistry* (ABC) employ biochemical and physiological approaches to investigate mechanisms of stress tolerance and nutrient efficiency. They investigate physiological and morphological responses and adaptation strategies to defined stresses or production conditions in the model plant Arabidopsis and in crop species to identify genes or processes that improve plant performance and quality. In a comprehensive approach, proteins were searched for that are involved in the tolerance of barley plants to salt stress. For this purpose, the two contrasting barley varieties Morex (salt tolerant) and Steptoe (salt sensitive; Fig. 41 A) were exposed to salt stress in hydroponics before analysis of the root plasma membrane proteome (Fig. 41 B). Out of 182 cultivar- or salinity stress-responsive proteins determined by mass spectrometry, a Membrane Steroid Binding Protein (MSBP) was identified that confers salt tolerance when expressed in yeast cells (Fig. 41 C). This finding points to a new membrane-related cellular mechanisms mediating salt tolerance in plants. In addition, the RG *ABC* identified a transcription factor which participates in the regulation of flavonoid biosynthesis as part of cold stress responses (Petridis et al., 2016, New Phytol.). Flavonoids protect plants from cold stress as they absorb photons and capture reactive oxygen species generated during photosynthesis.

The RG *MPE* clarified the physiological function of the membrane transporter AMT2;1 that is able to transport ammonia across the plasma membrane. Under nitrogen deficiency,

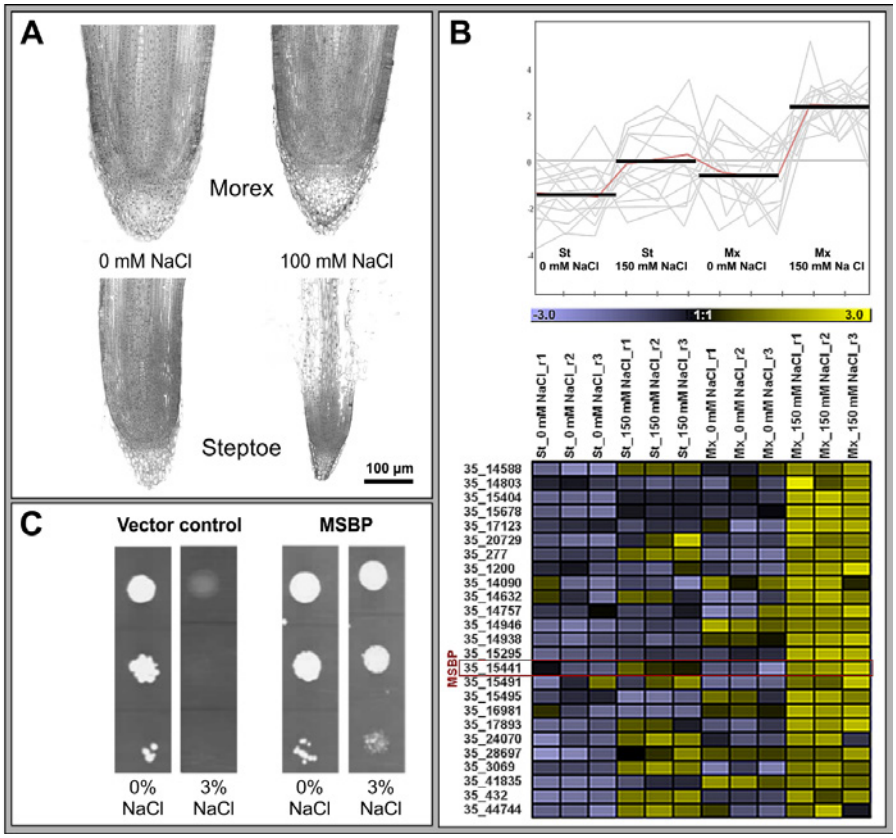

Fig. 41 Proteomanalyse zur Identifikation des Membran Steroid Bindeproteins (MSBP) in Gerstenwurzeln in Reaktion auf Salzstress. (A) Struktur von Wurzelspitzen der Gerstensorten Morex (salztolerant) und Steptoe (salzsensitiv) nach zehntägiger Exposition auf 150 mM NaCl. (B) Häufigkeitsprofile salzstressinduzierter Proteine in Morex oder Steptoe unter Kontroll- oder Saltstressbedingungen (oben) und Heat-Map-Visualisierung der relativen Häufigkeit von salzstressinduzierten Proteinen (unten). Bei LC-MS Analysen von drei unabhängigen biologischen Wiederholungen für jede Bedingung, wurde das Protein Nr. 35_15441 als MSBP identifiziert. (C) Zur Bestätigung, dass die funktionelle Expression von MSBP in der osmosensitiven Hefemutante Δhog1 zu Salztoleranz führt, wurden Hefekulturen in serieller 10-facher Verdünnung auf Agar mit 0 % oder 3 % NaCl angeimpft und für vier Tage bei 30°C inkubiert. Als Vektorkontrolle diente der pYES2-DEST52-Vektor ohne Insertion (H.-P. Mock, K. Witzel, G. Kunze and M. Melzer). ▪ Proteome analysis identified Membrane Steroid Binding Protein (MSBP) in the response of barley roots to salt stress. (A) Structure of the root tips of the barley cultivars Morex (salt-tolerant) and Steptoe (salt-sensitive) after 10 days of exposure to 150 mM NaCl. (B) Abundance profiles of salt stress-responsive proteins in Morex (Mx) or Steptoe (St) under control or salt stress conditions (upper panel) and heat-map of the relative abundance of stress-responsive proteins (lower panel). For each treatment three independent biological replicas were analyzed by LC-MS. Protein no. 35_15441 was identified as MSPB. (C) Yeast cultures were spotted in serial 10-fold dilutions onto agar containing 0% or 3% NaCl and incubated for four days at 30°C to confirm that functional expression of MSBP in the osmo-sensitive yeast mutant Δhog1 confers salt tolerance. As vector control served the pYES2-DEST52 vector without insertion (H.-P. Mock, K. Witzel, G. Kunze and M. Melzer).

kann. Unter Stickstoffmangel ist AMT2;1 vorwiegend in Cortexzellen lokalisiert, wo es zur Ammoniumaufnahme in Wurzeln beiträgt, während erhöhtes Ammoniumangebot zur Lokalisation in Perizykelzellen führt, wo AMT2;1 die Xylembeladung und damit die Translokation von Ammonium-N vermittelt (Fig. 42; Giehl et al. 2017, Mol. Plant). Des Weiteren wurden physiologische und molekulare Determinanten aufgeklärt, die die Interaktion von Fe mit anderen Schwermetallen bestimmen und für die Toleranz von Pflanzen gegen Fe-Mangel verantwortlich sind (Eroglu et al. 2016, Plant Physiol.; Eroglu et al. 2017, Plant Physiol.; Leskova et al. 2017, Plant Physiol.). Zudem wurde mithilfe einer kürzlich etablierten UPLC-MS/MS-basierten analytischen Plattform erstmalig auf metabolischer Ebene ein phytohormonelles Netzwerk des Sproßwachstums in Abhängigkeit eines Nährstoffmangels beschrieben (Eggert & von Wirén 2017; New Phytol.). In der Arbeitsgruppe *MT* wurden biochemische Eigenschaften und physiologische Funktionen von Bor-transportierenden Aquaporinen aufgeklärt (De Giorgio et al. 2016, Plant Cell; Kirscht et al. 2016, PLOS Biol.). Damit gehören diese Forschungsarbeiten zum Kern des *Forschungsschwerpunkt 5*, der sich primär der Anpassung von Pflanzen an ihre Umwelt widmet.

AMT2;1 localizes primarily to cortical cells where it contributes to ammonia uptake, while under elevated ammonium supply AMT2;1 localizes to pericycle cells, then mediating xylem loading and thus root-to-shoot translocation of ammonia-derived nitrogen (Fig. 42; Giehl et al. Mol. Plant). Moreover, the group uncovered physiological and molecular determinants affecting the interaction of Fe with other heavy metals and thus mediating tolerance to Fe deficiency (Eroglu et al. 2016, Plant Physiol.; Eroglu et al. 2017, Plant Physiol.; Leskova et al. 2017, Plant Physiol.). Using a recently established UPLC-MS/MS-based analytical platform allowed characterizing at the metabolic level a phytohormonal network underlying nutrient-limited shoot growth (Eggert & von Wirén, 2017; New Phytol.).

The *MT* RG characterized biochemical properties and physiological functions of boron-transporting aquaporins (De Giorgio et al. 2016, Plant Cell; Kirscht et al. 2016, PLOS Biol.). All these research topics belong to the core of *research theme 5*, which is primarily devoted to plant interactions with its environment.

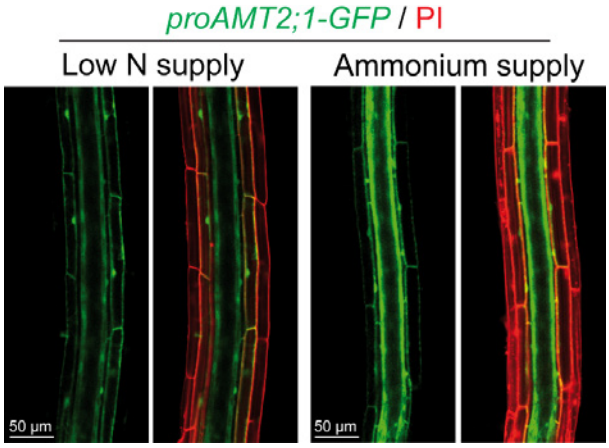

Fig. 42 Der Stickstoff-Ernährungszustand bestimmt die Lokalisation des Ammoniumtransportproteins AMT2;1 in Arabidopsiswurzeln. Unter Stickstoffmangel lokalisiert AMT2;1, das mithilfe einer Kopplung an ein grün fluoreszierendes Protein (GFP) sichtbar gemacht wurde, vorwiegend in Cortexzellen (links), während unter erhöhtem Ammoniumangebot AMT2;1 verstärkt in Perizykelzellen lokalisiert, die zur Xylembeladung beitragen. Äussere Wurzelzellen wurden mit Propidiumiodid (PI) angefärbt und fluoreszieren rot (Giehl et al. 2017; Mol. Plant). ▪ The nitrogen nutritional state determines the cell type-specific localization of the ammonium transport protein AMT2;1 in Arabidopsis roots. Under nitrogen deficiency, AMT2;1, visualized by coupling to green fluorescent protein (GFP), localizes primarily to cortical cells, whereas under ample ammonium supply AMT2;1 localizes to pericycle cells, which are involved in xylem loading. Outer root cells show red fluorescence after staining with propidium iodide (PI) (Giehl et al. 2017; Mol. Plant).

In einem biotechnologischen Ansatz hat die Arbeitsgruppe *Hefegenetik* (HEG) in der Hefe *Arxula adeninivorans* die Synthese- und Abbauwege von n-Butanol so modifiziert, dass die Ausbeute von n-Butanol erheblich gesteigert werden konnte (Rauter et al. 2016, Microb. Cell Fact.; Kasprzak et al. 2016, FEMS Yeast Res.; AMB Express). Des Weiteren konnten in *Arxula adeninivorans*-Stämmen mit überexprimierten Genen des Poly-Hydroxy-Alkanoat (PHA)-Stoffwechselwegs (β-Ketothiolase, Acetoacetyl-CoA-Reduktase, PHAs-Synthase) sowie des Phasin-Gens hohe Gehalte an PHB-V (Polyhydroxybutyrat-co-hydroxyvalerat) intrazellulär akkumuliert werden (Fig. 43; Biernacki et al. 2017). Das kostengünstig mit kohlenhydrathaltigen Reststoffen der Lebensmittelindustrie produzierte PHB-V dient u.a. als Ausgangsmaterial zur Herstellung von Verpackungsmaterialien oder Filamenten für den 3D-Druck.

Unter Einsatz zellbiologischer und biotechnologischer Methoden wurden in Kooperation zwischen *Struktureller Zellbiologie* (SZB) und *Pflanzlicher Reproduktionsbiologie* (PRB) die Dynamik posttranslational modifizierter Histone während der Pollenembryogenese untersucht (Pandey et al. 2017, Plant Reprod.) und in der Ag *PRB* weitere methodische Fortschritte bei der Zielsequenz-spezifischen Genommodifikation durch RNA-vermittelte Cas-Endonukleasen erreicht. Fig. 44 zeigt den prinzipiellen Mechanismus dieser Technologie. Es wurden u.a. aussagekräftige Tests zur funktionellen Validierung Zielsequenz-spezifisch designter Endonukleasen etabliert sowie mittels Haploidentechnologie eine effiziente genetische Fixierung von durch RNA-vermittelte Cas9-Endonuklease induzierten Veränderungen belegt (Budhagapatalli et al. 2016, Plant Methods; Schedel et al. 2017, Front. Plant Sci.). Diese Arbeiten tragen damit zur methodischen und inhaltlichen Weiterentwicklung des *Forschungsschwerpunkt 3* bei.

Perspektiven und Herausforderungen

Ein vorrangiges Ziel der Abteilung ist die Weiterentwicklung neuer Methoden der Genomeditierung, die genau vorhersagbare Modifikationen der genomischen DNA-Sequenz erlauben.

Employing metabolic engineering in the yeast *Arxula adeninivorans*, the *Yeast Genetics* (HEG) group has modified synthesis and degradation pathways in carbon metabolism to increase the yield of n-butanol (Rauter et al. 2016, Microb. Cell Fact.; Kasprzak et al. 2016, FEMS Yeast Res.; AMB Express). Overexpression of genes involved in poly-hydroxy-alkanoate (PHA) metabolism as well as of the phasein gene allowed converting waste metabolites into n-butanol, cis,cis-muconid acid or into PHB-V (polyhydroxybutyrate-co-hydroxyvalerate), which accumulates to up to 52.1% of yeast dry weight (Biernacki et al. 2017, AMB Express; Fig. 43). PHB-V, which is produced on basis of low-cost carbohydrate-containing residues from food industry, serves e.g. as precursor for the production of packaging materials or filaments for 3D-printing.

Using cell biological and biotechnological tools allowed the *Structural Cell Biology* (SZB) and *Plant Reproductive Biology* (PRB) group to investigate the dynamics of post-translationally modified histones during pollen embryogenesis (Pandey et al. 2017, Plant Reprod.) and the PRB group to

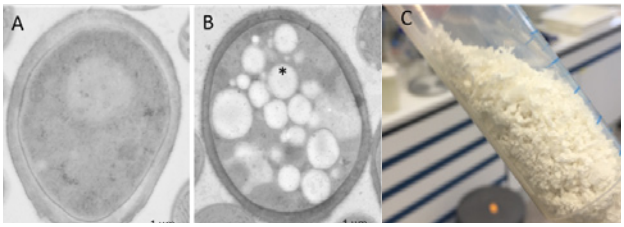

Fig. 43 Biotechnologische Herstellung von Ausgangsmaterialien für Kunststoffe in Hefe. A) Transmissionselektronenmikroskopische Aufnahmen von PHB-V-Einschlüssen in *Arxula adeninivorans*. Kontrollstamm ohne Einschlüsse. B) Aufnahme des PHB-V-Produktionsstammes. * markieren die Akkumulation von Polymereinschlüssen. C) Gereinigtes PHB-V -Copolymer [5 % HV], isoliert aus Hefezellen nach Zellaufschluss und Extraktion mit organischen Lösungsmitteln (G. Kunze, F. Bischoff and M. Melzer). ▪ Biotechnological production of precursors for plastic polymers. A) Transmission electron microscopy images of PHB-V inclusions in *A. adeninivorans*; control strain without inclusion bodies. B) PHB-V producing strain. * mark the accumulation of polymer inclusions. C) Purified PHB-V-co-polymer [5% HV] isolated from yeast cells after cell disruption and extraction by organic solvents (G. Kunze, F. Bischoff and M. Melzer).

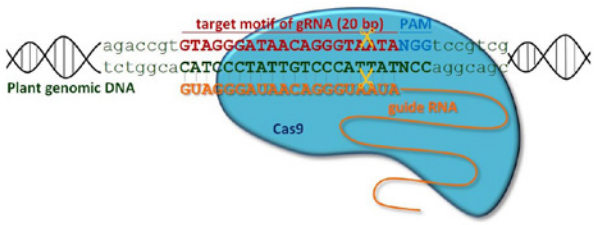

Fig. 44 Zielsequenz-spezifische Genommodifikation durch RNA-vermittelte Cas9-Endonukleasen (blau) mit Guide-RNA (orange), die ein synthetisches Zielsequenz-spezifisches 5'-Ende trägt (orangefarbene Nukleobasen). Der Enzym-RNA-Komplex bindet an eine genomische Zielsequenz (rote und blaue Nukleobasen) über komplementäre Basenpaarung. Wenn das Cas9-Protein richtig positioniert ist, schneidet es (gelbe Schere) beide Stränge im Zielmotiv der genomischen DNA. Die zelluläre Reparaturmaschinerie ist in gewissem Ausmaß fehleranfällig und verursacht zufällige Modifikationen des zu reparierenden genomischen Lokus (S. Schedel, J. Kumlehn).
▪ Site-directed mutagenesis of plant genomic DNA by Cas9-endonuclease. Cas9 protein (blue) complexes with a guide RNA (orange) that features a synthetic, target-specified 5'-end (orange nucleobases). This complex binds to the plant genomic target motif (red and blue nucleobases) via complementary base-pairing. Once the Cas9 protein is positioned appropriately, it cuts (as indicated by yellow scissors) both strands of the target DNA motif. The cellular DNA repair machinery is error-prone to some extent, which causes random modifications of the chosen genomic locus (S. Schedel, J. Kumlehn).

Diese Methoden sollen u. a. eingesetzt werden, um Gene zu modifizieren, die die abiotische Stresstoleranz oder Nährstoffeffizienz in Kulturpflanzen erhöhen. In Kooperation mit Ags anderer Abteilungen sollen vielversprechende allelische Varianten solcher Gene über QTL-Kartierungen relevanter Merkmale in Gersten- oder Weizenpopulationen oder über die Resequenzierung bekannter Gene in unterschiedlich effizienten Gersten- und Weizenlinien aus der Genbank identifiziert werden. Ein neu etabliertes Rasterelektronenmikroskop (Zeiss Gemini SEM300) in der Ag *SZB*, das mit einer Block-Face-Imaging-Einheit ausgestattet ist, ermöglicht 3D-Rekonstruktionen von größeren Gewebeproben. Die damit gewonnene Strukturinformation im Nanometerbereich wird Forschungsvorhaben unterstützen, die die Aufklärung pflanzlicher Effizienz-, Toleranz- oder Qualitätsmerkmale zum Ziel haben, wie z. B. die Standfestigkeit von Getreide.

In Nachfolge der Ag *HEG* soll eine Ag mit neuer thematischer Ausrichtung etabliert werden. Um das Profil der Abt. *PZB* im Bereich der Wurzelforschung zu stärken, soll ein Ag-Leiter (m/w) mit Forschungsschwerpunkt in der Wurzelphysiologie, -architektur und/ oder -entwicklung gewonnen werden. Diese neue Ag soll sich auch an der Entwicklung neuer Methoden in der Wurzelphänotypisierung engagieren.

advance site-directed genome modification using RNA-guided Cas9 endonuclease. Fig. 44 shows the basic principle of this technology. In this field, progress relates to the establishment of conclusive prevalidation tests for customized endonucleases as well as the efficient genetic fixation of site-specifically induced modifications (Budhagapatalli et al. 2016, Plant Methods; Schedel et al. 2017, Front. Plant Sci.). Thereby, these projects contribute to *research theme 3* in terms of both, content and methodology.

Plans, Opportunities and Challenges

One priority in departmental research is the advancement of novel methods in genome editing that allow precisely predictable modifications of the genomic DNA sequence. These approaches shall be employed, for instance, to modify genes that enhance abiotic stress tolerance or nutrient efficiency in cereals. In cooperation with groups of the other departments, promising variants of such genes shall be identified by QTL mapping of relevant traits in barley and wheat populations or by re-sequencing of known genes in lines with contrasting nutrient efficiency or stress tolerance. The *SZB* RG has established a new scanning electron microscope (Zeiss Gemini SEM300), which is equipped with a serial block face imaging unit to obtain 3D-images of larger plant tissue samples. Such structural information at nanometer resolution will greatly support research on the mechanistic understanding of efficiency, tolerance or quality traits, such as lodging resistance in crops.

In succession of the *HEG* group a group will be established with a new research focus. To strengthen the *PZB* profile in root research, the new group leader will be dedicated towards the physiology, architecture or development of plant roots. This group shall also engage in the development of new methods in root phenotyping.

Research Group: Molecular Plant Nutrition (MPE)

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Keywords

Nutrient Acquisition and Transport
Nutrient Sensing
Root System Architecture
Nutrient Efficiency Traits
Adventitious Root Formation
Stress Tolerance

Highlights

UPLC-MS/MS-based analysis platform is now fully operational and covers 70 precursors, conjugates, degradation products and active forms of auxins, cytokinins, gibberellins, abscisic and salicylic acids, brassinosteroids and strigolactones (Eggert & von Wirén, New Phytol. 2017).

Development of a novel method to determine elemental concentrations in Arabidopsis roots at cell type-specific resolution by combining fluorescent-activated cell sorting and high-resolution ICP-MS.

Intensive contribution to the characterization of Fe- and heavy metal-related transport and developmental processes (3 x Plant Physiol., 1 x J. Exp. Bot.).

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The *Molecular Plant Nutrition* research group investigates the transport and metabolism of mineral nutrients, their impact on phytohormonal regulation as well as their role in physiological and morphological adaptations to stress or to agricultural production conditions. Research includes nutrient sensing mechanisms, like the adaptation of root growth to local nutrient supplies or to systemic plant signals, mechanisms of nutrient enrichment in seeds as well as the redox- or nutrient-dependent regulation of stress responses.

Research Statement and Major Achievements

A major aim of the past two years was to uncover physiological and developmental processes in plants that are determined by the Fe nutritional status. A large problem for Fe-deficient plants is that all membrane transporters for Fe in plants are poorly specific for Fe but permeate also other heavy metals. This causes heavy metal toxicity and more severe Fe deficiency. We studied these processes in Arabidopsis and found that excess uptake of Zn induces Fe deficiency by interfering with Fe sensing in the transcriptional regulation of genes required for Fe acquisition and allocation. By contrast, metals like Ni, Cd or Mn hamper Fe acquisition and metabolism downstream of Fe sensing (Leskova et al. 2017, Plant Physiol.). For instance, excess Mn inhibits the membrane-bound Fe(III) reductase that is a central component of Fe acquisition by roots. Such inhibition is prevented by Fe deficiency-induced upregulation of the tonoplast Mn transporter MTP8 that serves for vacuolar compartmentalization of excess Mn (Eroglu et al. 2016, Plant Physiol.). Interestingly, MTP8 transports also Fe and is expressed during embryogenesis and germination of seeds. During these developmental phases, MTP8 mediates not only cell type-specific enrichment of Mn in subepidermal cells of cotelydons but also Fe re-allocation in vacuoles upon seed imbibition. Thereby, MTP8 improves germination and seed vigour under conditions of elevated external Mn availability (Eroglu et al. 2017, Plant Physiol.).

Adventitious root (AR) formation in the stem base of cuttings is the basis for propagation of many ornamental plant species. We used Petunia as model to study this developmental process. Based on our previous studies (Ahkami et al., 2014; Drüge et al., 2014), we now discovered that Fe is the most limiting mineral element for AR formation. Fe only stimulates

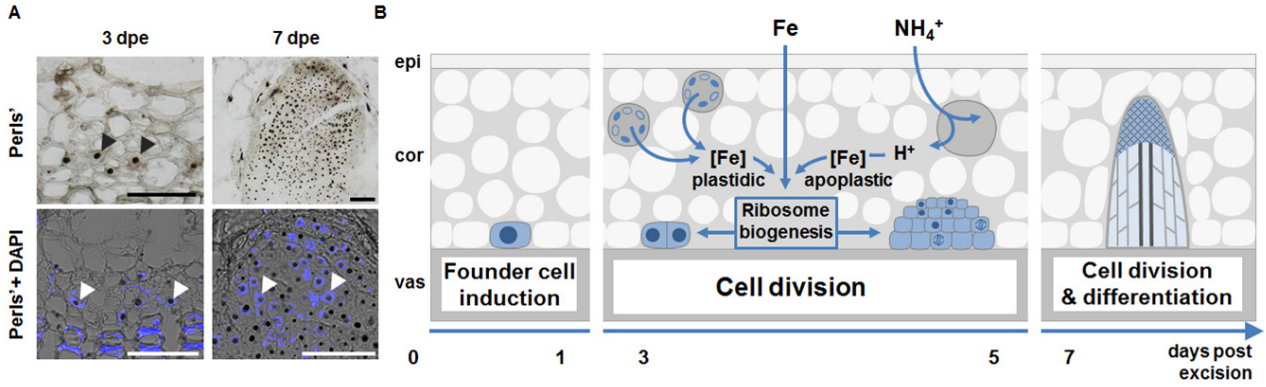

Fig. 45 (A) Localization of Fe by Perls'/DAB method in the stem base of *Petunia hybrida* cuttings during Fe stimulated adventitious root (AR) formation. Cross sections from 1-4 mm of the stem base are shown 3 and 7 days post excision (dpe). Black arrowheads show Fe localization in cambial cells 3 dpe. Additional staining with DAPI indicates nuclear localized Fe in meristematic cells (white arrowheads). Scale bar, 50 µm.
(B) Working model for the effects of Fe and NH_4^+ on adventitious root (AR) formation in *Petunia hybrida*. Fe performs a specific function in the rooting zone by activating ribosome biogenesis, crucial for growth of the meristematic cells of the developing AR. Under Fe-free conditions Fe associated with chloroplasts in cortical cell layers may be released to supply developing AR meristems. The uptake of NH_4^+ leads to a local acidification of the apoplast as a consequence of an increased net H^+ efflux, which in turn facilitates the mobilization of Fe precipitated in the apoplast; epi. epidermis; cor. cortex; vas. vasculature.

AR formation after local supply to the stem base, where it becomes highly enriched in nucleoli of meristematic cells and accelerates the emergence and elongation of ARs (Hilo et al., 2017, J. Exp. Bot., Fig. 45). Follow-up studies pursue the hypothesis that Fe activates biochemical processes in ribosomes.

During the past years, we have established a UPLC-MS/MS-based platform for the simultaneous analysis of phytohormones from different classes. This methodology allowed complementing a series of studies, in which phytohormonal changes turned out as major determinants for morphological or physiological plant traits (Yousef, Eggert et al. 2017, Nature Genet.; Hosseini et al., 2016; Front. Plant Sci.). Moreover, this platform was used to describe for the first time simultaneous changes in precursors, metabolites and active forms of phytohormones from different classes, which regulate shoot growth under nutrient-deficient conditions (Eggert & von Wirén, 2017; New Phytol.).

Significant advance has been made in the area of ammonium transport by showing that the unique ammonium transporter AMT2;1 in Arabidopsis has a role in root-to-shoot translocation of ammonium (Giehl et al., 2017, Mol. Plant). Moreover, new concepts have been built on ammonium-triggered physiological and morphological responses in plant roots, stating that ammonium sensing takes place at multiple steps along its transport, storage, and assimilation pathways (Liu and von Wirén, 2017; J. Exp. Bot.).

Embedding in Departmental and IPK Research Strategy

With major emphasis on the discovery of plant responses and adaptations to nutrient deficiencies, research topics in *MPE* make up a central component of research theme 5 (*Mechanisms of Resistance and Stress Tolerance*). As coordinator of this research focus, N. von Wirén takes over a conceptual role in designing research activities here. Together with colleagues from *MLU*, N. von Wirén is member of the program committee of the newly designed SFB proposal *Programs of plant plasticity* (to be defended in March 2018) and of another SFB initiative named *Proteins as mediators of plant traits – ProMPT*. These activities contribute to the integration of several IPK groups into the research landscape of the *MLU* and Halle area.

Moreover, the *MPE* RG offers IPK-wide and beyond access to its technical platforms consisting of UPLC-MS/MS (phytohormones), HR-ICP-MS (mineral elements), IR-MS (stable isotopes) and IC/LC-MS (primary metabolites and specific metabolite groups).

Plans, Opportunities and Challenges

In cooperation with a group from Stanford, we have characterized two new enzymes in the biochemical pathway of coumarin-type siderophores assisting iron acquisition in non-graminaceous plant species. Interestingly, these siderophores possess besides Fe(II)-chelating also Fe(III)-reducing capacities and are modulated in their chemical structure and composition by external pH and the type of available iron minerals. Here, a new research field has opened up that is addressed in cooperation with partners from the *Leibniz Institute ISAS*, Dortmund, and the *University of Vienna*.

Significant advance has also been made in the elucidation of signaling pathways that allow plants to form longer lateral roots under mild nitrogen deficiency. Employing association mapping in Arabidopsis, we have identified genes involved in brassinosteroid signaling to play a major role in lateral root expansion. After clarifying their role, approaches will be initiated to exploit this type of knowledge for crop improvement.

Involvement of N. von Wirén in the steering groups for the excellence cluster and SFB initiatives at the *MLU* provides an excellent opportunity for novel cooperations, e.g. in the area of electrophysiology (Michael Föller, human physiology), protein interactions and protein structure (Andrea Sinz, Jochen Balbach, Milton Stubbs) and nutrient signaling (Steffen Abel, *IPB* Halle).

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HEUERMANN, D.: Comparative analysis of phytohormone translocation, nitrogen metabolism and yield components under nitrate und urea nutrition in oilseed rape. (PhD Thesis) Martin-Luther-Universität Halle-Wittenberg, Naturwissenschaftliche Fakultät I Biowissenschaften, Halle/S. (2017) 149 pp.

Research Group: Applied Biochemistry (ABC)

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Keywords

Secondary Metabolites
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Abiotic Stress Defence
Anthocyanins
Coumarins

Highlights

Identification and characterization of *Arabidopsis thaliana* transcription factors related to phenylpropanoid metabolism in response to cold stress.

Phenylpropanoid patterns of blue and red potato tubers (gene bank accessions).

Characterization of a barley population with respect to phenylpropanoids and identification of a relevant glycosyltransferase.

Identification of genes relevant to cope with cryostress (Leibniz Pakt Project, KAIT)

EU Project ANTHOPLUS (Coordinated by A. Matros.)

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The main research interest of the research group is the biosynthesis and regulation of secondary metabolism, in particular of phenylpropanoids. Important aspects are their protective functions against abiotic and biotic stresses *in planta*, but also their potential health effects as a part of the human diet. Major goals are to gain insights into regulatory programs and mechanism of resource allocation into different branches of secondary metabolism and tissue-specific metabolite functions. Integrative approaches combining proteomics, metabolomics and transcriptome analysis are applied to study the integration of secondary metabolism regarding overall cellular defence mechanisms, in particular to abiotic stress.

Research Statement and Major Achievements

The potential beneficial health effects of anthocyanins were followed in the EU project Anthoplus and within the PhD work of Rongfan Wang (cereals) and Anne Oertel (potato). A major effort was to establish and scale-up preparative isolation of anthocyanins from different sources (in collaboration with ANTHOPlus partners). The potential use of purple barley and wheat lines for a healthy diet were studied by R. Wang (cooperation with RG *RGR*). In the ANTHOPlus project distinct anthocyanins were preparatively isolated alone or in defined combinations. The major sources were transgenic cell cultures with accumulation of anthocyanins by expression of regulatory factors and propagated at the bio-reactor scale by a Norwegian project partner. Anne Oertel characterized the metabolic profiles of potato tubers (57 gene bank accessions) accumulating blue or red anthocyanins and initiated studies on the underlying molecular background.

The analysis of regulatory components involved in the cold stress regulation of phenylpropanoids was continued. One of the factors was shown to be a component of the RNA silencing machinery. Stress experiments and subcellular localization of metabolites were performed to further characterize individual candidate genes. Two transcription factors were shown to be involved in regulation of anthocyan accumulation.

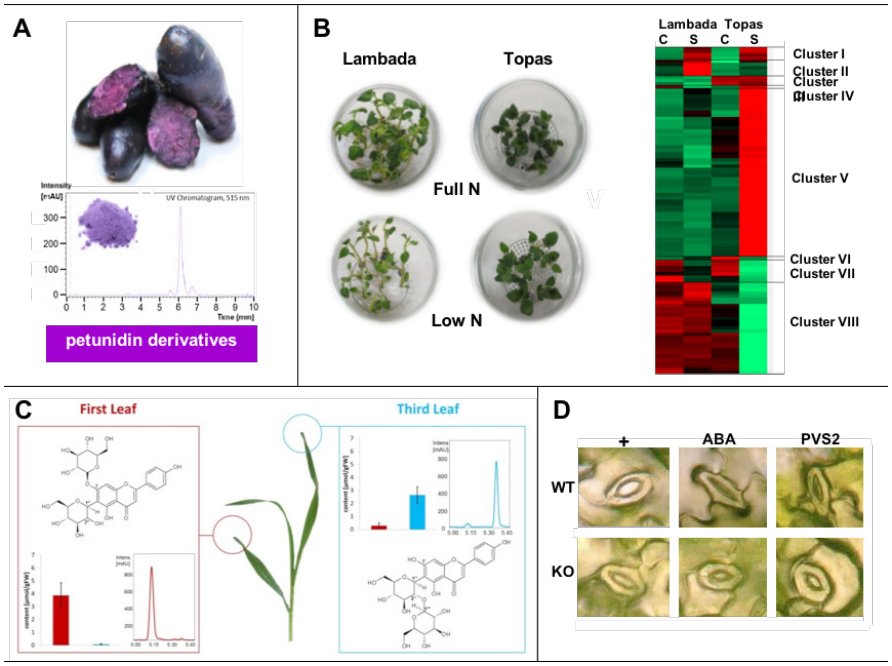

Fig. 46 (A) Metabolite profiling by LC-UV/MS of colored potato tuber from selected gene bank accession Blue Marker. (B) Comparative analysis of root proteome of two potato accessions (Lambada and Topas) contrasting in nitrogen use effiency. C: control, S: stress (N deficiency conditions). (C) Phenylpropanoid profiles of leaves of barley genotype Scarlett. During leaf development, a shift from saponarin to isovitexin-2-O``-glucoside is observed. (D) Changes in stomatal aperture in Arabidopsis WT and KO mutant in response to absisic acid and cryoprotectants (PVS2).

The participation of plastidal responses in cold stress adaptation is in the focus of ongoing work. In a joint project adaptation mechanisms relevant for cryoconservation of plant meristems are studied (Johanna Stock, collaboration with RG *CSB*). Involvement of coumarins in iron metabolism is studied in collaboration with the RG *MPE*.

The phenylpropanoid metabolism has been investigated in barley populations grown either in the field or under different conditions (cold stress, elevated CO_2) in growth cabinets (Dominic Brauch, collaboration with K. Pillen, Halle). Major aims are to correlate metabolic patterns with hyperspectral data of field grown plants and to identify novel regulatory genes of phenylpropanoid metabolism in barley. Hyperspectral imaging in combination with metabolite analysis was also performed for sugarbeet genotypes (N. Arens; collaboration with U. Seiffert and Fa. Strube). Three genotypes contrasting in pathogen response were grown at different light conditions. Metabolic profiles were correlated with hyperspectral image data and compounds potentially contributing to the hyperspectral signatures were identified.

The project on salt stress responses in barley mapping populations with contrasting tolerance has been continued with the functional characterization of candidate proteins identified by earlier proteome approaches. Field experiments with the parental lines and selected off-springs were performed in collaboration with a Tunisian partner lab (BASALT project; Leila Bennani).

Drought stress and nutrient limitation of selected potato cultivars were studied by proteomic approaches with a focus on the plasma membrane (A. Jozefowicz). Several novel candidates associated with a higher tolerance towards nitrogen limitation have been identified and are currently characterized in more detail (collaboration with RG *MT*).

Embedding in Departmental and IPK Research Strategy

Research in the *ABC* RG is situated within the *theme 4* and *5* and is focused on the regulation of phenylpropanoid metabolism in the context of developmental processes and the interaction of plants with their environment. Nutrient availability (e.g. nitrogen status, Fe deficiency) has a strong impact on the allocation of resources into different branches of secondary metabolites. Many stresses lead to particular profiles of phenylpropanoids, and frequently the metabolic changes show distinct temporal and spatial patterns. Due to these cellular connectivities research of the group has interaction with the other groups of the department and several other groups at the institute. In particular, we also contribute to the phytochemical characterization of gene bank accessions e.g. in tomato, potato, barley or wheat.

Plans, Opportunities and Challenges

A number of novel factors involved in cold stress adaptation of phenylpropanoid patterns have been identified. These candidates deserve further characterization in *A. thaliana* and cereals with respect to their mode of action and functional context. Collaboration has been started to assess the involvement of these candidates in phenylpropanoid related, response up to UV radiation or other abiotic stresses. A particular challenge will be the improvement of spatially resolved metabolic analysis by combining different approaches (microscopy, laser micro-dissection, mass spectrometry based imaging).

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STOCK, J., A. SENULA, M. NAGEL, H.-P. MOCK & E.R.J. KELLER: A simple method for shoot tip cryopreservation of Arabidopsis genotypes. Cryo Lett. 38 (2017) 364-371.

Articles in Compilations

2016

KELLER, E.R.J., M. GRÜBE, M.-R. HAJIREZAEI, M. MELZER, H.-P. MOCK, H. ROLLETSCHEK, A. SENULA & K. SUBBARAYAN: Experience in large-scale cryopreservation and links to applied research for safe storage of plant germplasm. In: LAMBARDI, M. & S. HAMILL (Eds.): Proceedings of the XXIX IHC - Int. Symp. on Micropropagation and *In Vitro* Techniques, Brisbane, Australia, August 17-22, 2014. (Series: Acta Horticulturae, Vol. 1113) Leuven: ISHS (2016) 239-249.

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2016

MOCK, H.P. (Ed.): Special Issue: Plant Proteomics: a bridge between fundamental processes and crop production. (Series: Biochimica et Biophysica Acta (BBA) - Proteins and Proteomics, Vol. 1864, No. 8): (2016) 179 pp.

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2016

MEISE, P., S. SEDDIG, A. SCHUM, A. JOSEFOWICZ, H.-P. MOCK, K. DEHMER, C. BÜNDIG & T. WINKELMANN: Trocken- und Stickstoffmangel – Stressreaktionen der Stärkekartoffel. Untersuchungen auf morphologischer, physiologischer und proteomischer Ebene im Projekt PROKAR. Kartoffelbau 67 (2016) 40-45.

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2016

ARENS, N.: Studies of the sugarbeet leaf metabolome and its hyperspectral reflectance signature responding to environmental stress. (PhD Thesis, kumulativ) Christian-Albrechts-Universität zu Kiel, Kiel (2016).

HÖPPNER, S.: Untersuchungen zum Carotinoid-Spektrum von Tomaten aus verschiedenen *Solanum lycopersicum* Genbank-Akzessionen. (Master Thesis) Hochschule Anhalt, Köthen, (2016) 71 pp.

2017

GRUHNE, J.: Eisenabhängige Suberin- und Cumarinsynthese in *Arabidopsis thaliana* und *Nicotiana tabacum*. (Bachelor Thesis) Hochschule Mittweida, Mittweida (2017) 57 pp.

WANG, R.: Physiological, phytochemical and molecular characterization of pigmented cereals. (PhD Thesis) Christian-Albrechts-Universität zu Kiel, Kiel (2017) 140 pp.

Research Group: Structural Cell Biology (SZB)

Head: Dr. Michael Melzer

Scientists

Dr. Marek Marzec

Aleksandra Muszyńska

Dr. Twan Rutten

Keywords:

Confocal Microscopy

Electron Microscopy

Live Cell Imaging

Morphology

Ultrastructure

Lodging Resistance

Highlights

Immunogold localization of chloroplasts to confirm that PsbS interactions are involved in the activation of energy dissipation in Arabidopsis. (Correa-Galvis et al. 2016, Nature Plants 2: 15225.).

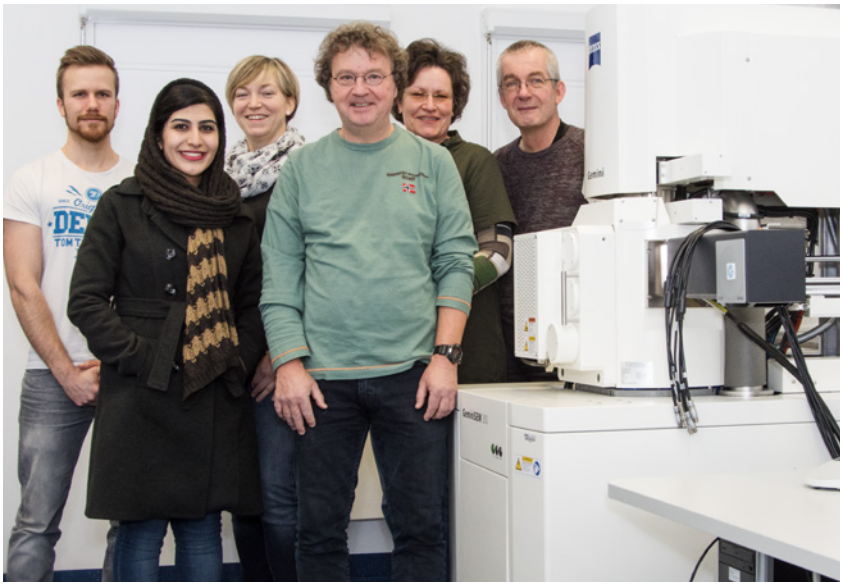
Contribution to Synthesis and transfer of galactolipids in the chloroplast envelope membranes of *Arabidopsis thaliana* published in PNAS (Kelly et al. (2016) 13: 10714-10719).

Identification of QTLs for lodging resistance in the rye genotype ´Stabilstroh`.

Aquisition of the Scanning Electron Microscope Zeiss Gemini300 including Gatan 3View System.

Funding

DFG, BLE



A major task of the research group as core facility for light and electron microscopy is to provide practical and theoretical advise to address research problems at the levels of tissues, cells, compartments and molecules by sophisticated cell biological techniques. Therefore the development of new protocols for plant tissue preparation for microscopy is an important aspect of our work. The overall research aim is the improvement of agronomically relevant traits in crops or of biotechnological procedures.

Research Statement and Major Achievements

In the framework of own research projects, internal and external cooperations, the group focusses mainly on the spatial distribution of plant enzymes and molecules as analyzed by electron or fluorescence microscopy.

In a joint DFG project with the RG *MPE* we try to identify molecular triggers for ammonium transporter (AMT) trafficking to target membranes in root cells to understand which intracellular signals trigger these processes. One of the major tasks is the identification of peptide domains involved in cell trafficking of AMTs in response to changing nitrogen status. The comparison of protein sequences of three AMTs that have shown different intracellular localization, revealed 10 potential domains related to protein trafficking. Currently, individual protein domains are functionally analyzed. Investigations on chromatin modifications during embryogenesis in comparison to gametogenesis disclose an important role of epigenetic markers for the induction of pollen embryogenesis. Furthermore, using molecular genetic studies and histological characterization, we were able to detect several QTLs that are responsible for the pronounced lodging resistance trait *Stabilstroh* in rye. In a recently started BLE project about the use of genetic diversity and innovative methods for breeding to reduce seed shattering, we currently perform cell biological and structural analyses of the abscission zone in various genotypes of grasses.

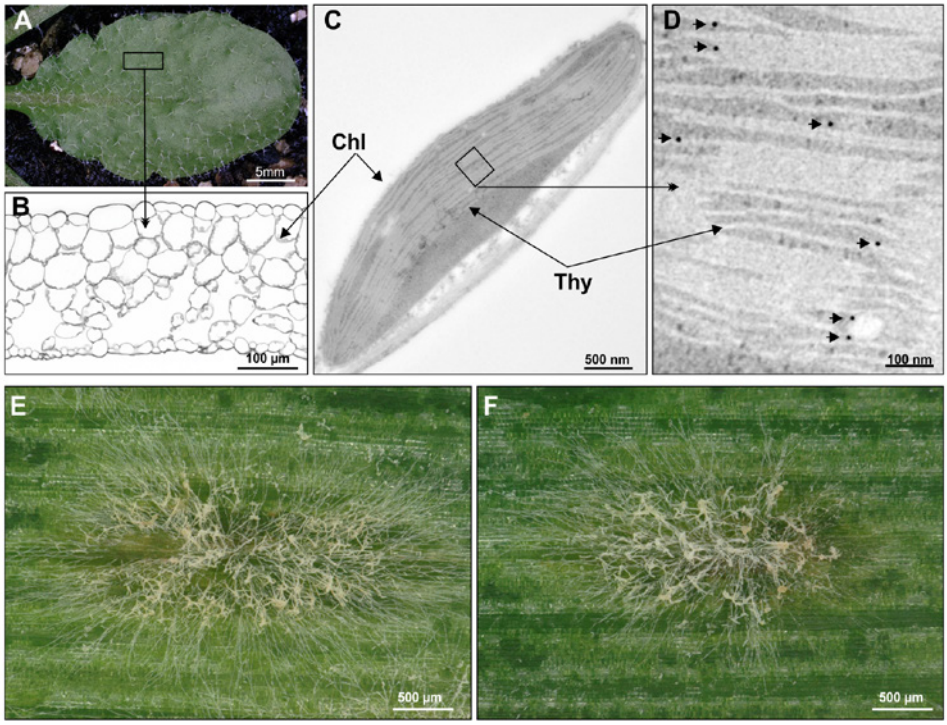


Fig. 47 Immunogold localization of the PsbS subunit of photosystem II in chloroplasts of Arabidopsis (A-D). Digital microscopy image of a fresh rosette leaf (A). Light microscopy image of a histological leaf cross section (B). Transmission electron microscopy images of chloroplast thylakoids after immunogold labelling of PsbS-proteins using 10 nm protein A-gold (C-D). Digital microscopy image of the epidemis of barley leaves after powdery mildew infection (E-F). Leaves of the variety *Sebastian* show a larger infected area (E) compared to the mutant hvd14. (F) with a mutation in a gene encoding a strigolactone receptor. Chl, chloroplast; Thy, thylakoid (M. Melzer and M. Marzec).

In cooperation with the group *Photosynthesis and Stress Physiology of Plants* of the *University of Düsseldorf* we were able to confirm by immunogold localization of chloroplasts that PsbS interactions are involved in the activation of energy dissipation in Arabidopsis (Fig. 47 A-D).

Due to its important role in cereal yield formation an investigation of spike morphology was carried out in close collaboration with the RG *PBP*. As the mechanisms behind cessation of spikelet formation and subsequent degradation of the apical spike are largely unknown, 3D reconstructions based on serial sectioning has been applied to document morphological changes in the apical spike of barley between the stages of cessation of growth until its degradation. In cooperation with the RG *PSG* the resistance of the barley mutant hvd14.d to powdery mildew infection was examined. Preliminary results show that plants with a mutation in a gene encoding for the strigolactone receptor are more resistant to an infection, in comparison to the wild type variety. The infection rate was about half of that observed in the control variety *Sebastian*, while those colonies that did develop were significantly smaller (Fig. 47 E-F).

Embedding in Departmental and IPK Research Strategy

Studies on pollen embryogenesis and the role of strigolactones in plant development contributes to the IPK research theme 3 *Mechanisms of Plant Reproduction*. Research on lodging resistance of a rye genotype with the trait *Stabilstroh*, studies on ammonium transporters under nitrogen deficiency (DFG) and seed shattering in grasses (BLE) are attributable to IPK Research theme 5 *Mechanisms of Resistance and Stress Tolerance*. Furthermore, based on several running internal cooperations within all departments of the IPK, the group is also closely connected to IPK *research themes 1*, *2* and *4*.

In cooperation with Klaus Pillen from the *Science Campus Plant Based Bioeconomy Halle* we are working on the structural characterization of barley husks.

Moreover, the *SZB* group serves IPK-wide as central facility for light and electron microscopy.

Plans, Opportunities and Future Challenges

In cooperation with the Department of Genetics, Katowice/Poland the group strives to establish a collection of mutants in genes involved in strigolactone biosynthesis and signalling as a new tool for molecular, physiological, and histological investigation of the role of strigolactones in barley.

As coordinator of specific applications for experiments M. Melzer contributes to a project application about the development of a novel optical spectroscopy instrument for optical structural-chemical identification and diagnosis in the *Horizon2020* programme.

The group will also continue the optimization of High Pressure Freezing and sample contrasting for serial block face imaging, as plant tissue preparation for microscopy close to the native state is still a major challenge.

Peer Reviewed Papers

2016

BUDHAGATAPALLI, N., S. SCHEDEL, M. GURUSHIDZE, S. PENCS, S. HIEKEL, T. RUTTEN, S. KUSCH, R. MORBITZER, T. LAHAYE, R. PANSTRUGA, J. KUMLEHN & G. HENSEL: A simple test for the cleavage activity of customized endonucleases in plants. Plant Methods 12 (2016) 18.

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BIERNACKI, M., M. MARZEC, T. ROICK, R. PÄTZ, K. BARONIAN, R. BODE & G. KUNZE: Enhancement of poly(3-hydroxybutyrate-*co*-3-hydroxyvalerate) accumulation in *Arxula adeninivorans* by stabilization of production. Microb. Cell Fact. 16 (2017) 144.

DREISSIG, S., S. SCHIML, P. SCHINDELE, O. WEISS, T. RUTTEN, V. SCHUBERT, E. GLADILIN, M.F. METTE, H. PUCHTA & A. HOUBEN: Live cell CRISPR-imaging in plants reveals dynamic telomere movements. Plant J. 91 (2017) 565-573.

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THIRULOGACHANDAR, V., A.M. ALQUDAH, R. KOPPOLU, T. RUTTEN, A. GRANER, G. HENSEL, J. KUMLEHN, A. BRÄUTIGAM, N. SREENIVASULU, T. SCHNURBUSCH & M. KUHLMANN: Leaf primordium size specifies leaf width and vein number among row-type classes in barley. Plant J. 91 (2017) 601-612.

TIKHENKO, N., N. POURSAREBANI, T. RUTTEN, T. SCHNURBUSCH & A. BÖRNER: Embryo lethality in wheat-rye hybrids: dosage effect and deletion bin mapping of the responsible wheat locus. Biol. Plant. 61 (2017) 342-348.

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YOUSSEF, H.M., K. EGGERT, R. KOPPOLU, A.M. ALQUDAH, N. POURSAREBANI, A. FAZELI, S. SAKUMA, A. TAGIRI, T. RUTTEN, G. GOVIND, U. LUNDQVIST, A. GRANER, T. KOMATSUDA, N. SREENIVASULU & T. SCHNURBUSCH: VRS2 regulates hormone-mediated inflorescence patterning in barley. Nat. Genet. 49 (2017) 157-161.

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Articles in Compilations

2016

KELLER, E.R.J., M. GRÜBE, M.-R. HAJIREZAEI, M. MELZER, H.-P. MOCK, H. ROLLETSCHEK, A. SENULA & K. SUBBARAYAN: Experience in large-scale cryopreservation and links to applied research for safe storage of plant germplasm. In: LAMBARDI, M. & S. HAMILL (Eds.): Proceedings of the XXIX IHC - Int. Symp. on Micropropagation and *In Vitro* Techniques, Brisbane, Australia, August 17-22, 2014. (Series: Acta Horticulturae, Vol. 1113) Leuven: ISHS (2016) 239-249.

2017

MARZEC, M.: Strigolactone Signaling in Plants. In: EL-ESAWI, M. (Ed.): Phytohormones - Signaling Mechanisms and Crosstalk in Plant Development and Stress Responses. (2017) 101-117.

Research Group: Plant Reproductive Biology (PRB)

Head: Dr. Jochen Kumlehn

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Keywords

Site-directed Genome Modification
Cas9 Endonuclease
Genetic Engineering
Zygotic, Somatic and Pollen Embryogenesis
Haploid Technology
Resistance to Fungal and Viral Pathogens

Highlights

Stable gene replacement in barley by targeted double-strand break induction (Watanabe et al., J. Exp. Bot. 2016).

Functional validation of BROAD LEAF1 which determinates barley leaf width by restricting lateral cell proliferation (Jöst et al., Current Biol. 2016).

Establishment of efficient *Brachypodium spec.* transformation technology as part of a comprehensive research platform for the interaction with the oomycete *Ustilago bromivora* (Rabe et al., eLife 2016).

Cas9-induced mutagenesis in tobacco followed by efficient chimera dissolution and genetic fixation in doubled haploids (Schedel et al. Front. Plant Sci. 2017).

Establishment of durable resistance to rust fungi in barley and maize by ectopic expression of the wheat disease resistance gene Lr34 (Böni et al., Plant Biotechnol. J. 2017; Sucher et al., Plant Biotechnol. J. 2017).

Funding

BMBF, BMEL, DFG, Land Sachsen-Anhalt, Industry (KWS, ENZA Zaden/NL), EU (ERA-CAPS)

The *Plant Reproductive Biology* (PRB) research group has a strong focus on the establishment of enabling technologies such as genetic transformation, site-directed genome modification, live cell dissection, analysis and manipulation as well as the generation of genetically fixed plants from haploid cells. By providing this biotechnological platform which is mainly devoted to the temperate cereals, the group aims to facilitate basic research as well as approaches to the improvement of crop plant performance. Particular emphasis is laid upon biological mechanisms associated with plant reproduction as well as plant-pathogen interactions.

Research Statement and Major Achievements

The major current focus of the *PRB* group is directed to the field of site-directed genome modification. Using the monocot barley and the dicot tobacco, a prevalidation test for customized endonucleases such as TALENs and RNA-guided Cas9 was developed which allows for their quantitative validation (Budhagatapalli et al., Plant Methods 2016). In cooperation with colleagues from the *MPIPZ* Cologne, stable gene replacement via homology-based double-strand repair was demonstrated using the meganuclease I-SceI targeting a synthetic sequence integrated into the barley genome (Watanabe et al. 2016, J. Exp. Bot.). While site-directed mutagenesis using RNA-guided Cas9 endonuclease is performed on a routine basis in barley, maize and tobacco, it was demonstrated that the use of haploid technology is highly instrumental for chimera dissolution and genetic fixation of mutations (Schedel et al., Front. Plant Sci 2017, Fig. 48).

An RNA sequencing approach conducted in cooperation with colleages from the Universities of Hamburg and Hohenheim resulted in a comparison of transcript profiles of wheat pollen undergoing normal vs. embryogenic development (Seifert et al., BMC Plant Biology 2016). In cooperation with the *SZB* RG of IPK, the dymanics of post-transcriptionally modified histones were investigated during barley pollen embryogenesis (Pandey et al., Plant Reproduction 2017).

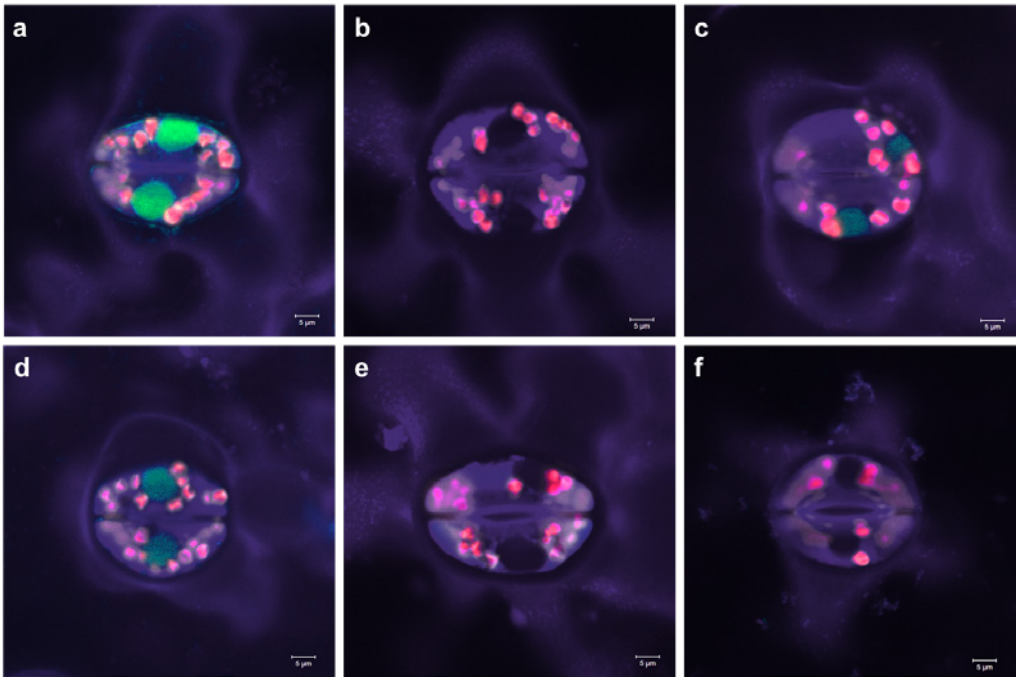

Fig. 48 Different levels of target gene functionality as shown by green fluorescence in nuclei of homozygous Green fluorescence protein (GFP) mutants of tobacco induced by RNA-guided Cas9-endonuclease. (A) GFP WT plant, (B) F130G mutant, (C) ΔD129 mutant, (D) ΔD129/N130V mutant, (E) knock-out mutant by reading frame shift, and (F) wild-type control plant. Analysis was performed using a confocal laser scanning microscope (taken from Schedel et al., Front. Plant Sci 7, 2017, article 1995).

Further studies were devoted to leaf development as a determinant of overall plant performance. A concerted effort with several research groups of three IPK departments revealed that leaf width is specified by the leaf primordium size, which itself was found to be different in 2- and 6-rowed barley, with the latter forming broader leaves (Thirulogachandar et al., Plant J. 2017). Together with colleagues from the University of Potsdam and the *GGR* RG of IPK, it was further demonstrated that the INDETERMINATE DOMAIN protein BROAD LEAF1 limits barley leaf width by restricting lateral cell proliferation (Jöst et al., Current Biol. 2016).

Genetic engineering was also broadly used in studies on the interaction of cereals with pathogenic fungi and oomycetes. In cooperation with colleagues from the *Technical Universities of Aachen* and *Munich*, a new grass-specific signaling pathway for polarized defence of fungal pathogens was elucidated, in which the Jacalin-Lectin domain of modular proteins plays a pivotal role (Weidenbach et al., Molecular Plant 2016). The long-standing cooperation with the IPK RG *PSG* has further resulted in the functional validation of a LRR/Malectin receptor-like kinase gene and a cellulose synthase-like D2 gene both of which confer resistance of barley to the powdery mildew-causing fungus (Rajaraman et al., Front. Plant Sci. 2016, Douchkov et al., New Phytologist 2016). In addition, the novel principle of plant-induced silencing of fungal genes entailed an effective protection of wheat spikes from being infected by *Fusarium culmorum (*Chen et al., J. Exp. Bot. 2016).

Embedding in Departmental and IPK Research Strategy

By providing cutting edge genetic engineering and haploid technologies, the *PRB* group is a major integrator of the network between all IPK's departments. *PRB* head Jochen Kumlehn is one of the coordinators of IPK's strategic research theme 3 *Mechanisms of Plant Reproduction*. In this context, the group is involved in research on reproductive processes such as meiosis, the initiation of embryogenesis and pollen development pathways. Within the *Physiology and Cell Biology* Department, the *PRB* group most intensely cooperates with the *MPE* and *SZB* groups. Moreover, the *PRB* group is also actively involved with its *PARASIT* project in the *ScienceCampus Halle*.

Plans, Opportunities and Challenges

The *PRB* RG aims to strengthen its international leading role in the development of site-directed genome modification in cereals. The major challenge in this field is to extend the technology from current methods of site-directed mutagenesis towards a precisely predictable modification of genomic DNA sequences, including edits aiming to change sequence motif functionality as well as exchanges of entire alleles. Furthermore, the *PRB* group will intensify its efforts to establish biotechnologies to be used to significantly improve the performance of so far under-utilitzed crops such as *Camelina sativa*, *Chenopodium quinoa* and grain amaranths.

Peer Reviewed Papers

2016

BUDHAGATAPALLI, N., S. SCHEDEL, M. GURUSHIDZE, S. PENCS, S. HIEKEL, T. RUTTEN, S. KUSCH, R. MORBITZER, T. LAHAYE, R. PANSTRUGA, J. KUMLEHN & G. HENSEL: A simple test for the cleavage activity of customized endonucleases in plants. Plant Methods 12 (2016) 18.

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Articles in Compilations

2016

KUMLEHN, J.: Embryogenesis and plant regeneration from isolated wheat zygotes. In: GERMANÀ, M.A. & M. LAMBARDI (Eds.): *In vitro* embryogenesis in higher plants. (Series: Methods in molecular biology, Vol. 1359) New York, NY [u.a.]: Humana Press (2016) 503-514.

2017

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TILL, B.J., B.J. HOFINGER, A. SEN, O.A. HUYNH, J. JANKOWICZ-CIESLAK, L. GUGSA & J. KUMLEHN: A protocol for validation of doubled haploid plants by enzymatic mismatch cleavage. In: JANKOWICZ-CIESLAK, J., T. TAI, J. KUMLEHN & B.J. TILL (Eds.): Biotechnologies for plant mutation breeding: protocols. Cham: Springer International Publishing (2017) 253-262.

Editorships

2016

EZURA, H., T. ARIIZUMI, J. GARCIA-MAS & J. ROSE (Eds.): Functional Genomics and Biotechnology in Solanaceae and Cucurbitaceae Crops. (Series: Widholm J., J. Kumlehn & T. Nagata (Eds.): Biotechnology in agriculture and forestry, Vol. 70) Berlin Heidelberg: Springer (2016) 265 pp.

2017

JANKOWICZ-CIESLAK, J., T. TAI, J. KUMLEHN & B.J. TILL (Eds.): Biotechnologies for plant mutation breeding: protocols. Cham: Springer International Publishing (2017) 339 pp.

Theses

2016

TRAUTWEIN, H.: Etablierung eines in planta Funktionalitätstests für Zielsequenz-spezifisch programmierbare Endonukleasen. (Bachelor Thesis) Hochschule für Angewandte Wissenschaften, Hamburg (2016) 94 pp.

2017

AUDIJE DE LA FUENTE, S.: Production of barley (*Hordeum vulgare* L.) doubled haploids via interspecific crosses. (Diploma Thesis) Universidad Politécnica de Madrid, Madrid (2017) 145 pp.

DIRKS, J.: Untersuchung des Einflusses der ATG-Kontext-Sequenz auf die Translationseffizienz. (Master Thesis) Martin-Luther-Universität Halle-Wittenberg, Naturwissenschaftliche Fakultät III, Institut für Agrar- und Ernährungswissenschaften, Halle/S. (2017) 47 pp.

GROSSE, M.: Gerichtete Mutagenese Methionin-Aminopeptidase-codierender Gene durch gRNA-vermittelte Cas9-Endonuklease. (Master Thesis) Ernst-Moritz-Arndt-Universität, Greifswald (2017) 123 pp.

HOHMANN, J.: Die Anwendung der gRNA/Cas9-induzierten Mutagenese in nahrungsrelevanten Nutzpflanzenarten. (Bachelor Thesis) Martin-Luther-Universität Halle-Wittenberg, Naturwissenschaftliche Fakultät III, Institut für Agrar- und Ernährungswissenschaften, Halle/S. (2017) 53 pp.

SCHEDEL, S.: Genetische Veränderung von Tabak mittels Zielsequenz-spezifizierter Endonukleasen. (PhD Thesis) Leibniz Universität Hannover, Naturwissenschaftliche Fakultät, Hannover (2017) 133 pp.

Patents

2016

HOUBEN, A., R. KARIMI ASHTIYANI, T. ISHII, N. STEIN & J. KUMLEHN: Generation of haploid plants. (Industrieanmeldung), Veröffentlichung: 03.03.2016, IPK-Nr. 2014/01. EP 14182719.6 (2016).

Research Group: Yeast Genetics (HEG)

Head: Prof. Dr. habil. Gotthard Kunze, Dr. Martin Giersberg (temp. since 12.12.2017)

Scientists

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Keywords

Arxula adeninivorans
Biofuel
Tannic Acid Catabolism
Biocatalysts
Biosensors
Arbuscular Mycorrhizal Fungi

Highlights

Transgenic *A. adeninivorans* strains produce up to 52.1% of the dry cell weight of poly-(hydroxy butyrate - hydroxyvalerate) copolymers with 12.3%mol poly-hydroxyvalerate (submitted in Microbial Cell Factories).

Elucidation of the complete tannic acid and protocatechuate degradation pathway in *A. adeninivorans* (Frontiers Microbiol.).

First time separation and identification of hormone-active compounds using a combination of chromatographic separation and yeast based reporter assay (Sci. Total Environ. (2017)).

Selection of first binding proteins for the elements Terbium and Europium.

Enzymatic degradation of diclofenac and sulfamethoxazole via recombinant laccase synthesized in *A. adeninivorans.*

Influence of branched-chain amino acids on n-butanol synthesis in *A. adeninivorans* (Microbial Cell Factories (2016)).

Funding

BMBF, BMWi (ZIM), EU (FP7-PEOPLE-2013-INT), Land Sachsen Anhalt, Industry

The activities of the *Yeast Genetics* research group are focused on non-pathogenic yeast species like *Arxula adeninivorans.* These yeasts are used for recombinant protein production in chemical industry, for the degradation of plastics and pharmaceuticals or to reduce the purine content in beer and food. They can also serve as gene-donor, biocatalyst for biofuels or the bioaccumulation of rare earth elements. As components in biosensors they are used for the monitoring of waste water, feed and food and for medical research. In addition, *arbuscular mycorrhizal fungi* are used to analyse fungus – plant root interactions.

Research Statement and Major Achievements

Arxula adeninivorans is a versatile non-pathogenic organism for both, basic and applied research due to its remarkable characteristics (Fig. 49). It utilises a broad range of sole carbon and nitrogen sources, exhibits a temperature-dependent dimorphism, is thermo-, osmo- and salt tolerant and shows excellent growth and secretion characteristics. Moreover, the genome of *Arxula* is completely sequenced and annotated enabling us to explore and exploit its portfolio of enzymes and entire metabolic pathways.

A. adeninivorans is capable of tannic acid and protocatechuate catabolism and the particular genes as well as the respective encoding proteins involved in the pathway (tannase 1 and 2, gallic acid decarboxylase, catechol 2,3-dioxygenase) have been isolated and characterised. In a transgenic approach yeasts were applied to convert waste metabolites into higher-value commodity chemicals like cis,cis-muconic acid. Furthermore it serves as a suitable biocatalyst for the synthesis of biotechnologically relevant products like 1-butanol, 2-butanol, 2-butanone, 2,3-butanediol, 2,5-furanedicarboxylic acid and poly-(hydroxybutyrate-hydroxyvalerate) copolymers because all essential prerequisites and components for heterologous gene expression are available. Many specialised methods have been established to construct customised industrial strains. These resulting strains synthesise recombinant esterases for the

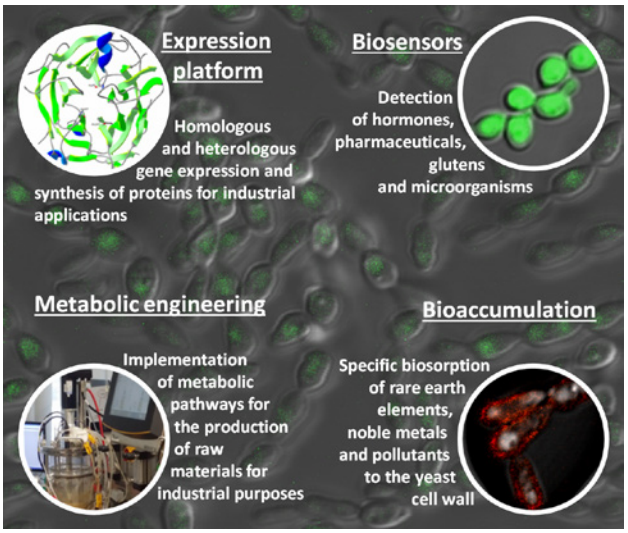


Fig. 49 Overview of major research fields in the yeast genetics group. For details see text. Yeast pictures were taken by Twan Rutten (SZB/PZB).

synthesis of mono esters from symmetric dicarbonic acids or symmetric diols as spacer groups for medical chemistry and polymer applications. In addition strains are under construction to synthesise a multi-enzyme complex (PURINOsom) with immobilised recombinant enzymes (purine nucleoside phosphorylase, adenine deaminase, xanthine oxidase, guanine deaminase and urate oxidase) to decrease the purine content in foods for patients suffering from gout. Other strains produce recombinant cutinases, laccases and cytochrome P450 for the biotechnological recycling of electronic scrap or the enzymatic removal of harmful substances like pharmaceuticals from wastewater. There are also strains available to improve feed quality by new enzymes with lignocellulolytic activities (e.g. arabinanase) or for the recovery of rare earth elements.

Yeasts are also used as biocompound for the detection of hormones, dioxins, pharmaceuticals or bisphenol A in tap water, mineral water and waste water. Assays and biosensors are based on transgenic *A. adeninivorans* cells which include the respective human receptors and a specifically activatable reporter gene expression module. The respective hormone response elements are designed as estrogen/androgen/progesterone/glucocorticoid/dioxin/pharmaceuticals/bisphenol A screen assays with biochemical measurements or as microbial biosensors with an amperometric detection method. First assays based on these sensor compounds are already commercialized and under investigation to set up an international standard assay (DIN, ISO). In addition, yeast cell based multi-bioautography receptor binding assays combined with thin layer chromatography for the identification and quantification of hormone active substances as well as cell free receptor dimerisation assays for the detection of ligand mediated receptor dimerisation have been developed.

Besides yeasts, *arbuscular mycorrhizal fungi* (AMF) are in focus of the research group. AMF are able to establish a symbiotic relationship with 70-90% of land plant species and obviously, this interaction has a major impact on the entire soil ecosystem. AMF improve the uptake of phosphorus and nitrogen by plants, improve salt and drought tolerance and are essential to protect plants from root pathogens. Since environmental conditions influence the composition of the AMF population, a set of autochthone AMF was selected from different places in Germany and subsequently taxonomically classified. This compilation was the basis to establish *in vivo* and *in vitro* AMF lines as core of a strain collection. The lines were tested as soil additive for the production of high quality tomatoes in the greenhouse and concerning their suitability as new technological approach for the effective propagation of fruit trees and conifers *in vitro*.

In addition, biosensors based on DNA-DNA/RNA hybridisation, as well as binding protein-ligand interaction were developed and adapted for identification and classification of AMF but also for detection of glutens in food and microbial contaminants in wine and beer.

Embedding in Departmental and IPK Research Strategy

The research of the *Yeast Genetics* Group is embedded in the IPK research theme 5 *Mechanisms of Resistance and Stress Tolerance*. Collaborations exist with the IPK groups *MPE*, *ABC*, *SZB* and *PAK*.

Plans, Opportunities and Challenges

Until the group leader´s retirement in 2019 research will focus (1) on the elucidation of new anabolic and catabolic pathways in the yeast *Arxula adeninivorans*, (2) on the characterization of new transporters and binding proteins, and (3) on new biotechnological products, metabolic engineering, bioaccumulation, biocatalysts and biosensors (predominantly financed from industry). After this time a transfer of this research field to a university or a research institute is intended.

Peer Reviewed Papers

2016

KASPRZAK, J., F. BISCHOFF, M. RAUTER, K. BECKER, K. BARONIAN, R. BODE, F. SCHAUER, H.M. VORBRODT & G. KUNZE: Synthesis of 1-(*S*)-phenylethanol and ethyl (*R*)-4-chloro-3-hydroxybutanoate using recombinant *Rhodococcus erythropolis* alcohol dehydrogenase produced by two yeast species. Biochem. Eng. J. 106 (2016) 107-117.

KASPRZAK, J., M. RAUTER, S. DENTER, K. BECKER, K. BARONIAN, R. BODE, F. SCHAUER, M. PIONTEK, H.M. VORBRODT & G. KUNZE: Synthesis of ethyl (*R*)-mandelate using recombinant *Carboxydothermus hydrogenoformans* alcohol dehydrogenase produced by two yeast species. J. Mol. Catalysis B-Enzymatic 133 (2016) 176-186.

KASPRZAK, J., M. RAUTER, J. RIECHEN, S. WORCH, K. BARONIAN, R. BODE, F. SCHAUER & G. KUNZE: Characterization of an *Arxula adeninivorans* alcohol dehydrogenase involved in the metabolism of ethanol and 1-butanol. FEMS Yeast Res. 16 (2016) fow018.

MALAK, A., K. BARONIAN & G. KUNZE: *Blastobotrys* (*Arxula*) *adeninivorans* – a promising alternative yeast for biotechnology and basic research. Yeast 33 (2016) 535-547.

PHAM, H.T.M., A. CHAMAS, A. NIETER, M. GIERSBERG, T. RUTTEN, L. GEHRMANN, K. HETTWER, J. TUERK, S. UHLIG, K. SIMON, K. BARONIAN & G. KUNZE: Determination of glucocorticoids using photometric (A-YGS) and spectrofluorometric (A-YGFS) bioassays based on modified *Arxula adeninivorans* cells: applications in environmental analysis. Sensors Actuat. B 223 (2016) 540-549.

RAUTER, M., J. KASPRZAK, K. BECKER, J. RIECHEN, S. WORCH, A. HARTMANN, M. MASCHER, U. SCHOLZ, K. BARONIAN, R. BODE, F. SCHAUER, H. MATTHIAS VORBRODT & G. KUNZE: Aadh2p: an *Arxula adeninivorans* alcohol dehydrogenase involved in the first step of the 1-butanol degradation pathway. Microb. Cell Fact. 15 (2016) 175.

ZABEK, A., J. SWIERKOT, A. MALAK, I. ZAWADZKA, S. DEJA, K. BOGUNIA-KUBIK & P. MLYNARZ: Application of ^{1}H NMR-based serum metabolomic studies for monitoring female patients with rheumatoid arthritis. J. Pharm. Biomed. Anal. 117 (2016) 544-550.

ZÜHLKE, M.-K., R. SCHLÜTER, A.-K. HENNING, M. LIPKA, A. MIKOLASCH, P. SCHUMANN, M. GIERSBERG, G. KUNZE & F. SCHAUER: A novel mechanism of conjugate formation of bisphenol A and its analogues by *Bacillus amyloliquefaciens*: Detoxification and reduction of estrogenicity of bisphenols. Int. Biodeter. Biodegr. 109 (2016) 165-173.

2017

BIERNACKI, M., M. MARZEC, T. ROICK, R. PÄTZ, K. BARONIAN, R. BODE & G. KUNZE: Enhancement of poly(3-hydroxybutyrate-co-3-hydroxyvalerate) accumulation in *Arxula adeninivorans* by stabilization of production. Microb. Cell Fact. 16 (2017) 144.

BIERNACKI, M., J. RIECHEN, U. HÄHNEL, T. ROICK, K. BARONIAN, R. BODE & G. KUNZE: Production of (R)-$_{3}$-hydroxybutyric acid by *Arxula adeninivorans*. AMB Express 7 (2017) 4.

CHAMAS, A., H.T. PHAM, M. JÄHNE, K. HETTWER, S. UHLIG, K. SIMON, A. EINSPANIER, K. BARONIAN & G. KUNZE: Simultaneous detection of three sex steroid hormone classes using a novel yeast-based biosensor. Biotechnol. Bioeng. 114 (2017) 1539-1549.

CHAMAS, A., H.T.M. PHAM, M. JÄHNE, K. HETTWER, L. GEHRMANN, J. TUERK, S. UHLIG, K. SIMON, K. BARONIAN & G. KUNZE: Separation and identification of hormone-active compounds using a combination of chromatographic separation and yeast-based reporter assay. Sci. Total. Environ. 605-606 (2017) 507-513.

MEIER, A., S. WORCH, E. BÖER, A. HARTMANN, M. MASCHER, M. MARZEC, U. SCHOLZ, J. RIECHEN, K. BARONIAN, F. SCHAUER, R. BODE & G. KUNZE: Agdc1p – a gallic acid decarboxylase involved in the degradation of 1 tannic acid in the yeast *Blastobotrys* (*Arxula*) *adeninivorans*. Front. Microbiol. 8 (2017) 1777.

WILLIAMS, J., A. TRAUTWEIN-SCHULT, G. KUNZE & K. BARONIAN: Environmental and metabolic parameters affecting the uric acid production of *Arxula adeninivorans*. Appl. Microbiol. Biotechnol. 101 (2017) 4725-4736.

ZÜHLKE, M.-K., R. SCHLÜTER, A. MIKOLASCH, D. ZÜHLKE, M. GIERSBERG, H. SCHINDLER, A.-K. HENNING, H. FRENZEL, E. HAMMER, M. LALK, U.T. BORNSCHEUER, K. RIEDEL, G. KUNZE & F. SCHAUER: Biotransformation and reduction of estrogenicity of bisphenol A by the biphenyl-degrading *Cupriavidus basilensis*. Appl. Microbiol. Biotechnol. 101 (2017) 3743-3758.

Articles in Compilations

2017

BISCHOFF, F., A. CHAMAS, K. LITWINSKA, F. MATTHES & G. KUNZE: Applications of *Blastobotrys* (*Arxula*) *adeninivorans* in biotechnology. In: SATYANARAYANA, T. & G. KUNZE (Eds.): Yeast diversity for human welfare. Singapore: Springer (2017) 455-479.

CHAMAS, A., H.T.M. PHAM, K. BARONIAN & G. KUNZE: Biosensors Based on Yeast/Fungal Cells. In: SIBIRNY, A.A. (Ed.): Biotechnology of Yeasts and Filamentous Fungi. Cham: Springer International Publishing (2017) 351-371.

WORCH, S. & I. LEMKE: Gene expression analysis in *Arxula adeninivorans*: A nested quantitative real time PRC approach. In: SATYANARAYANA, T. & G. KUNZE (Eds.): Yeast diversity for human welfare. Singapore: Springer (2017) 251-256.

Editorships

2017

SATYANARAYANA, T. & G. KUNZE (Eds.): Yeast diversity for human welfare. Singapore: Springer (2017) XIV, 486 pp.

Theses

2016

FABER, M.: Charakterisierung zweier Rapskultivare auf Bormangeltoleranz durch Metabolit-Element- und BOR-Transportprotein-Analysen. (Bachelor Thesis) Hochschule Anhalt, Köthen (2016) 104 pp.

KASPRZAK, J.: Alcohol dehydrogenases as biocatalysts for the production of enantiomerically pure chiral alcohols. (PhD Thesis) Ernst-Moritz-Arndt-Universität, Greifswald (2016) 141 pp.

MATIEBE, A.: Genomweite Identifizierung von Bortransportern und Charakterisierung der Bor-Aufnahmekinetik in zwei Raps (*Brassica napus*) Kultivaren, die sich in ihrer Bormangel-Toleranz unterscheiden. (Bachelor Thesis) Hochschule Anhalt, Köthen (2016) 66 pp.

MÜLLER, J.: Rekombinante Expression und biochemische Charakterisierung von drei 2,3-Butandiol-Dehydrogenasen aus *Arxula adeninivorans* und *Klebsiella pneumoniae.* (Bachelor Thesis) Hochschule Anhalt, Köthen (2016) 56 pp.

SCHATZ, J.: Arbeiten zur Adaption des bakteriellen Cohesin-Dockerin-Systems in Hefen. (Bachelor Thesis) Hochschule Anhalt, Köthen (2016) 51 pp.

2017

BISCHOFF, F.: Identifizierung und Charakterisierung dreier Cutinasen von *Arxula adeninivorans* und deren Einsatz zum Abbau von Polyestern. (PhD Thesis) Ernst-Moritz-Arndt-Universität, Greifswald (2017) 152 pp.

BOHNDORF, A.: Nutzung der Protoplastenfusion zur Herstellung höherploider *Pelargonium crispum*-Hybriden (*P.× crispum*). (Master Thesis) Hochschule Anhalt, Studiengang Biotechnologie, Köthen (2017).

RESO, J.: Untersuchungen zur rekombinanten Expression und Charakterisierung von bakteriellen Cellulosom-Komponenten in der Hefe *Arxula adeninivorans.* (Bachelor Thesis) Hochschule Anhalt, Studiengang Biotechnologie, Köthen (2017).

Unabhängige Arbeitsgruppen

Die unabhängigen Arbeitsgruppen stellen ein Instrument der Förderung wissenschaftlicher Nachwuchskräfte dar. Ohne in eine der vier wissenschaftlichen Abteilungen des Institutes eingegliedert zu sein bieten sie den Wissenschaftlerinnen und Wissenschaftlern die notwendigen Rahmenbedingungen, um eigene Forschungsthemen zu erschließen, internationale Sichtbarkeit zu erlangen und sich für spätere Leitungsfunktionen zu qualifizieren.

Independent Research Groups

To promote junior researchers, the independent research groups provide excellent scientists with conditions facilitating the raise of their scientific reputation. Without being integrated in one of the four scientific departments, independent research groups enable their heads to qualify for the next career step and to proceed own research projects with enhanced autonomy and visibility .

Independent Heisenberg Research Group: Plant Architecture (PBP)

Head: PD Dr. Thorsten Schnurbusch

Scientists

Dr. Ahmad M. Alqudah

Dr. Zifeng Guo

Omar Heliel (Egyptian Scholarship)

Dr. Ravi Koppolu

Dr. Naser Poursarebani

Dr. Shun Sakuma (JSPS Fellow)

Dr. Johannes Thiel

Venkatasubbu Thirulogachandar

Dr. Helmy M. Youssef

Gizaw M. Wolde

Keywords

Developmental and Molecular Genetics

Inflorescence Architecture

Cereal Spike

Spikelet

Floret

Highlights

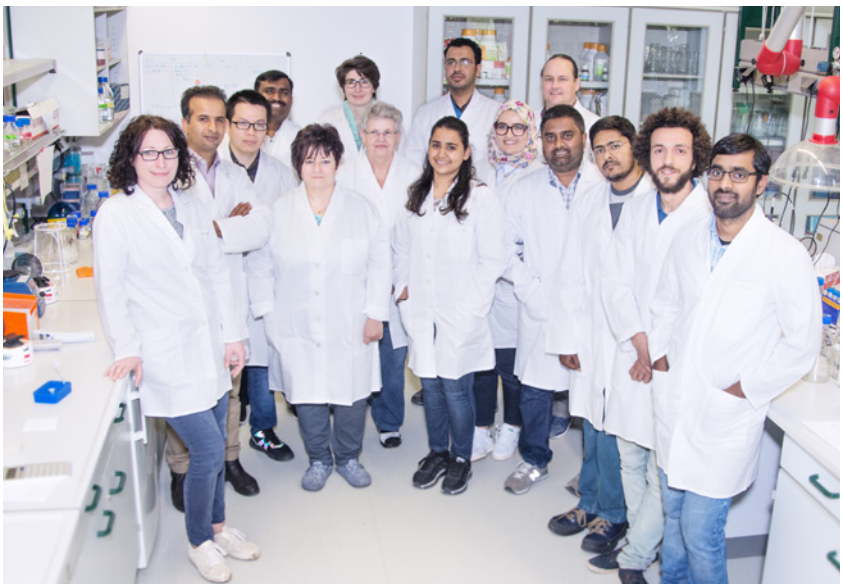
July 2016, Start of the European Research Council (ERC) Consolidator Grant (ERC-2016-CoG #681686), HORIZON 2020, "LUSH SPIKE - Genetic and Molecular Determinants of Spikelet Survival in Cereal Crops".

October 2016, Start of the BMBF, Pflanzenzüchtungsforschung Grant, OSIRIS consortium, "An RGEN and GWAS approach for new spike architecture in wheat".

January 2017, NATURE GENETICS paper about *Vrs2* published.

Funding

ERC, DFG, BMBF, IWYP, BMEL, WGL, JSPS, Industry



Our understanding of the molecular genetics of spike or spikelet development is very limited in small grain cereals. Functional knowledge of genes, which regulate key developmental traits such as inflorescence branching, spikelet initiation or abortion, is almost completely lacking in most of our cereal crops. We are utilizing natural spike variants from wheat and induced spike mutants from barley to clarify the genetic make-up of genes underlying developmental phenotypes for reduced and increased grain number per spike.

Research Statement and Major Achievements

Towards a better understanding of the genetic and molecular determinants of spikelet survival in cereal crops: One promising avenue for improving grain yield of cereal crops, including wheat and barley, involves reducing spikelet mortality. Spikelets, the grain-bearing units of cereal spikes, usually form in excess and subsequently abort during development; increased spikelet survival is linked to increased numbers of grains per spike. Therefore, reducing spikelet mortality is an intriguing approach to improve grain yield. In barley, the number of spikelets per spike at the awn primordium (AP) stage represents the maximum yield potential per spike. After the AP stage, significant spikelet mortality results in fewer grains per spike. Our group's previous results clearly indicated that spikelet survival in barley is highly genetically controlled and that the period from AP to tipping represents the most critical pre-anthesis phase related to spikelet reduction and grain yield per spike. However, the underlying genetic and molecular determinants of spikelet survival remain to be discovered. Within the ERC-funded LUSH SPIKE project we pursue an ambitious research program with an emphasis on using available genetic resources to isolate and functionally characterize Mendelized QTL, to reveal gene regulatory networks determining spikelet survival during the critical spike growth period, and to elucidate spatio-temporal patterns of metabolite and phytohormone distributions in spike and spikelet sections during the critical growth period, using mass spectrometric imaging. The results we obtain will also advance our understanding of how to improve yields of other cereal crops such as wheat.

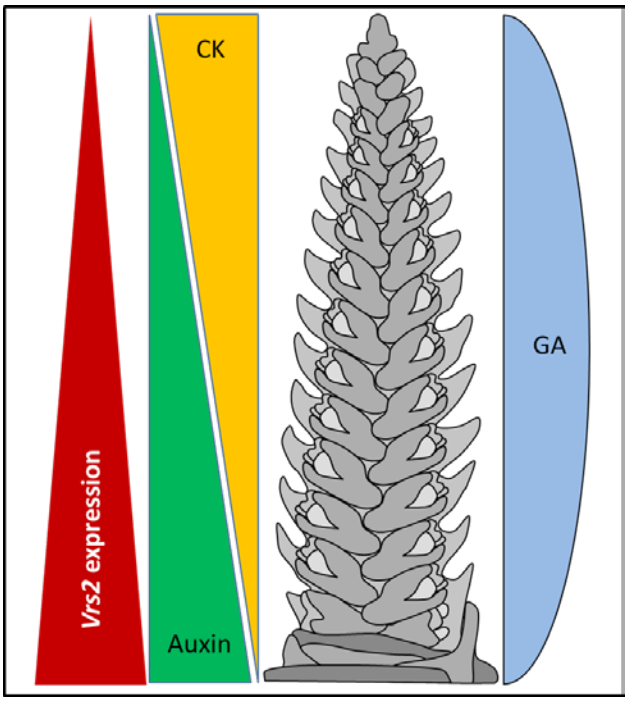


Fig. 50 Low-resolution model showing the overall trend of *Vrs2* expression in relation to auxin, cytokinin (CK) and gibberellin (GA) concentrations during barley spike development. Auxin concentrations along the spike followed *Vrs2* transcript levels from different spike sections in a basal–apical fashion.

CRISPR-induced allelic variation for novel spike architecture genes in wheat: Grain number is one important yield component of wheat's grain yield and measurable either as per unit area, per plant, or per spike. A further increase in the number of grains per plant can be achieved by modified spike architecture with enhanced reproductive sink capacity, and thus, producing more potential grain sites. The wheat and barley spike is characterized by sessile spikelets directly borne on the main axis, forming a branchless spike. However, wheat and barley mutants that display non-canonical spike-branching have been characterized in our laboratory of which one tetraploid wheat mutant, Miracle Wheat (i.e. *branched head*, *bh*^{t}), produced significantly more grains per spike that consequently led to higher spike yield. Moreover, we positionally cloned and identified mutant alleles of two other spike architecture genes that resulted in branch formation. Therefore, the above-mentioned genes represent exciting targets for engineering novel spike architecture in hexaploid wheat to potentially produce more spikelets and subsequently more grains per spike. During the BMBF-funded OSIRIS project, we therefore will apply genome engineering technology derived from the bacterial CRISPR/CAS immune system, to knock-out these genes in hexaploid wheat.

VRS2 regulates hormone-mediated inflorescence patterning in barley (Nat Genet 49: 157-161): Limited molecular information is available about how grain-bearing inflorescences, called spikes, are formed and maintain their regular, distichous pattern. In this study we elucidated the molecular and hormonal role of *Six-rowed spike 2* (*Vrs2*), which encodes a SHORT INTERNODES (SHI) transcriptional regulator during barley inflorescence and shoot development. We showed that *Vrs2* is specifically involved in floral organ patterning and phase duration by maintaining hormonal homeostasis and gradients during normal spike development and similarly influences plant stature traits. Furthermore, we established a link between the SHI protein family and sucrose metabolism during organ growth and development that may have implications for deeper molecular insights into inflorescence and plant architecture in crops (Fig. 50).

Embedding in Departmental and IPK Research Strategy

Work within the independent *HEISENBERG-Research Group PBP* relates predominantly to the IPK research theme 4 *Growth and Metabolism*.

Plans, Opportunities and Challenges

Our ongoing work, collaborations and activities may provide sufficient opportunities to continue our seminal studies in the research area of spike and spikelet growth and development in wheat and barley. Future challenges will be to generate reporter- or sensor lines (stable transformants) for sophisticated phenotypic, microscopic and cellular analyses of developmental phenotypes. The planned acquisition of a new microscope (Raman- and Brillouin spectroscopy; RG *SZB*) may help reaching this level of analysis.

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2016

ALQUDAH, A.M., R. KOPPOLU, G.M. WOLDE, A. GRANER & T. SCHNURBUSCH: The genetic architecture of barley plant stature. Front. Genet. 7 (2016) 117.

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Other Papers

2017

GUO, Z.: Save Floret! Save yield! Save life! 18. Kurt von Rümker-Vorträge. Vortr. Pflanzenzücht. 86 (2017) 13-20.

YOUSSEF, H.M.: Genotypic and phenotypic analysis of the SPIKE row-type in barley (*Hordeum vulgare* L.). 18. Kurt von Rümker-Vorträge. Vortr. Pflanzenzücht. 86 (2017) 67-74.

Theses

2016

YOUSSEF, H.M.: Genotypic and phenotypic analysis of the spike row-type in barley (*Hordeum vulgare* L.). (PhD Thesis) Martin-Luther-Universität Halle-Wittenberg, Institut für Agrar- und Ernährungswissenschaften der Naturwissenschaftlichen Fakultät III, Halle/S. (2016) 140 pp.

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GUO, Z.: Physiological and genetic analyses for the determination of grain number in wheat. (PhD Thesis) Martin-Luther-Universität Halle-Wittenberg, Institut für Agrar- und Ernährungswissenschaften der Naturwissenschaftlichen Fakultät III, Halle/S. (2017) 225 pp.

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Independent Research Group: Domestication Genomics (DG)

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Keywords

Domestication

Cereal Crops

Population Genomics

Genome Assembly

Crop Wild Relatives

Computational Methods

Highlights

Barley genome paper published in Nature.

Articles on past and present barley diversity published in Nature Genetics.

Wild emmer genome published in Science.

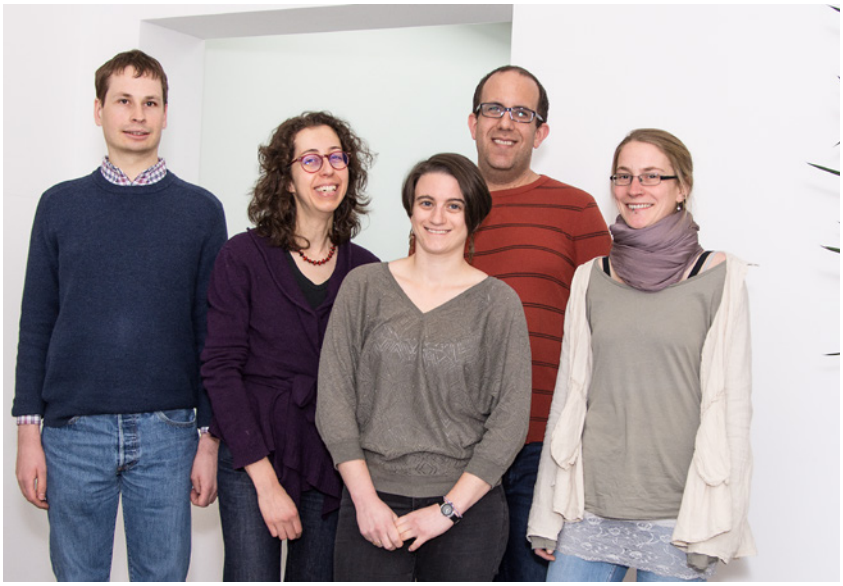
Leadership award of the International Wheat Genome Sequencing Consortium awarded to Martin Mascher.

DFG project on gene regulation in wild and domesticated barley started.

BMBF projects on wheat and barley genomics started.

Funding

DFG, BMBF, Leibniz-SAW, WCH



The research group *Domestication Genomics* studies domestication and adaptation processes and their interaction with genetic diversity in crops and their wild relatives with a focus on the temperate cereals barley, wheat, and rye. Key research goals are: (i) tracing the demographic development and adaptation of cereal crops as they expanded their range from the initial site of domestication into Europe (ii) understanding the molecular consequences of domestication on patterns of nucleotide diversity, gene expression and gene regulation (iii) elucidating the relationship between crops and their extant wild relatives and progenitors.

Research Statement and Major Achievements

The International Barley Genome Sequencing Consortium has recently reported a reference genome sequence assembly of the barley cv. Morex. In frame of this work, we have established a general workflow for constructing chromosome-scale assemblies of Triticeae genomes using three-dimensional (3D) contact probabilities obtained by means of chromosome conformation capture sequencing (Hi-C). This allowed us to derive, for the first time, a linear order of the vast non-recombining regions of the barley genome. The barley genome sequence will arguably represent the most important resource for barley genetics and genomics in the coming years. Moreover, the initial analysis of the barley genome sequence revealed (i) an extreme depletion of genetic diversity in pericentromeric regions in elite material, (ii) Triticeae-specific expansions of agronomically important gene families relevant for nutrient transport and starch breakdown, and (iii) key features of the 3D organization of chromatin in the interphase nucleus.

In frame of international consortia, we applied the computational methods developed for assembling the barley genome to wheat. Chromosome-scale assemblies were constructed for a wild emmer wheat accession (Zavitan), a durum variety (Svevo), and the reference accession of bread wheat (Chinese Spring).

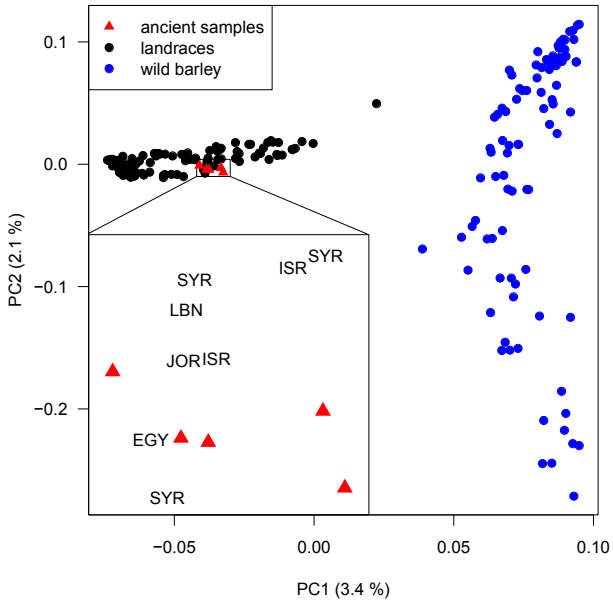


Fig. 51 Ancient barley sequences were compared to exome sequence data for a present-day diversity panel. Principal component analysis (PCA) showing ancient samples projected onto the PCA axes for the present-day diversity panel. The inset magnifies the PCA space around the ancient samples. ISR, JOR, SYR, LBN and EGY represent closely related landraces from Israel, Jordan, Syria, Lebanon and Egypt, respectively. The proportion of variance explained by each principal component is indicated in parentheses.

Together with Israeli archeologists and German archaeogeneticists, we analyzed DNA sequences retrieved from barley grains recently excavated in a Chalcolithic cave site in the Judean desert. The ancient samples were put into the context of extant barley diversity by joint analysis with exome sequences from 267 wild and domesticated barleys. Our key finding was that the ancient barley samples are closely related to modern landraces from the Southern Levant, presumably because key domestication and adaptation processes had been finished by 4000 BC.

In frame of the Leibniz-funded *BRIDGE* project, we are currently leading the computational analysis of genotypic profiles of 20,000 wild and domesticated barley accessions. In collaboration with the RGs *GGR*, *RGR* and *BIT*, we have so far analyzed data for 15,000 domesticated barleys. This dataset has already (i) highlighted a history of recent intentional admixture between major germplasm groups due to breeders' efforts, (ii) enabled the mapping of highly heritable spike traits by means of GWAS, and (iii) led to the assembly of genetically defined core collections (Fig. 51).

Embedding in Departmental and IPK Research Strategy

Our research on population genomics of cereal crops and their wild relatives in context of IPK's gene bank collection contributes to the IPK research themes *Genome Diversity and Evolution* and *Concepts for the Valorization of Genetic Resources*. We contribute to in-depth molecular characterization of plant genetic resources and to developing means for leveraging genotypic passport for gene bank management. Moreover, we collaborate with other research groups at IPK on computational projects. Our computational pipelines for sequence analysis are also available to other research groups.

Plans, Opportunities and Challenges

We will continue our involvement in the international wheat and barley genome sequencing. After the completion of one barley reference genome, research will focus on (i) resequencing diverse germplasms including domesticated and wild accessions for comprehensive population genetic analysis, and (ii) constructing chromosome-scale genome assemblies of multiple genotypes to integrate large-scale structural variants in the analysis. The recent advances in sequencing and assembly methodologies have made genome assembly and large-scale resequencing feasible in minor crops such as oats and rye. We have committed ourselves to perform chromosome-scale sequence assembly and population genomic analyses in frame of international rye and oat genome sequencing consortia. We will use RNA sequencing data of F1 hybrids between wild and domesticated barley to study the contribution of cis- and trans-regulation of gene expression in interaction with an environmental stress. In collaboration with the *CSF* group and international collaborators, we plan to use chromosome conformation capture sequencing in combination with cytological methods to study chromosome organization throughout the cell cycle. Future research projects will require the analysis of high-throughput datasets of increasing volume and complexity. Key challenges include (i) maintaining a powerful storage and compute infrastructure, (ii) keeping track of algorithmic innovations and (iii) hiring scientists with the necessary computational expertise.

Peer Reviewed Papers

2016

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Independent Junior Research Group: Abiotic Stress Genomics (SGN)

Head: Dr. Markus Kuhlmann (until 31.05.2016)

Scientists

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Dr. Christiane Seiler (INNO-GRAIN MALT)

Dr. Nese Sreenivasulu (Guest, Counsellor, IRRI)

Dr. Vito Butardi (Guest, IRRI)

Seyed Hashemipetroudi (Guest, GABIT)

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Korana Surdonja (INNO-GRAIN MALT)

Hongwen Wang (Graduate School)

Keywords

Terminal drought

Absisic acid

Tiller formation

Barley row type (2-rowed/6-rowed)

DNA methylation

Small regulatory RNA

Highlights

New Project IDRIB funded by Leibniz WissenschaftsCampus Halle "Pflanzenbasierte Bioökonomie"

Funding

ICN funded Junior Research Group

INNO-GRAIN MALT (BMBF)

Graduate School (DFG)

Terminal drought can have severe impact on crop production. Especially, the reproductive stages are highly sensitive causing severe yield losses. Our lab is interested in revealing the molecular mechanisms contributing to stable yield in barley under drought mainly by addressing the research topics (a) altered grain number and (b) seed filling efficiency.
We use integrative genomics approaches to derive gene regulatory networks as well to identify the key regulatory targets, including small regulatory RNA and DNA methylation during the spike meristem differentiation and seed development.

Research Statement and Major Achievements

Cultivated barley, derived from its wild progenitor *Hordeum vulgare ssp. spontaneum,* is among the world's earliest domesticated crop species and today represents the fourth most abundant cereal in both area and tonnage harvested. Approximately three-quarters of global production is used for animal feed, 20% is malted for use in alcoholic and non-alcoholic beverages, and 5% as an ingredient in a range of food products. So improving barley crop yield is one of the most important challenges for research scientists, based on its food and commercial values.

Barley plant architecture is crucial for grain yield and is determined by plant height, tiller number, grain number, grain size, and spike size and spikelet number in a spike, associated with barley productivity. The tiller number in barley is an important agronomic trait for grain production. In the project funded by the *Leibniz Graduate School Yield Formation in cereals-overcoming yield-limiting factors* we are investigating the molecular mechanisms for generating tillers in barley.

The plant hormone abscisic acid (ABA) mediates plant responses to different kinds of abiotic stress such as drought stress and is involved in long-distance signaling in plants. It is the key signal regulating stomatal aperture, seed development, embryo maturation, synthesis of storage products (proteins and lipids), desiccation toleran-

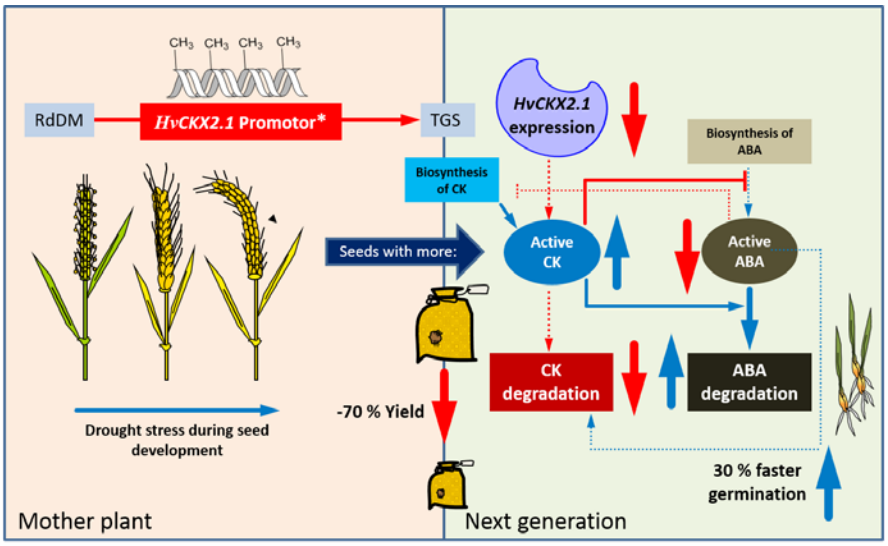


Fig. 52 Sequencing of small RNA under drought stress conditions in barley led to the identification of heterochromatic small RNAs with homology to the promoter of *HvCKX2.1. CKX2.1* belongs to a class of cytokinin oxidases, and the gene is expressed during germination. Terminal drought resulted in an increase of DNA methylation in the promoter region. Grains derived from drought stressed plants showed an increased shoot emergence rate. This behaviour could be mimicked by transgenic barley plants with elevated ABA levels during grain development. (Surdonja K, Eggert K, Hajirezaei M-R, Harshavardhan V, Seiler C, von Wirén N, Sreenivasulu N, Kuhlmann M, Increase of DNA methylation at the HvCKX2.1 promoter by terminal drought stress in barley. Epigenomes 1 (2017) 9. dx.doi.org/10.3390/epigenomes1020009). (Graphic: Kai Eggert)

ce and is involved in apoptosis and maintenance of dormancy (inhibition of germination). In concert with other plant signaling molecules, ABA is also implicated in mediating responses to pathogens and wounding. Certainly, ABA homoeostasis in the plant is tightly controlled by a balance between biosynthesis, inactivation and degradation. But its function in tiller development has been unknown.

In order to increase drought resistance independent transgenic lines (LOHi) have been generated that are post transcriptionally silenced for ABA 8'-hydroxylase genes (RNAi). Surprisingly the transgenic lines showed more tillers resulting in increased yield under control conditions. It was found that during development a temporal increase in ABA content in the late vegetative phase occurs. The followed decrease of ABA content is affected in the two transgenic lines, correlating with the extended phase of active tiller outgrowth. The described phenotype was observed at phytochamber and greenhouse conditions as well as in field near conditions after applying terminal drought stress treatment.

Initial transcriptome analysis performed by microarray hybridization revealed a new interplay of the plant hormones absisic acid and strigolactone. Strigolactones are plant hormones, identified in the dicotyledonous model plant *Arabidopsis thaliana* and also described for the well analyzed monocotyledons model rice, repressing the outgrowth of lateral organs. The synthesis of absisic acid and strigolactone include all-trans-beta-carotene as precursor. We could identify a gene encoding an all-trans/9-cis-beta carotene isomerase with homology to the *A. thaliana DWARF27* (*D27*) gene. The analyzed transgenic plants with elevated levels of ABA after anthesis showed a clear ABA dependent reduction of *HvD27* mRNA in roots. Based on sequence similarity several genes involved in strigolactone biosynthesis and signal perception could be identified. Based on the transgene approach, supported by their expression pattern the involvement of *CCD7*, *CCD8* and *MAX1* homologous genes in barley on strigolactone production could be confirmed. Analysis of LOHi barley root exudates revealed the reduced presence of 5-deoxy-strigol, the main active compound involved in the inhibition of lateral organ outgrowth. To validate the gene function of HvDWARF27 as regulator of tiller outgrowth virus induced gene silencing was performed. Therefore, in collaboration with *RG PSG* a part of the coding region of HvD27 was inserted into the sequence of the barley stripe mosaic virus and barley plants cv. Black Hulless infected. After confirmation of successful infection and transcriptional suppression of the target gene the phenotype of enhanced tiller outgrowth could be confirmed.

Within the described project we were able to identify and quantify the bioactive plant hormone 5-deoxy-strigol in barley for the first time. Furthermore, using our transgenic approach we could identify HvD27 as important key enzyme, interconnecting absisic acid and strigolactone biosynthesis. The transcriptional activity of HvD27 is suppressed by elevated concentration of ABA in the root and thereby strigolactone mediated suppression of lateral organ outgrowth reduced after anthesis (Fig. 52).

Peer Reviewed Papers

2016

HASHEMI, S.H., G. NEMATZADEH, G. AHMADIAN, A. YAMCHI & M. KUHLMANN: Identification and validation of *Aeluropus littoralis* reference genes for quantitative real-time PCR normalization. J. Biol. Res. (Thessalon.) 23 (2016) 18.

HOSSEINI, S.A., M.-R. HAJIREZAEI, C. SEILER, N. SREENIVASULU & N. VON WIREN: A potential role of flag leaf potassium in conferring tolerance to drought-Induced leaf senescence in barley. Front. Plant Sci. 7 (2016) 206.

YAMUNARANI, R., V. RAMEGOWDA, G. GOVIND, H.G. JALENDRAKUMAR, M. UDAYAKUMAR & A.G. SHANKAR: Effect of Zn application on its uptake, distribution and concentration of Fe and Cu in finger millet [*Eleusine coracana* (L.) Gaertn.]. J. Plant Nutr. 39 (2016) 569-580.

2017

DE GUZMAN, M.K., S. PARWEEN, V.M. BUTARDO, C.M. ALHAMBRA, R. ANACLETO, C. SEILER, A.R. BIRD, C.P. CHOW & N. SREENIVASULU: Investigating glycemic potential of rice by unraveling compositional variations in mature grain and starch mobilization patterns during seed germination. Sci. Rep. 7 (2017) 5854.

RADCHUK, V., D. RIEWE, M. PEUKERT, A. MATROS, M. STRICKERT, R. RADCHUK, D. WEIER, H.-H. STEINBIß, N. SREENIVASULU, W. WESCHKE & H. WEBER: Down-regulated sucrose transporters HvSUT1, HvSUT2 affects sucrose homeostasis along its delivery path in barley grains. J. Exp. Bot. 68 (2017) 4595-4612.

SANDMANN, M., P. TALBERT, D. DEMIDOV, M. KUHLMANN, T. RUTTEN, U. CONRAD & I. LERMONTOVA: Targeting of *A. thaliana* KNL2 to centromeres depends on the conserved CENPC-k motif in its C-terminus. Plant Cell 29 (2017) 144-155.

SURDONJA, K., K. EGGERT, M.-R. HAJIREZAEI, V. HARSHAVARDHAN, C. SEILER, N. VON WIRÉN, N. SREENIVASULU & M. KUHLMANN: Increase of DNA methylation at the HvCKX2.1 promoter by terminal drought stress in barley. Epigenomes 1 (2017) 9.

THIRULOGACHANDAR, V., A.M. ALQUDAH, R. KOPPOLU, T. RUTTEN, A. GRANER, G. HENSEL, J. KUMLEHN, A. BRÄUTIGAM, N. SREENIVASULU, T. SCHNURBUSCH & M. KUHLMANN: Leaf primordium size specifies leaf width and vein number among row-type classes in barley. Plant J. 91 (2017) 601-612.

Other Papers

HASHEMIPETROUDI, S.H., G. NEMATZADEH, G. AHMADIAN, A. YAMCHI & M. KUHLMANN: Expression analysis of salt stress related expressed sequence tags (ESTs) from *Aeluropus littoralis* by quantitative real-time PCR. Biosci. Biotech. Res. Comm. 9 (2016) 445-456.

Theses

2017

VENKATASUBBU, T.: Dosage of duplicated and antifunctionalized homeobox proteins influences leaf and spikelet development in barley (*Hordeum vulgare* L.). (PhD Thesis) Martin-Luther-Universität Halle-Wittenberg, Naturwissenschaftliche Fakultät I - Biowissenschaften, Halle/S. (2017) 165 pp.

WANG, H.: Genetic manipulation of the cross-talk between abscisic acid and strigolactones and their biosynthetic link during late tittelring in barley. (PhD Thesis) Martin-Luther-Universität Halle-Wittenberg, Naturwissenschaftliche Fakultät I Biowissenschaften, Halle/S. (2017) 114 pp.

Independent Emmy Noether Research Group: Metalloid Transport (MT)

Head: Dr. Gerd Patrick Bienert

Scientists

Dr. Manuela Désirée Bienert

Till Arvid Diehn

Dr. Benjamin Pommerrenig

Dr. Christoph Spitzer

Dr. Jiye Rhee

Keywords

Metalloid Biology

Nutrient Transport

Boron-Deficiency Tolerance

Arsenic Toxicity

Transport Mechanisms

Aquaporin

Highlights

Setting up a soil growth cultivation system which allows working with defined and repeatable boron deficiency conditions in high-throughput phenotyping facilities.

Identification of boron deficiency tolerant Arabidopsis accessions.

Discovery that floral Nodulin26-like Intrinsic type4 Proteins (NIP4s) from *Brassica napus* are functional boron channels.

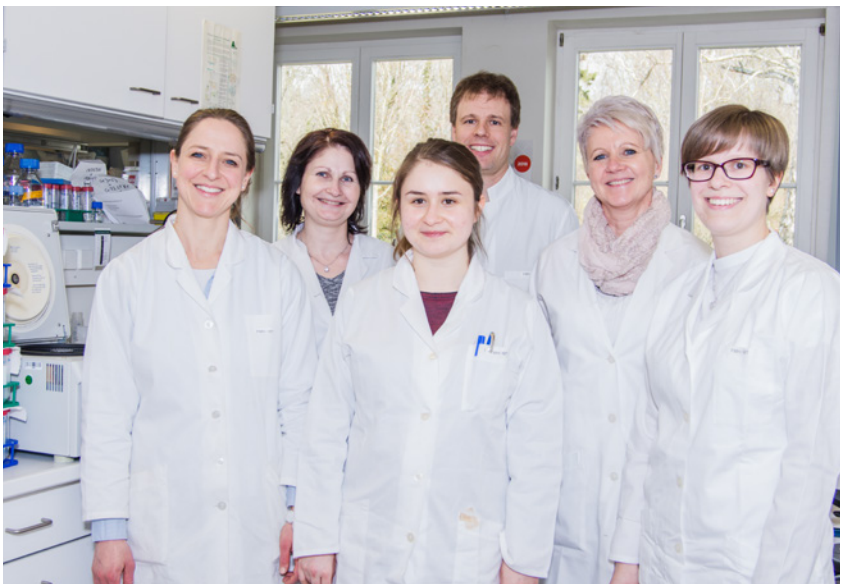
Boron deficiency causes ectopic expression of a meristematic master regulator gene in cortex cells of Arabidopsis roots (Fig. 53).

Unraveling of the functional evolution of modern plant metalloid transport proteins originating from bacterial transport systems.

Rapid kinetic measurements of transmembrane hydrogen peroxide transport processes using a multimixer stopped-flow system.

Funding

DFG



The main objective of the DFG-funded Emmy Noether research group is to elucidate functions, biochemical reactions and transport pathways of metalloids in crop plants as well as their adaptive responses to metalloid deficiency and toxicity. We focus on the essential plant nutrient boron and on the highly toxic and carcinogenic element arsenic. To this aim, a combination of detailed physiological measurements, elemental analyses, exhaustive transcriptomic and metabolomic profiling, transport studies and targeted molecular analyses are employed, both in plants as well as in heterologous expression systems.

Research Statement and Major Achievements

Our hitherto findings have provided a variety of new aspects and novel insights into the mechanisms regulating the B nutritional status in *B. napus* and Arabidopsis. Obtained information and follow-up results will reveal B-efficiency mechanisms and underlying genomic loci and help to understand plant responses upon B-deficiency. This knowledge will assist to develop B-efficient genotypes which will contribute to a more sustainable agriculture. We established a soil-substrate growth system, which allows working with defined and repeatable B-deficiency conditions at different developmental stages of crop plants. The growth system is of high benefit for the entire B research community. It can be used for various plant species and is suitable for automated phenotyping facilities. We have screened and identified highly B-deficiency tolerant *B. napus* and Arabidopsis genotypes. These genotypes represent a valuable set of plants which allows unraveling B-efficiency mechanisms and mechanisms regulating the B nutritional status at the genetic, molecular, and physiological level. Having identified B-deficiency tolerant *B. napus* and Arabidopsis genotypes allows us to experimentally benefit from the advantages which either the crop or the model plant system offers. A byproduct of our screenings is the acquired knowledge on various root architecture traits of various genotypes in both plant species which represent the basis for further studies unrelated to the micronutrient B. Understanding root characteristics is a timely topic in basic research but also from the point of view of breeders as it holds potential

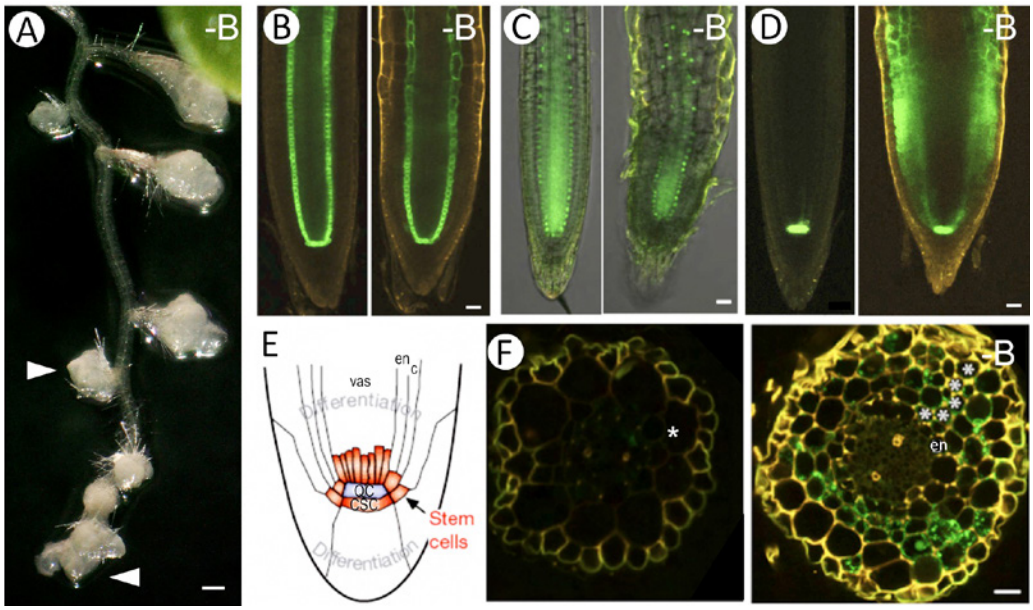


Fig. 53 Boron deprivation has profound impacts on Arabidopsis root morphology. A) Arabidopsis seedlings transferred to boron depleted media develop characteristic primary and lateral root swelling (arrowheads). Arabidopsis root expressing an endodermis (en) marker (B), an endodermis/vasculature (vas) marker (C) and a quiescent center marker (D) on boron containing (left) and depleted (right) media. E) Quiescent center (QC)-driven signaling prevents surrounding stem cells such as the columella stem cells (CSC) from differentiating (Sarkar et al., 2007). F) Root sections of Arabidopsis seedlings expressing GFP-ER under the control of the QC specific promoter transferred to boron-depleted media. Boron deprivation leads to fluorescent signals of the QC marker in cortex cells. Asterisks denote cortex (C) cells. Scale bars are 250 µm (A) and 20 µm (B-F). (Dr. Christoph Spitzer).

for the exploitation and manipulation of genes to increase yield and yield stability of crops.

We have identified and molecularly characterized numerous B transport proteins from *B. napus* cultivars with contrasting B-deficiency tolerances. This information allows understanding in detail the uptake and translocation processes of metalloids at the cellular level. Novel channel features and characteristics have been identified. Our observations that certain Nodulin26-like Intrinsic Proteins (NIPs) possess selectivities for specific metalloids (B versus As) have not only important implications for our molecular understanding of channel selectivity features but also for the potential development of nutrient-efficient elite lines which take up little or no As or do not translocate it to the edible parts of the plant while having or gaining an increased nutrient efficiency. Moreover, we have made substantial progress in unraveling the (functional) evolution of plant NIPs. While originating from bacterial As resistance operons, the horizontal gene transfer of NIP genes to algae allowed a subsequent functional diversification and neofunctionalization with respect to plant metalloid transport processes. NIP channel functioning allowed plants to fine-tune and regulate the distribution of the nutrients B and Si and therewith to successfully colonize land.

We generated detailed knowledge on short-term (Fig. 53) and long-term B-deficiency response reactions at the metabolic, molecular, and morphological level and with respect to growth parameters and phytohormone signaling.

Embedding in Departmental and IPK Research Strategy

The research strategy of the Emmy Noether group matches the research strategy of the IPK as part of the research themes 4 and 5. (*Growth and Metabolism* & *Mechanisms of Resistance and Stress Tolerance*). This is reflected by very fruitful co-operations with several other groups of different IPK departments. Moreover, two unique core facilities of the Institute, the Genebank and the phenotyping facilities, are heavily integrated in the identification of genotypes with beneficial metalloid-related traits. The research concept of the group contributes to key objectives of the IPK:

i) The envisaged improvement of B (+Si)-efficiency in crops will improve sustainable food production by reducing the need for supplementing fertilizers in agricultural crop production while increasing plant stress tolerance.

ii) The generation of crops with highly reduced toxic As levels will decrease exposure of humans to health risks.

Plans, Opportunities and Challenges

Based on the scientific achievements and promising lines of research it is intended to permanently establish and foster the *MT* RG within the European scientific community in close connection to the IPK network.

G.P. Bienert is member of the Programme Committee for the DFG-funded SPP 2089 which provides an excellent opportunity for novel co-operations and initiatives.

Peer Reviewed Papers

2016

DI GIORGIO, J.A., G.P. BIENERT, N.D. AYUB, A. YANEFF, M.L. BARBERINI, M.A. MECCHIA, G. AMODEO, G.C. SOTO & J.P. MUSCHIETTI: Pollen-specific aquaporins NIP4;1 and NIP4;2 are required for pollen development and pollination in *Arabidopsis thaliana*. Plant Cell 28 (2016) 1053-1077.

KIRSCHT, A., S.S. KAPTAN, G.P. BIENERT, F. CHAUMONT, P. NISSEN, B.L. DE GROOT, P. KJELLBOM, P. GOURDON & U. JOHANSON: Crystal structure of an ammonia-permeable aquaporin. PLoS Biol. 14 (2016) e1002411.

MEDRAÑO-FERNANDEZ, I., S. BESTETTI, M. BERTOLOTTI, G.P. BIENERT, C. BOTTINO, U. LAFORENZA, A. RUBARTELLI & R. SITIA: Stress regulates aquaporin-8 permeability to impact cell growth and survival. Antioxid. Redox Sign. 24 (2016) 1031-1044.

ZIERER, W., M.-R. HAJIREZAEI, K. EGGERT, N. SAUER, N. VON WIRÉN & B. POMMERRENIG: Phloem-specific methionine recycling fuels polyamine biosynthesis in a sulfur-dependent manner and promotes flower and seed development. Plant Physiol. 170 (2016) 790-806.

Articles in Compilations

2017

BIENERT, M.D. & G.P. BIENERT: Plant aquaporins and metalloids. In: CHAUMONT, F. & S.D. TYERMAN (Eds.): Plant aquaporins. From transport to signaling. (Series: Signaling and communication in plants) Cham: Springer International Publishing (2017) 297-332.

Theses

2016

FABER, M.: Charakterisierung zweier Rapskultivare auf Bormangeltoleranz durch Metabolit-Element- und BOR-Transportprotein-Analysen. (Bachelor Thesis) Hochschule Anhalt, Köthen (2016) 104 pp.

MATIEBE, A.: Genomweite Identifizierung von Bortransportern und Charakterisierung der Bor-Aufnahmekinetik in zwei Raps (*Brassica napus*) Kultivaren, die sich in ihrer Bormangel-Toleranz unterscheiden. (Bachelor Thesis) Hochschule Anhalt, Köthen (2016) 66 pp.

Independent Research Group: Meiosis (ME)

Head: Dr. Stefan Heckmann

Scientists

Yun-Jae Ahn

Dr. Maria Cuacos Marcos

Stefan Steckenborn Diaz Coria

Mohammad Abdelmordy Ayoub

Keywords

Meiosis

Homologous Recombination

Barley

Chromosomes

Meiotic Chromosome Axis

Highlights

BMBF-funded junior research group Meiosis starts at IPK.

Gransts4Targets awarded by BAYER.

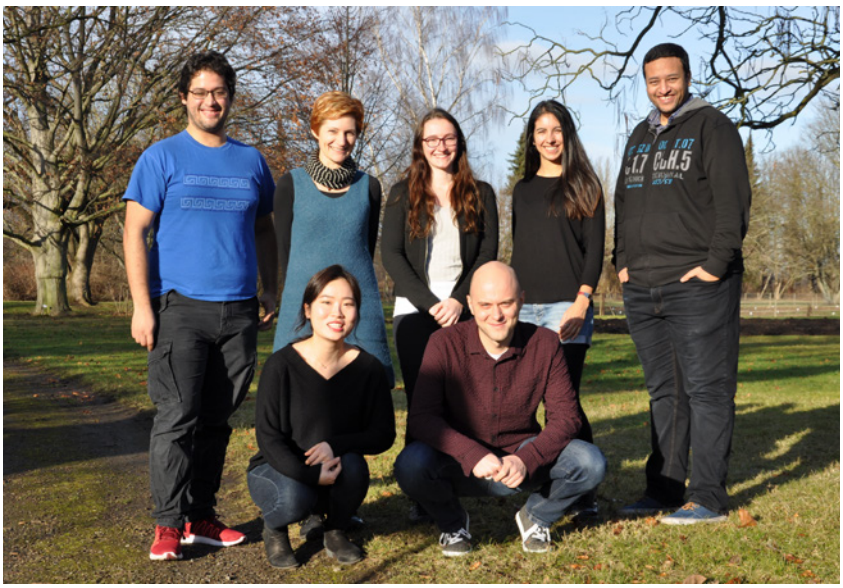
Successful *in planta* delivery of compounds during barley meiosis.

Flow-cytometric isolation of meiotic cells.

ITN MEICOM granted by EU

Funding

BMBF, BAYER



The research group primarily funded by the *Federal Ministry of Education and Research* (BMBF) is interested in the process of plant meiosis that generates genetic variation through homologous recombination. We aim to better understand the underlying mechanisms of meiotic recombination control and chromosome axis remodelling as well as to translate acquired knowledge particularly from *Arabidopsis thaliana* into barley (*Hordeum vulgare*) in order to modify the frequency and distribution of meiotic recombination events.

Research Statement and Major Achievements

Particularly in cereal crops such as barley (*Hordeum vulgare*) meiotic recombination events are limited both in terms of their total number and in their distribution to distal chromosome regions (CO heterogeneity) and this represents major challenges for plant breeding. By utilizing molecular genetics, proteomic and cytogenetic approaches the BMBF-funded and in October 2016 established independent RG *Meiosis* (ME) aims to better understand the underlying mechanisms of meiotic recombination control and programmed meiotic chromosome axis remodelling using *Hordeum vulgare* and *Arabidopsis thaliana*. Ultimately, we aim to translate acquired knowledge particularly from *Arabidopsis thaliana* into barley in order to manipulate the frequency and distribution of meiotic recombination events.

To achieve these objectives various approaches including genome editing, proteomics, flow-cytometry and various imaging approaches are employed. In the first project we aim to better understand the phenomena of CO heterogeneity found in barley by using barley and Arabidopsis as comparative models (different genome size and structure). To do so, cytological methods for different barley genotypes have been established. The second project aims to identify whether genes identified in Arabidopsis that limit the number of recombination events also limit their number in barley. The third project aims to explore whether artificially induced DNA double strand breaks being either randomly genome-wide or site-specifically induced trigger meiotic recombination. Furthermore, a method to apply compounds *in planta* during barley meiosis

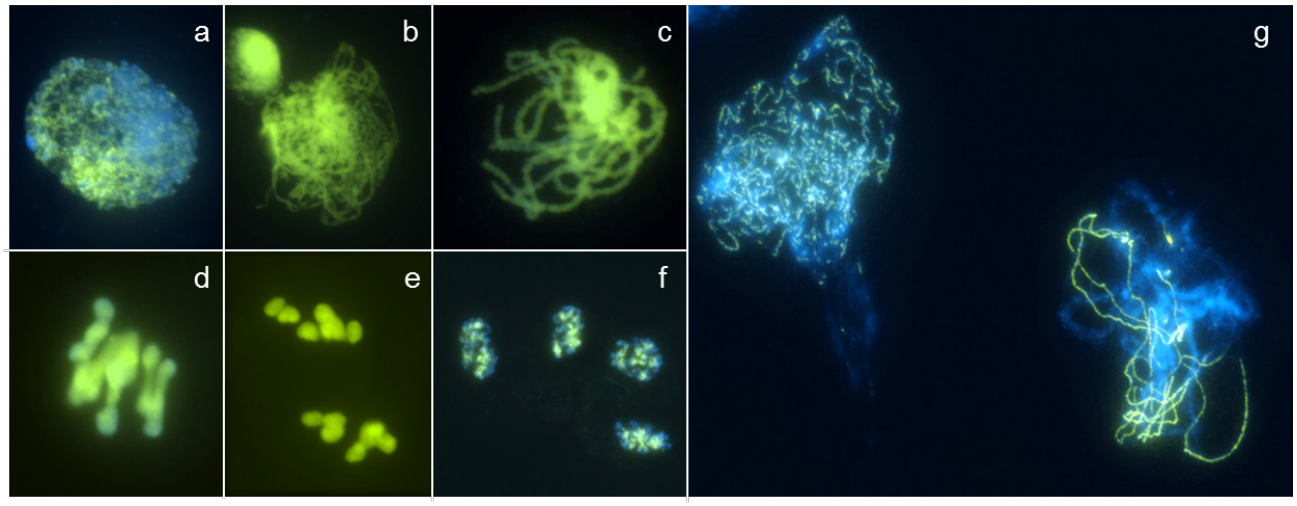


Fig. 54 (a-f) Chromosome spreads of different meiotic stages from barley plants treated with EdU (incorporated into newly-replicated DNA) shows successful uptake of the compound in meiotic cells; DNA in blue and EdU in yellow. (g) Isolated meiotic cells (left: early pachytene, right: mid pachytene) from reproductive *Arabidopsis thaliana* tissue by flow-cytometry showing ASY1 (meiotic chromosome axis component) labelling in yellow and DNA in blue.

has been established to screen by cytological and molecular means the effect of compounds impacting epigenetic marks or post-translational protein modifications on the meiotic recombination landscape in barley (Fig. 54 a-f). Additionally, we were able to isolate meiotic cells from reproductive plant tissue by flow-cytometry (Fig. 54 g) and this will allow biochemical and immunological studies on isolated meiotic cells.

Embedding in Departmental and IPK Research Strategy

Plant breeding, which harnesses the natural genetic variation that arises during meiosis, will have a key role for Food Security in the future by improving crop varieties. We are closely-linked to the research efforts and aims of the department *Breeding Research* specifically in the area of applied chromosome biology by studying plant meiotic chromosome behavior and meiotic recombination assuring genetic diversity. We contribute with our research on meiosis to the IPK research theme 3 *Mechanisms of Plant Reproduction* by studying meiotic chromosome biology and homologous recombination during meiosis.

Plans, Opportunities and Challenges

One of our goals is to visualize meiosis live since so far observations of plant meiosis are primarily limited to the microscopic analysis of fixed meiotic cells. Live-cell imaging of meiosis has great potential to improve our understanding of the spatiotemporal events taking place during meiosis. To do so, plants expressing fluorescent protein fused to meiotic candidates were generated and their analysis will profit from the availability of the requested fluorescent light-sheet microscope at the IPK allowing time-lapse microscopy of living plant material.

Another important achievement has been the flow-cytometric isolation of meiotic cells from Arabidopsis (Fig. 54 g). We will now refine this procedure, try to extend it to barley and develop protocols for subsequent immunological analysis by high-resolution imaging or for biochemistry approaches.

We have been also successful in the establishment of a reliable method to deliver compounds into living barley plants during meiosis (Fig. 54 a-f). We are now ready to test the effect of different *epi-drugs* on the frequency and distribution of recombination events in barley.

Bioinformatics at the IPK

Coordinator Systems Analysis and Modelling: Dr. Andrea Bräutigam (until 30.09.2017)
Coordinator Biodiversity Informatics: Dr. Uwe Scholz

Fig. 55 Bioinformatic Centre

Bioinformatics activities are distributed among seven research groups over all departments and within an independent research group and the groups collectively address research topics spanning efficient data management, data publication, genomics, phenomics and integrative analyses for systems biology.

Life sciences continue to integrate bioinformatics and experimental biology and thus the demand for bioinformatics services and collaborations keeps increasing. The IPK addresses this demand by embedding dedicated groups with bioinformatics expertise within the departments and ensures harmonized, coherent efforts and timely solutions through coordination.

To fulfil the bioinformatics needs of the experimental research groups at the IPK the bioinformatics activities are divided into two coordination subject areas. Dr. Andrea Bräutigam coordinates the section *Systems Analysis and Modelling* which includes the RG *Network Analysis and Modelling*, *Image Analysis* and Dr. Anja Hartmann as Bioinformatician in the Department of *Physiology and Cell Biology*. Dr. Uwe Scholz coordinates the section *Biodiversity Informatics* which includes the RG *Genebank Documentation*, *Bioinformatics and Information Technology*, *Domestication Genomics* and the bioinformatics activities within the RG *Quantitative Genetics*. Both coordinators tightly interact to address the overlapping topics.

The IPK has continued the restructuring of the bioinformatics groups. Dr. Andrea Bräutigam joined the IPK in January 2016 to fill the position vacated by Prof. Dr. Falk Schreiber and focuses on transcriptome analyses, model development and system biology approaches. Dr. Evgeny Gladilin moved from Heidelberg University to Gatersleben and currently develops advanced algorithms and an integrative software environment for quantitative analysis of high-throughput image data from multi-modal plant imaging and phenotyping platforms.

The IPK is excellently integrated in German and European bioinformatics initiatives. The *German Network for Bioinformatics Infrastructure* (de.NBI), a project financed

by German *BMBF*, unites over 30 German research institutions. From the networks inception in 2015, IPK has been successfully coordinating the service unit focused on plant bioinformatics called *GCBN* – German Crop BioGreenformatics Network. With this leading role in *GCBN* and in *de.NBI* we are also contributing to the European *ELIXIR* initiative. *ELIXIR* is the distributed infrastructure for life-science information and unites over 20 European countries. Last but not least we are actively collaborating within the *DivSeek* initiative. With this participation, we are contributing to a community driven effort that aims to use digital data to unlock the potential of crop diversity stored around the globe.

The IPK continues to develop resources for the internal and external research community. The experimental focus on phenomics is underpinned by theoretical support. The IPK has spearheaded the development of the phenomics standards *MIAPPE* (Minimal Information About a Plant Phenotyping Experiment). It also provides an infrastructure for data publication in a digital resource center called *PGP* (Plant Genomics and Phenomics Research Data Repository) which is based on the e!DAL-software. Data sets are published with *DOI* (Digital Object Identifier) and fulfil the FAIR principles (Findable – Accessible – Interoperable – Reusable).

In 2016 and 2017 the coordinators have set up an internal course program to support the education of graduate students and postdoctoral fellows in bioinformatics and data analysis: courses in basic and advanced R programming (introduction, statistics, and population genetics) and courses in efficient use of functions in Excel form the basis of education while advanced topics such as bioinformatics for biologists (within the framework of *PLANT 2030*) and big data analysis (within the framework of *de.NBI*) allow deeper insights and more specific hands-on learning geared towards biologists with none to limited prior bioinformatics expertise. By linking teaching efforts with major German and international research initiatives such as *PLANT 2030* and *de.NBI*, outreach beyond the IPK towards the national and international research communities is enabled. The international visibility of these teaching activities is demonstrated by the reuse of the published training material under the DOIs 10.5447/IPK/2016/59 and 10.5447/IPK/2017/17.

The bioinformatics groups look back on many scientific achievements within the reporting period, in particular its continued stewardship for *Triticeae* genomes. With the publication of a high quality barley genome sequence in 2017 that builds upon the earlier work of an initial assembly from 2012 IPK has extended its barley genomics resources including publicly available access tools. The barley genome has been joined by additional *Triticeae* genomes of rye and wild emmer which are both already published. Finally, IPK is a major stakeholder in the preparation and polishing of a new wheat genome sequence version which has been already made publicly available and awaits publication.

These bioinformatics activities are manifestations of IPK's evolution into a digital resource center for plant genomics and phenomics. A substantial example is the *EURISCO* database hosted and maintained mainly by IPK personnel and infrastructure. *EURISCO* is the European Search Catalogue for Plant Genetic Resources and provides information about 1.9 million accessions of crop plants and their wild relatives, preserved *ex situ* by almost 400 European institutes.

More detailed information on the scientific progress and coordination efforts can be found in the reports of the individual research groups.

PostDoc Board

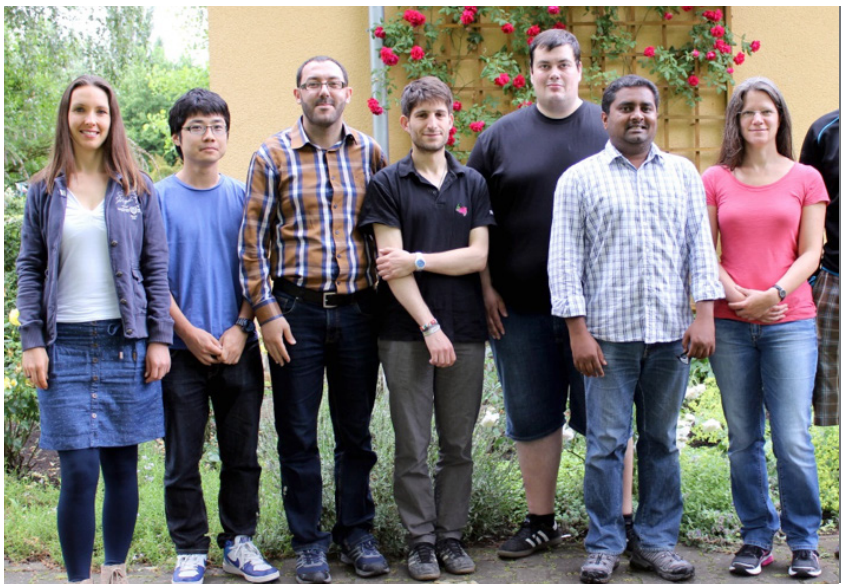


Fig. 56 IPK PostDoc Board in 2016 (from left to right: Dr. Anja Hartmann, Dr. Takayoshi Ishii, Dr. Ahmad M. Alqudah, Dr. Jonathan Brassac, Dr. Matthias Jost (Vize), Dr. Jeyaraman Rajaraman, Dr. Daniela Nowara (chair))

The main objectives of the *PostDoc Board* are the representation of the IPK PostDoc community and communication of their needs and wishes to the *Board of Directors*. Furthermore, we provide information to PostDocs for their individual career planning and help them to gain valuable skills through scientific and non-scientific courses or mini-symposia. To stay up-to-date with the needs and wishes of the PostDocs, we meet with them twice per year.

In June 2016 the *PostDoc Board* organized a PostDoc Retreat with the topic *Career planning in science and alternative career paths*. Six speakers talked about career perspectives for young scientists at IPK, their experience as professors at German universities, career possibilities in the private sector and as a teacher.

In November 2016, the *PostDoc Board* hosted a mini-symposium with representatives from *Kooperationsstelle EU der Wissenschaftsorganisationen* (KoWi), *Japan Society for the Promotion of Science* (JSPS), and *Volkswagen foundation* who gave an overview about their respective programs and useful advices for writing a proposal. Dr. Patrick Bienert gave tips for applying for an Emmy Noether fellowship.

To help the PostDocs gaining valuable skills, the *PostDoc Board* organized two courses in the reporting period. The first was a three-day course about university didactics, and the second course was a two-day course about proposal writing.

Members of the *PostDoc Board* represented IPK in 2016 and 2017 at different external events: *sciencemeetscompanies* in Halle, *Wirtschaftsforum Harz* in Wernigerode, and *Leibniz-Kolleg* in Berlin (2016) and in Brandenburg (2017). In both years, we provided an informative quiz about crop plants for the visitors of IPK's Day of the Open Door.

In the beginning of September 2017 the *PostDoc Board* organized its third Summer School. 15 PhD students from all over Europe visited the institute in frame of the IPK *Summer School of Modern Crop Design* for a week. During this week they were taught by IPK Postdocs about the use of old varieties and modern tools to develop advanced breeding material, phenomics, sequencing techniques, the basics of QTL analysis, cytogenetics and phylogenetic analysis. Five renowned guest speakers reported about their latest research and discussed lively with the students during lunch. In the afternoon the students went to the labs to apply their newly obtained knowledge.

End of September 2017 a large party for all IPK employees was carried out. The party was initiated and planned by the *PostDoc Board* chair Dr. Daniela Nowara and organized with the help of several IPK employees. Everyone enjoyed a nice afternoon with good food and some sportive activities

Mid October the *PostDoc Board* got a new chair: Dr. Matthew Haas.

New Elements in the PhD Graduate Program and improvements in the PhD Student Board

Fig. 57 Student Board members in 2017 (from left to right: Christian Hertig, Krishna Mohan Pathi, Alevtina Ruban, Vanessa Paffrath, Daniela Impe, Robert Hoffie, Zahra Nemati, Mona Schreiber, Kamatchi Ulagappan, Steven Dreissig, Stefan Hiekel)

The IPK *Graduate Program* is the fundamental basis for PhD students at IPK for a target-oriented, quick and structural progression of their doctoral study. Basic program points include the maintenance of a study record book, the participation in the PhD seminar and soft and hard skill courses. To maintain a high standard of the doctoral study, in collaboration with the IPK directorate, the *PhD Student Board* (PSB) works on the constant improvement of the program.

Changes in the personnel and organization of the *PSB* took place this year. The chair was taken over in January 2017 by Daniela Impe and many members joined to work together. To ensure an efficient and fast communication among the board members and between the *PSB* and the institute, the email account of the *PSB* has been revived and is extensively in use. Furthermore, the webpage of the *PSB* was completely redesigned. Now the tasks of the *PSB* are described and board members are listed with their responsibility and contact information. Additionally, the *Help Desk* and a *Newcomer´s guide* were introduced as new instruments to help students to be settled quickly. Actual information can be checked at the corner *Latest News*. Furthermore, a new poster was designed, which gives more information about the *PhD Student Board*.

One of the achievements of the *PSB* was the improvement of the PhD seminar. The *PSB* prepared new evaluation sheets with an easy pointing system that enables the audience to have a quick and efficient evaluation of the speakers. Additionally, the procedure of the seminar and the regulations for speakers have been clearly described.

Further improvement comprises the restructuring of the lecture series, which were part of the IPK Graduate Program. The lectures rarely took place in the past and are now replaced by consolidated series of talks from each department termed as *Departmental Day*. In this event, the group leaders or a representative of all working groups from one department will present their actual research. In this way, the PhD Students and other interested people have a great opportunity to get a comprehensive overview about the actual research of one department. The event is organized by the *PSB*. The first *Departmental Day* took place in November 2017 and the result has been a great success.

In addition, the *PSB* also organizes the annual *Beagle Award* for PhD Students. This Award is dedicated to support young scientists who are at the beginning of their career. A jury assigned by the *PSB* and representative board members judge the scientific work and the social commitment of the applicants. The awarding ceremony is organized by the *PSB* as well. The ceremony took place during the *Institute´s Days* in October 2017 and the award has now been presented for the seventh time. The price was bestowed for Sebastian Beier due to his noteworthy achievements throughout his doctoral study at IPK.

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	Genebank Documentation (DOK), Dr. Helmut Knüpffer
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Genome Analysis, Dr. Patrick Schweizer	Pathogen Stress Genomics (PSG), Dr. Patrick Schweizer
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Dept. Molecular Genetics
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Research Groups
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Seed Development (SE), Dr. Bruno Müller
Gene Regulation (GR), Prof. Dr. Thomas Altmann (temp.)
Phytoantibodies (PAK), Prof. Dr. Udo Conrad
Assimilate Allocation and NMR (AAN), Dr. Ljudmilla Borisjuk
Image Analysis (BA), Dr. Evgeny Gladilin
Network Analysis and Modelling (NAM), Prof. Dr. Thomas Altmann (temp.)

Dept. Physiology and Cell Biology
Prof. Dr. Nicolaus von Wirén

Research Groups
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Applied Biochemistry (ABC), Dr. Hans-Peter Mock
Structural Cell Biology (SZB), Dr. Michael Melzer
Plant Reproductive Biology (PRB), Dr. Jochen Kumlehn
Yeast Genetics (HEG), Dr. Martin Giersberg (temp.)

Independent Research Groups

Research Groups
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Domestication Genomics (DG), (junior research group), Dr. Martin Mascher
Metalloid Transport (MT), (Emmy Noether group, DFG), Dr. Gerd Patrick Bienert
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Coordination System Analysis and Modelling: N. N.

[1)] Management

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