LEIBNIZ-INSTITUT FÜR
PFLANZENGENETIK UND
KULTURPFLANZENFORSCHUNG

IPK
LEIBNIZ-INSTITUT

RESEARCH REPORT

2020/2021

IMPRESSUM

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Leibniz
Association

CONTENT

INDEPENDENT RESEARCH GROUPS

SATELLITE
COLLECTIONS
NORTH

MAIN LOCATION

The **Leibniz Institute of Plant Genetics and Crop Plant Research** (IPK) is a member of the Leibniz Association. It is organised as a non-profit foundation under public law. According to its statutes, the Institute conducts basic and application-oriented research on crop plants. The Institute resides at three locations, the headquarter in Saxony-Anhalt and two branch stations in Mecklenburg-Western Pommerania.

»The global competition for ideas remains our driving force«

Foreword by Prof. Dr. Andreas Graner

The Leibniz Institute of Plant Genetics and Crop Plant Research stands for scientific excellence to investigate the genetic, biochemical and physiological principles underlying the evolution of crop plant diversity and spark innovations to improve crop plant performance in a changing environment.

To leverage the potential of the multidisciplinary research the institute operates two large and unique research infrastructures, the Federal *Ex situ* Gene Bank for agricultural and horticultural crop plants and a phenotyping platform for non-invasive imaging of plants which is epitomised by the Plant Cultivation Hall, termed PhenoSphere. Scientists from more than 30 countries bring in new ideas and help strengthen our global research network with public and private partner institutions. At the national level, the institute closely interacts via joint appointments with the neighbouring universities at Halle and Göttingen.

In this research report, we look back at two challenging years. On the one hand, these were coined by the Corona Pandemic, severely curbing science communication, including the organisation of conferences and workshops, open house days and academic teaching. On the other hand, the digitalisation of workflows was further advanced, and novel ways of online communication were established that helped to handle lockdown situations. Despite the vagaries of the pandemic, and based on the enthusiasm and commitment of the staff, the scientific programme yielded remarkable highlights and trendsetting developments.

Being a leading centre for fundamental and applied crop plant research, the activities summarised in the present report were published in more than 350 reviewed publications. Similarly, extramural funding exceeded 10 million Euro per year including an European Research Council (ERC) consolidator grant and two ERC starting grants. To acknowledge their outstanding work, scientists received prestigious awards, were elected as members of academies and received professorships at universities. In addition to the departmental groups, independent research groups represent a platform for young scientists to explore novel research themes and gain international visibility. In a similar vein, two young investigator groups were established to help promote early-career scientists on their way to independence.

In 2022 we celebrate the 200th anniversary of Johan Gregor Mendel. His meticulous studies resulting in the description of the rules of inheritance published in 1865 have laid the foundation of genetics as a scientific discipline. His work has inspired researchers across the globe and blazed the trail for innovations in crop plant research that have been and will be instrumental for food security and environmental safety. The people at IPK are proud to contribute to these efforts by converging scientific excellence with societal relevance.

We thank you for your interest
and hope you will enjoy reading

Andreas Graner

FACTS & FIGURES 2020/2021

467 Employees

Nations **35**

30 Research Groups

2020 **190**
2021 **189**
Publications **379**

235
2021 **159**
2020 **76**
Lectures

Bachelor **18**
Master **21**
Dissertations **15**
Graduations **54**

PHENOSPHERE

110 Growth Containers

360 Rhizo Boxes

FEDERAL *EX SITU* GENE BANK

Accessions **151348**

Genera **758**

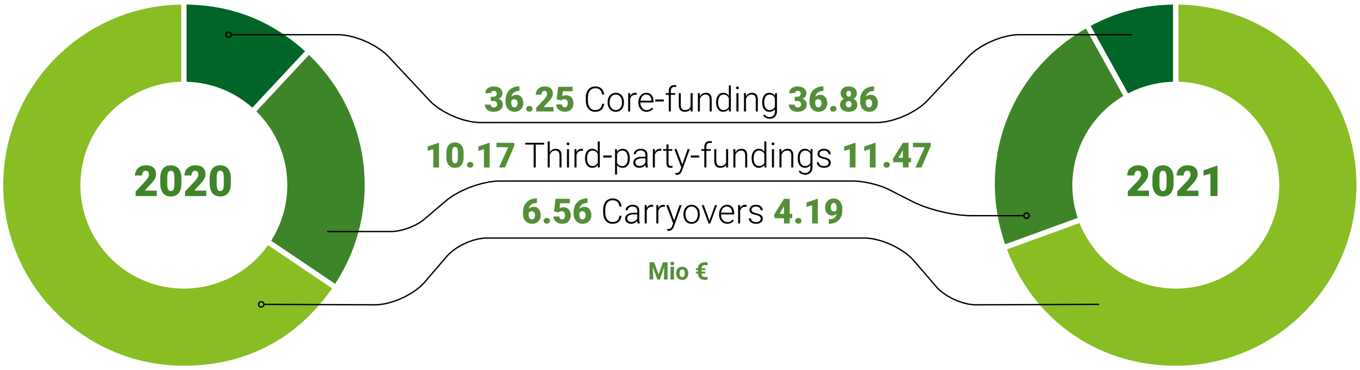
Species **2912**

Greenhouse Area **7100** sqm

75 ha Field Trials Area

Phyto Chamber **220** sqm

FUNDING



Total funding 52.98 Mio €

Total funding 52.52 Mio €

THIRD PARTY FUNDING

2020		2021
Industry		**Industry**
1.61	Private sector	1.53
Public		**Public**
2.05	EU	1.39
3.0	BMBF	3.87
0.99	BMEL	1.49
0.22	BMWi	0.17
1.76	DFG	1.70
0.12	Leibniz	0.25
0.02	LSA	0.86
0.40	Others	0.21
10.17 Mio €	total	11.47 Mio €

THE INSTITUTE IN 2020 AND 2021

IPK is a place where scientific continuity remains intertwined with innovative approaches, concepts and technologies. By its research the Institute is committed to converge scientific excellence with relevance for society and mankind. Against this backdrop, the research programme of the Institute is rooted in the four scientific departments, which provide the disciplinary expertise to cover five thematic areas of fundamental and applied plant research. Beside the departmental research, independent research groups represent launching pads for young scientists to explore novel topics and to advance their professional career. To support early career development at the postdoctoral stage, two "Young Investigator" groups were initiated in 2021. The aim of these groups is to give young researchers an opportunity to gain independence upon obtaining their own funding to establishing their own research programme.

Over the past years, the world has become aware that innovations along with transformative changes are needed to successfully face the global challenges that directly or indirectly bear on food security and the environment. Also, the Corona pandemic reminded us of the devastating consequences of infectious diseases that had almost fallen into oblivion during the past century.

Despite restrictions and public lock downs the Institute managed to continue its ambitious research programme during the time of this particular challenge. Delays in the execution of third-party funded projects could be compensated in some cases by the provision of additional resources from funding agencies. Up to 40 percent of the staff moved to home office and personal communication was replaced by video conferences. At the same time, conferences, workshops, lectures and also team meetings and discussions became multimedia and purely electronic. Scientific exchange was kept alive but dramatically changed. Notwithstanding these obstacles, the Institute looks back at two years of exiting research. In the following, an overview is presented on key developments, which are described in more detail in the reports of the departments and research groups.

ORGANISATIONAL AND STRUCTURAL DEVELOPMENTS

Staff development

Compared to the reporting period 2018/2019, there is a slight reduction, by about three percent in the number of staff from 482 to 467 employees.

Research groups

Excellence in research is contingent on the dynamic adaptation of the research infrastructure resulting in the opening of new groups to explore novel fields or to continue working along established lines. As summarised below, several new research groups have been established and existing groups have been thematically refocused by new appointments or were discontinued.

Department Genebank

As of January 1, 2020, Stephan Weise took over the leadership of the research group "Genebank documentation", which after the retirement of its former head, Helmut Knüpffer was provisionally headed by Markus Oppermann since 2018. As of December 31, 2020, the research group "Genome Diversity" was closed. As of January 1, 2021, the independent research group "Domestication Genomics" headed by Martin Mascher was integrated into the Department, where it now strengthens the research programme "Taxonomy and Evolution".

Department Breeding Research

In 2020, the research group "Kinetochore Biology" was established. The group, led by Inna Lermontova, spun off the research group "Chromosome Structure and Function", where it initially formed a project group. As of March 31, 2021, the "Gene and Genome Mapping" group was discontinued upon retirement of the group leader, Marion Röder. As of October 1, 2020, the research group “Biotrophy and Immunity” was continued under provisional leadership of Dimitar Douchkov, after Armin Djamei had moved to the University of Bonn.

Department Molecular Genetics

The head of the research group "Acclimation Dynamics and Phenotyping", Astrid Junker, left the IPK on December 31, 2020, to take up an appointment in the private sector. Kerstin Neumann from the former research group "Genome Diversity" was appointed to continue the group, now "Automated Plant Phenotyping" with readjusted focus. The Young Investigator group "Integrated Mechanistic Models" under the leadership of Mary-Ann Blätke was opened on January 1, 2021 to strengthen the departmental research programme "Seed Biology".

Department Plant Physiology and Cell Biology

As of December 31, 2020, the research group "Yeast Genetics" was closed. A Young Investigator group "Sustaina-

Impressions of the seed storage facility at the Federal Ex situ Gene Bank in Gatersleben. Cereal seeds are stored for the long-term at minus 18 degrees Celsius.

ble Nutrient Management" headed by Diana Heuermann started on April 1, 2021. Her research provides input in the departmental research programme "Physiology and Biochemistry". In addition, Jiajing Zhu, who has worked for several years at the Carnegie Institution for Science, Department of Plant Biology, at Stanford, will conduct research at IPK for an initial two years, starting on March 1, 2021. Her work is supported by funds from the FEM-Power project.

Independent Research groups

The Emmy Noether group “Metalloid Transport” was closed by September 30, 2020 when Patrick Bienert took up an appointment by the Technical University of Munich.

Department Administration and Central Services

After the former Administrative Director had left the Institute by the end of June 2021 administrative responsibilities were taken over on a provisional basis by the Managing Director. On July 1, 2021, Britt Leps was appointed provisional head of the group “Technology Transfer and Legal Matters”.

APPOINTMENTS

In the reporting period, two scientists left the Institute to continue their academic careers as professors. In 2020, Armin Djamei (head of “Biotrophy and Immunity”) and Patrick Bienert (head of “Metalloid Transport”) were appointed as professors (W3) at the University of Bonn and the Technical University of Munich.

Training and young scientists

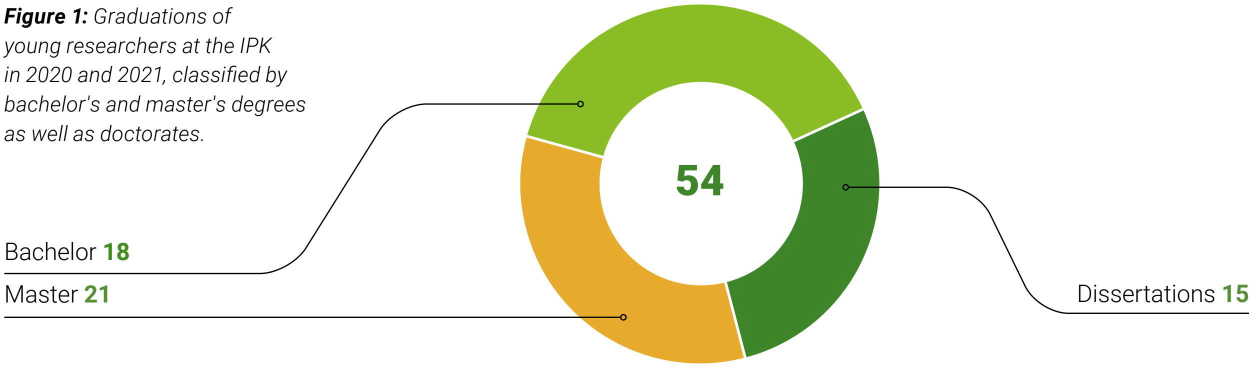
In the years 2020 and 2021, a total of 54 final theses were prepared at the Institute. A classification according to Bachelor's, Master's and PhD degrees can be found in Figure 1.

In addition to the teaching activities of our scientists at various universities, the supervision of these Bachelor's, Master's and PhD students is of great importance. All PhD students are enrolled in a structured doctoral programme at IPK, which was developed in cooperation with the Leibniz ScienceCampus Halle and is regularly updated. The curriculum comprises seminars, courses and internships, and serves to expand theoretical and technical know-how. A further focus is the acquisition of so called "soft skills".

A PhD Student Board represents the interests of this group of young scientists and organises the Plant Science Student Conference, in close collaboration with PhD students from the Leibniz Institute of Plant Biochemistry (IPB) in Halle.

IPK also supports the professional development of young postdoctoral fellows. The PostDoc Board provides guidance for creating a professional identity. Thanks to the provision of a self-administered budget, various training opportunities and seminars are offered to help support career building. Every other year, the PostDoc Board organises a summer school. The PhD and PostDoc Board meet with the Board of Directors at least once a year to discuss

Figure 1: *Graduations of young researchers at the IPK in 2020 and 2021, classified by bachelor's and master's degrees as well as doctorates.*



the status quo and to further develop their programmes.

For IPK, the promotion of young talents also involves a parallel commitment to vocational training and further education. In the area of vocational training in various professions the Institute employed in 2020 and 2021 17 and 13 apprentices, respectively. In addition, seven dual BSc students in "Biotechnology" enrolled at Anhalt University of Applied Sciences, Köthen and two students enrolled in “Computer Science” at Otto-von-Guericke University, Magdeburg conducted their dual study programme at the Institute.

PRIZES AND AWARDS

In the reporting period, researchers of the IPK were honoured for their scientific work. Andreas Graner was admitted to the Indian National Science Academy in January 2020.

In January 2020 Martin Mascher received the Günter and Anna Wricke Prize for his work on improved sequencing of cereal genomes. In spring 2021, Nils Stein has been awarded the medal of the Royal Physiographic Society and the Mendelian Society in Lund (Sweden) for his contributions in the field of cereal genomics. Nicolaus von Wirén was appointed as a member of the National Academy of Science Leopoldina in July 2021. The Young Scientist Award 2021 of the Society of Experimental Biology in London was awarded to Amanda Camara for her contribution "How to walk the line? – Simulating a condensation pathway for holocentric chromosomes".

The society of the friends and supporters of IPK awards every year in an alternating scheme the Gatersleben research price for an outstanding PhD thesis and the Mansfeld price for an outstanding Master thesis. Nominations are invited from universities in German speaking countries. In 2020 the Gatersleben research award was bestowed on Alevtina Ruban (Martin Luther University of Halle) for her thesis on “Analysis of the B chromosomes undergoing root-specific elimination during the embryogenesis of Aegilops speltoides”. In 2021, the Mansfeld award was bestowed on Lydia Kienbaum (University of Hohenheim) for her thesis on “Comparison of deep learning and traditional

Snapshot of the 2021 Plant Science Student Conference organised by PhD students. Virtual meeting spaces and self-selected avatars enabled direct interaction between participants in a game-like manner and stimulated discussions during the poster presentation.

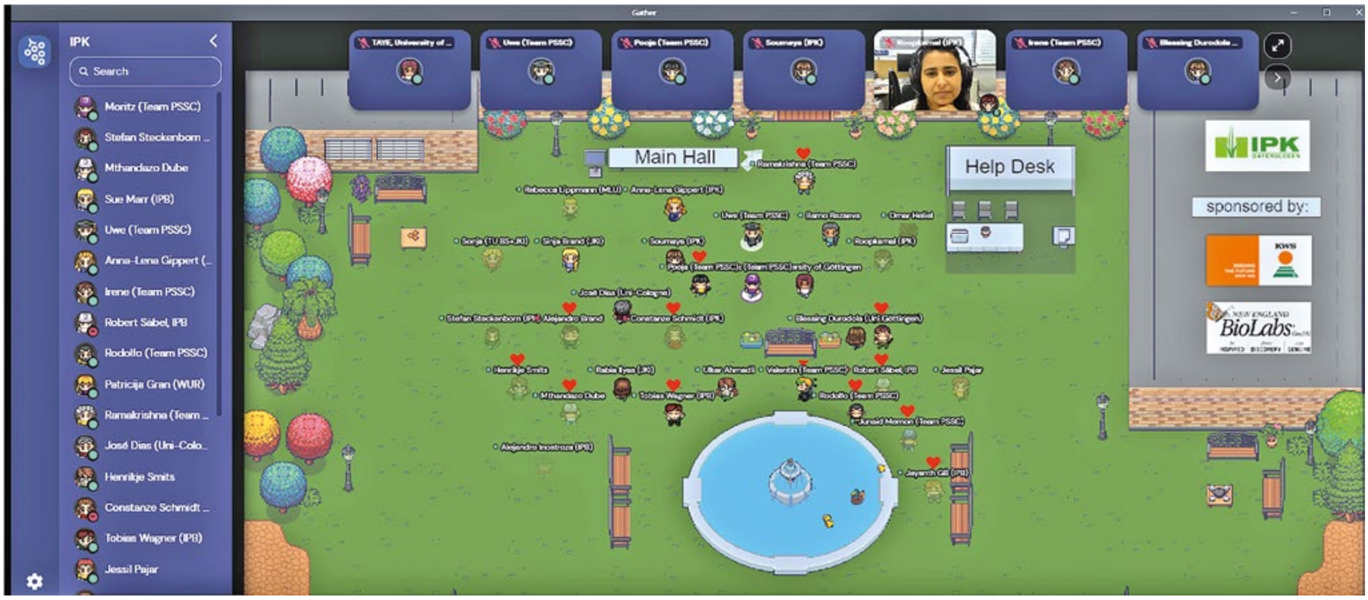


image analysis approaches in the example of maize cob detection and parameter extraction". Finally, the Beagle Award was bestowed by the IPK PhD Student Board on Dominic Knoch (2020) and Mohan Pathi (2021) for their scientific achievements and their manifold social activities during their time as PhD students at the Institute.

GENDER EQUALITY

IPK is committed to implement measures to improve gender equity and gender balance in science. The Institute strives to leverage the potential of female scientists, which has gone unheeded over the past decades. Ranking among the first institutions to receive a "berufundfamilie" (profession and family) certificate IPK aims at providing a professional environment which provides a nursing ground for excellent science and at the same time is supportive of the needs of (mostly) young families.

Because of the underrepresentation of female applicants for group leader positions, the Institute places major emphasis on the attraction of female scientists in the recruiting phase.

The overriding goal of gender equality work is to eliminate the underrepresentation of female scientists in leadership positions. To this end, a major focus was placed on personnel recruitment and career development. Based on funding from the ESF and the EU (FEM POWER program) a new recruitment format was implemented to attract applications from female scientists and provide support for the establishment of a research group. The recruitment package includes a two-year employment along with resources to run a research lab and mentoring by an experienced IPK scientist to provide a starting pad for the acquisition of third-party funding. In March 2021, the first female scientist recruited under the new format started her work at IPK.

CAREER DEVELOPMENT

In the area of career development, a new structure was introduced in 2021 with the establishment of so-called Young Investigator groups, which serve to support young scientists in the post-doc phase. The aim of the new funding format is to increase the scientific visibility and independence of talented scientists. The intermediate step of a Young Investigator Group, which lasts a maximum of four years, is intended to enable the development and management of a research group. Young Investigator groups are based on extramural funding acquired by the group leader and organisationally assigned to a host department, which also provides additional support and resources. The first two groups were established in 2021.

RESEARCH INFRASTRUCTURES

The Institute operates two major research infrastructures which provide materials and scientific services. These are essential components for the implementation of the research agenda. Moreover, they provide biological resources and access to experimental facilities for external uses at the national and international level.

Conservation of potato accessions at the Groß Lüsewitz Branch of the Gene Bank as in vitro cultures.

Impression of the IPK PhenoSphere Container Compartment.

Federal *Ex situ* Gene Bank

The Federal *Ex situ* Gene Bank houses seeds, tubers and plants amounting to ca 150,000 accessions covering about 3,000 botanical species. Ranking among the largest *Ex situ* facilities in the world, more than 10,000 samples are distributed to users across the globe annually. To advance the utilisation of genetic resources for research and breeding the services offered by the Gene Bank are upgraded by providing digitised information including passport data, consolidated phenotypic information, and molecular data. In this way the Federal *Ex situ* Gene Bank is being advanced into a bio digital Resource Centre, which will successively increase its value as a research infrastructure. To facilitate a genotype to phenotype mapping, the accession-based wheat and barley collections were extended by the generation of “precision collections” that are represented by "immortal" homozygous genotypes which in turn are being genotyped. The genetic characterisation of collections is complemented at the phenotypic level by the curation and evaluation of legacy data as well as the generation of new information on agronomically relevant traits. A further pillar of the bio digital Resource Centre is represented by the advancement of the IPK data warehouse and the web portals to facilitate speedy and informed access to information related to Plant Genetic Resources and to provide interfaces for data exchange with other related systems.

Phenotyping

The Institute houses an abundance of facilities for growing plants, amounting to 255 m² of controlled environment chamber space, about 6,800 m² of greenhouse space and 80 ha of experimental field space. Phenotyping platforms, installed in two greenhouses and one controlled environment chamber have enabled an almost complete automation of the acquisition of whole plant phenotypic data

The worldwide unique “IPK PhenoSphere” research facility allows for a highly automatised and non-destructive phenotyping of plants under strictly controlled environmental conditions. It comprises a Rhizotron System for the analysis of root growth and a Container System for the analysis of the above-ground plant development. The Rhizotron System with a capacity of 360 large Rhizotrones, each with a size of 60 x 90 x 5 cm includes a high-resolution monochrome camera to capture root growth while in parallel top and side view RGB cameras are recording shoot development. The container system is equipped with an automatically positionable multi-sensor camera system ("PhenoCrane") to record a wide range of above-ground characteristics. It allows phenotyping under field like scenarios with wide ranges in air temperature, humidity and illumination settings mimicking the sunlight spectrum and intensity including fast changes and diurnal courses. Further, carbon dioxide concentration can be adjusted. The large volume containers (max. 110 containers with 1 cubic meters of soil volume each) allow to grow plant stands and to control watering and soil temperature. The PhenoCrane multisensor platform which has been completed in September 2021 is equipped with an RGB camera, a FluorCam 3D laser scanner and hyperspectral camera (VNIR 350 900 nm). In 2021, the facility became fully functional and experimental operation has commenced. As a substantial extension of the existing NMR facility the mounting of a super-wide-bore NMR instrument (Bruker AVANCE Neo 500 MHz NMR) for non-invasive analysis and visualisation of organs, structures and constituents in whole plants approaches is nearing completion.

Microscopy, Analytics and DNA-Sequencing

The visualisation of cell and tissue ultrastructure is enabled by a combination of latest state of art laser scanning microscopy, super high resolution light microscopy and electron microscopy. Similarly, state-of-the-art chromatography and mass spectroscopy are available for the structural and functional analysis of nutrients and metabolites, as well as for the identification of proteins and peptides. For the quantitative analysis of mineral elements and isotopes new ICP-MS and IR-MS equipment was installed, respectively.

The nucleotide sequencing capacity of the Institute has been further expanded by upgrading the PAC-BIO single molecule sequencing equipment to accelerate data processing.

Information Technology and Digitalisation

Modern Life Sciences require the generation and analysis of large data sets from “omics” experiments, including numerous environmental parameters. Imaging technology is also becoming a significant driver of the growing level of digitisation of biological data. Over the reporting period, IPK’s data storage and computing power has been continuously ramped up. Currently, it amounts to 850 terabytes of data online and 1.5 petabytes in archived format. The computer infrastructure comprises high-performance compute server (in total 444 CPU cores, 11.5 terabyte RAM) and one “simple linux utility resource management cluster (Slurm cluster with 14 CPU compute nodes and 436 cores, 9.5 terabyte RAM as well as 1 GPU compute node with 48 cores, 1 terabyte RAM and 6 GPUs). In order to both ensure that the data are available and freely accessible in a permanent and structured way to allow biological questions to be addressed, the Institute has been actively participating in initiatives such as "de.NBI" (German Network for Bioinformatics Infrastructure), "ELIXIR" (European Infrastructure Network for the Life Sciences), DataCite and the National Research Data Infrastructure (NFDI) initiative; the latter seeks to ensure that scientific data remain FAIR – findable, accessible, interoperable and reusable. In this context, every accession in the Gene Bank has received a unique digital identifier. In addition to the Gene Bank’s information system, IPK also hosts a large number of other databases (including the barley genome explorer BARLEX, the BRIDGE portal for barley genomics and the WiLDSI portal to explore the use of digital sequence information).

Optimisation of campus grid

By the end of 2021 the optimisation of the infrastructure for energetic provision on the Gatersleben campus, which was initiated in 2015 has been completed. The construction measure included a comprehensive refurbishment, expansion and optimisation of the energy systems on the IPK campus in Gatersleben. In particular, the electro technical systems, the building automation and the heating and cooling systems were part of the energy optimisation. As a result, the security of energy supplies and the resilience of the campus grid were enhanced and adapted to the increased demand of electricity.

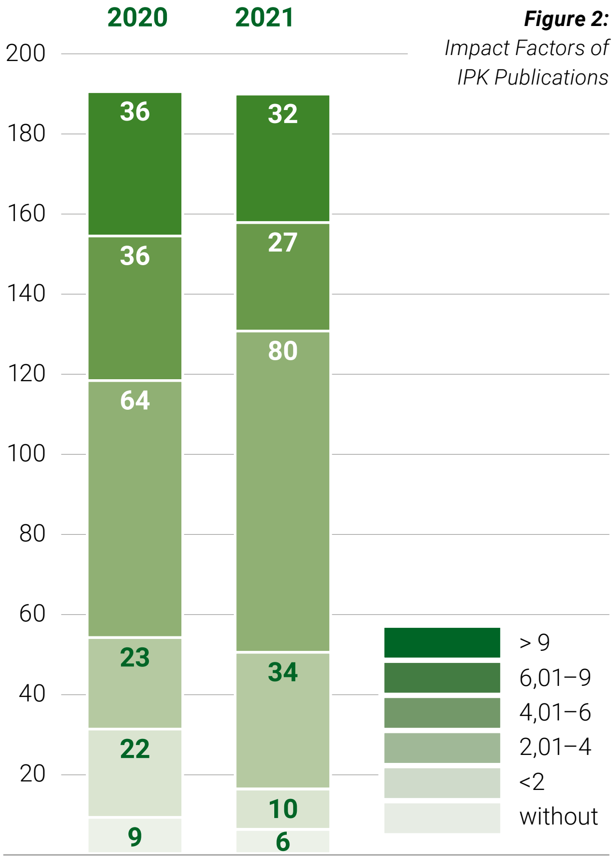


Figure 2:
Impact Factors of IPK Publications

PUBLICATIONS

In the reporting period a total of 379 papers were published in peer reviewed journals (190 in 2020 and 189 in 2021). 68 of these in journals with an impact factor greater than nine (Fig 2), reflecting a continuous trend towards publication in high impact journals. A complete list of the publications is given in the appendix of this report (page 108).

KNOWLEDGE AND TECHNOLOGY TRANSFER

During the reporting period, two invention disclosures were reported by IPK researchers. Both inventions were claimed, whereby one invention was declared a trade secret after internal examination for usability and patentability and the other (joint invention with a company) was transferred because it was contractually bound. The latter will be registered by the company as an industrial property right. In the reporting period two licence agreements on IPK technology were signed. IPK was able to acquire funds for a two-year project within the framework of the WIPANO funding programme of the BMWi (funding priority "Public Research – Further Development of Inventions") with the objective of generating further data and transferring the invented technology to other crop species.

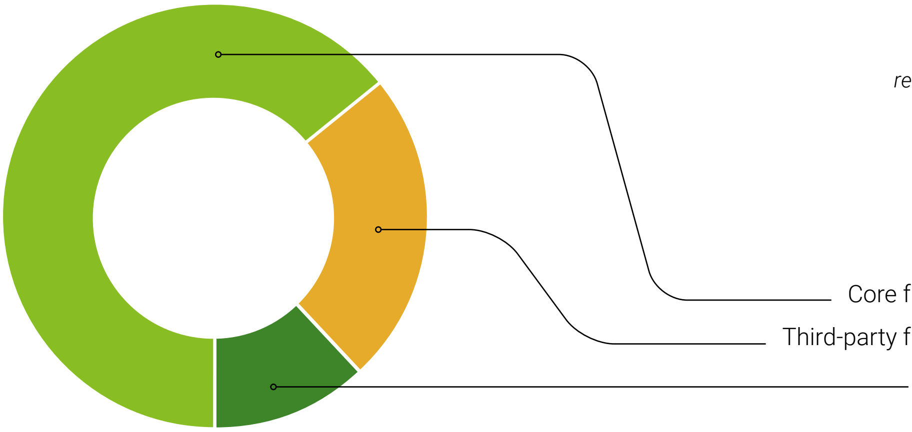


Figure 3: *Development of total revenues in 2020 and 2021 in percent.*

Core funding **68%** (2020) · **70%** (2021)

Third-party funding **19%** (2020) · **22%** (2021)

Others **12%** (2020) · **8%** (2021)

Further activities concerned the ongoing portfolio management, as well as portfolio streamlining and the investigation of exploitation options for contractually uncommitted know-how, as well as the planning of an application for the further development and validation of inventions via WIPANO. In 2021, considerations and first steps were taken with regard to a stronger focus on the screening of technology approaches and know-how accompanying new research projects.

FUNDING

In 2021 the total income amounted to 52.52 million euro including third-party grants and own income (2020: 52.98 million euro). This figure includes, on the one hand, the Institute's core funding amounting to 36.86 million euro (2020: 36.25 million euro) and, on the other hand, self-financing funds carried over from the previous year amounting to 4.19 million euro (2020: 6.56 million euro) and transferable cash balances totalling 7.03 million euro (2020: 9.84 million euro). (Figure 3)

In terms of appropriation, personnel accounted for approximately 48 percent (2020: 47 percent) of total expenditures in 2021 and equipment accounted for 27 percent (2020: 31 percent). In 2021 investments in scientific equipment were covered by core funding and by a BMBF-funded project (DPPN) to rig the "IPK-PhenoSphere" facility. Institutional funds were primarily used to optimise the supply and distribution of energy on the campus. The development and structure of total expenditures from 2018 to 2021 are shown in figure 5.

Third-party funding

In 2020 and 2021 third-party funding amounted to 10.17 and 11.47 million euro, respectively. (Figure 4) To increase the resilience of third party funding the effort of diversification bore fruit. Excellent basic research was made possible by the acquisition of extensive funding from the German Research Foundation (DFG) but also in the acquisition of European funding. Worthy of particular mention are two ERC starting grants (MEIOBARMIX, TRANSFER) that were won in 2021 by young research group leaders. In addition, a large EU project (AGENT) is being coordinated at the Institute. An overview of third-party funded projects is given in the appendix to this report (page 128) The figures also demonstrate that the Institute is a sought-after partner for collaboration with other research institutions and the private sector, especially plant breeding. The majority of the income results from such co-operations. A major funding line was the German Plant Phenotyping Network – DPPN of the BMBF, in which one of three research infrastructure nodes have been established at IPK. Similarly, the AVATARS joint project is funded by the BMBF and coordinated by the IPK.

Third-party-funding	**2018**	**2019**	**2020**	**2021**
EU	1.62	1.66	2.05	1.39
BMBF	7.08	6,16	3.00	3.87
BMEL	1.21	1.15	0.99	1.49
BMWi	0.22	0.13	0.22	0.17
DFG	1.21	1.64	1.76	1.70
Leibniz	0.26	0.11	0.12	0.25
LSA	0.21	-0.30	0,02	0.86
Others	0.08	0.27	0.40	0.21
Private sector	2.08	1.85	1.61	1.53
total	**13.97**	**12.67**	**10.17**	**11.47**

Figure 4: *Third-party funding (Comparison of third-party funding raised by the IPK Leibniz Institute in the years 2018 – 2021.)*

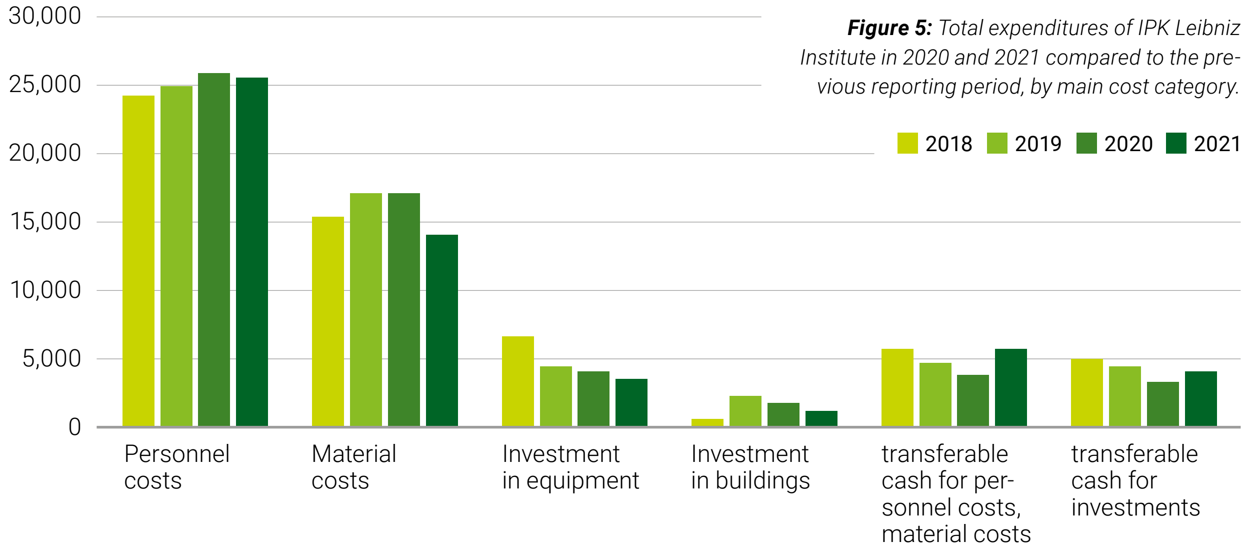


Figure 5: *Total expenditures of IPK Leibniz Institute in 2020 and 2021 compared to the previous reporting period, by main cost category.*

Research Co-operations and Collaborations

Co-operation with and teaching at nearby universities is an important draw for young scientists, links complementary research competencies, and develops the research landscape at the regional level. Based on joint appointments the Institute entertains tight links with the Martin-Luther-University in Halle (MLU) (3x W3, 1x W2, 1x W1) and the University of Göttingen (W3). A second joint appointment with the latter is underway. The links of IPK with the academic sector are further strengthened by two associated professorships of IPK scientists at MLU and one at the University of Kassel. In addition, IPK scientists teach at numerous universities totalling to 72 and 82 course hours per semester-week in 2020 and 2021, respectively. Scientists at the Institute were also involved in supervising students. In this context, 15 PhD students successfully defended their theses. In addition, 21 Master and 18 Bachelor theses were completed. Supposedly because of the Sars-Cov-2 pandemic, the numbers declined in 2021 by more than 50 percent.

To initiate cooperation with the DFG-funded Cluster of Excellence on Plant Science (CEPLAS) in North Rhine-Westphalia two joint workshops were held, and a joint strategy paper for the establishment of a cross-regional "Centre for Translational Plant Biodiversity Research" (TransCend) was adopted. At the international level, the cooperation with the "Institute of Genetics and Developmental Biology" of the Chinese Academy of Sciences was renewed in July 2021 for another period of five years.

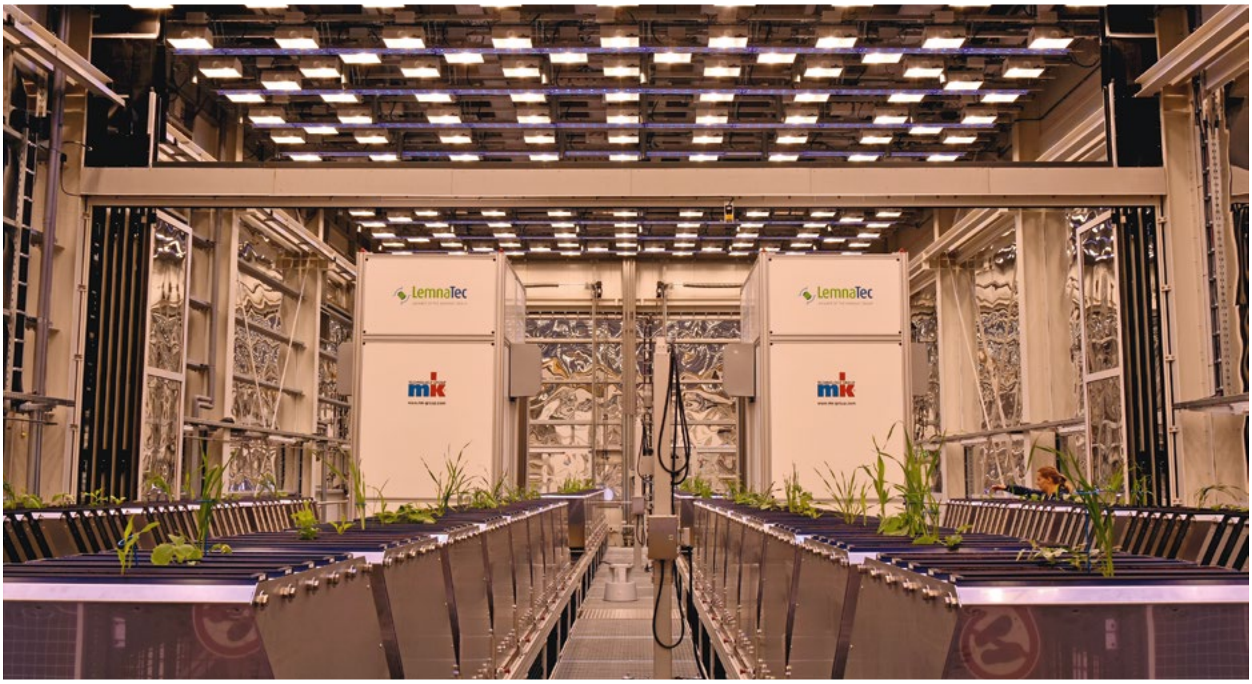
LEIBNIZ SCIENCE CAMPUSES AND LEIBNIZ RESEARCH NETWORKS

For many years, the Institute has been actively involved in shaping Leibniz research campuses, research alliances and networks. In 2020, the **Leibniz ScienceCampus "Phosphorus Research Rostock"** (P-Campus), founded in 2015, entered a further funding phase. Under the leadership of the Leibniz Institute for Baltic Sea Research Warnemünde, the P-Campus combines the interdisciplinary expertise of five Leibniz institutes and the University of Rostock. Together, the aim is to find answers and strategies for comprehensive research into the element phosphorus, which is essential for all life processes, its diverse chemical compounds and modes of action in agriculture and the environment as well as in technical and industrial processes. In addition to basic and applied research, new technologies for phosphorus use are to be developed and transferred to industry.

The Leibniz ResearchCampus Halle – "Plant-Based Bioeconomy" was consolidated in the reporting period as the **"ScienceCampus Halle"** (WCH). The aim remains the networking and cooperation of regionally neighbouring Leibniz institutes and the Martin Luther University Halle-Wittenberg. The “ScienceCampus Halle” integrates the relevant scientific disciplines of plant-based agricultural sciences, biology, biochemistry, biotechnology and links these competences with environmental, social and economic research and teaching areas. This enables a fundamental examination and assessment of plant-scientific and biotechnological innovations and the associated social and economic processes. After two successful funding periods, the structure of this network is now being consolidated by the participating partners.

A further bundling of competencies takes place at the level of Leibniz research networks. The IPK is involved in two of these networks. The **Leibniz Research Network "Biodiversity"** (LFN) bundles and networks the competencies of 18 Leibniz institutions in the environmental, life, regional, social and economic sciences. The LFN was originally founded in 2008 as the Leibniz Biodiversity Research Network (LVB) on the initiative of the institutions and has been continued as a research network since 2021.

The **Leibniz Research Network "Bioactive Compounds"** comprises Leibniz Institutes from four sections of the Leibniz Association and achieves better integration in drug development, food security and related areas. The main goal of the Leibniz Research Network is to further develop the topic-related communication platform on which the participating institutes as well as external partners can exchange professional, methodological and technical expertise. In addition, based on its own work on stem cells



Rhizotron system in the PhenoSphere for automated digital phenotyping of above- and below-ground plant parts.

in cereals, the IPK is associated with the Leibniz Research Network "Stem Cells and Organoids" established in 2021.

To contribute to and benefit from interdisciplinary research in the field of agricultural sciences, the IPK is participating in the **Strategy Forum "Conflicts of objectives in sustainable biomass production"**. The mandate is to elicit the Leibniz Association's interdisciplinary expertise for overcoming conflicts of objectives in agricultural and aquatic production systems. The members develop a methodological framework and research approach for sustainable biomass production systems.

SCIENTIFIC LIBRARY AND INFORMATION SERVICES

The scientific library houses about 82,700 media units related to the main research areas of the Institute. The main task of the library is to provide literature for the researchers on site, but the neighbouring biotech companies also make use of the service. The IPK's participation in the DEAL contracts with Wiley and SpringerNature is an important step for the Open Access process. This leads to an improved information supply for all participating institutions by extending reader access to the entire journal portfolio of the respective publishers. Authors also have the opportunity to publish their research results in Open Access. The Institute supports the open science initiatives of the Leibniz Association. In 2021, 95 publications (2020: 86) were published in genuine "Open Access" journals and 55 publications (2020: 44) in hybrid journals. The IPK is a member of the ORCID Germany consortium led by TIB Hannover. The "Open Researcher and Contributer ID" (ORCID) ensures a uniform, general and open standard of author identification. Due to active information and support services within the Institute, about 90 percent of the researchers at IPK are registered at www.orcid.org.

WORK OF THE BOARDS

The Scientific Advisory Board advises the Board of Directors and the Board of Trustees on scientific and technical matters. In 2020, the Scientific Advisory Board was primarily concerned with peer review of the Molecular Genetics and Physiology and Cell Biology departments. In 2021, the focus of the review was on the research work of the independent research groups and the two departments Genebank and Breeding Research. In 2020 the Board of Trustees held its meeting in December, and in 2021 the board convened in March and November, respectively.

SCIENTIFIC COMMUNICATION

Due to the pandemic restrictions, on-site conference activities had to be severely curbed. During the reporting period, the IPK organised the "International Conference of the Working Group Seed Science and Certification" of the German Society of Plant Breeding (GPZ) & Section IV Seeds (VDLUFA), titled "Seed Production in Times of Climate Change" in March 2021, with 216 participants from 33 countries as an online event in Gatersleben. The **"International Symposium on Rye Breeding & Genetics"** as an online conference in June 2021 was organised in Gatersleben as well. In total 160 researchers from 30 countries took part in this event. The **"Cytogenetics Meeting 2021"**, organised jointly by GPZ, Senckenberg and IPK, took place in September 2021 in Görlitz as the only meeting in presence in the reporting period with a total number of 65 participants from the United Kingdom, the Czech Republic and Germany. Also, in November 2021 the “6th Conference of Cereal Biotechnology and Breeding” was jointly organised with the EUCARPIA Cereals Section in Budapest (Hungary) as an online event with 120 participants from 28 countries. The IPK PhD-Students jointly with the PhD-Students of our partner institute, the Leibniz-Institute of Plant Biochemistry (IPB), organised the PSSC in June 2021 as an online conference. More than one-hundred students took part in the four days event. PhD students in plant or crop research and bioinformatics were invited to present their research results in talks and poster sessions. In addition keynote lectures and workshops from academia and industry where organised.

A project funded together with the Leibniz Institute DSMZ (**WiLDSI-VorweRts** – Scientific approaches to solutions for digital sequence information for preparing further advice) will give the international research community a voice in the preparation of the next UN negotiations at the Biodiversity Conference (COP 15) in China. The background is the political debates on digital sequence information (DSI) from Genetic Resources (GR) under the CBD and the Nagoya Protocol. The aim of the project is to maintain free accessibility for all areas of life sciences including plant research. Within the framework of the project, several workshops with stakeholders were organised in Germany and Brussels (Belgium) and several publications, which provide a scientifically grounded basis to support the negotiations where published. An international scientific network on DSI has been formed with more than 50 researchers from 6 continents and is still growing. The Network’s mission is to contribute to policymakers´ and other stakeholders’ understanding of DSI, its applications and contributions to research supporting biodiversity conservation and public health, as well as highlighting the global benefits of open access to DSI databases.

In recent years, the IPK has made further efforts to intensify the transfer of knowledge to society and to provide it with a broader and medially up-to-date basis. Examples of this are the intensified press work including the reworking of the IPK Journal, the redesign of the Institute's website and intensified activities in the social media with a focus on Twitter. Due to the limited opportunities to visit the Institute as a result of the pandemic, a virtual tour of the Institute was developed, which is anchored on the homepage and will continuously be updated. The aim of these measures is to give users all over the world an improved insight into the research activities at the Institute.

The IPK was a partner and host of the Journalists' College of the Leopoldina National Academy of Sciences. On 22 October 2021, 25 journalists were guests at the IPK. Under the title "Agriculture and Food – Resources for the Future" insights into current research were provided and discussed in lectures and guided tours. As a result of the event, further contacts were made and, as a consequence, reports on the work of the IPK became published. A separate series of events in the Year of Bioeconomy was targeted to students from high school classes. The project "Crops4Future" was one of 32 selected projects funded by the BMBF within the Federal Year of Bioeconomy. Two live talks were attended by 50 students and a large number on the internet. These discussion rounds with young researchers of the IPK were broadcast live and can be accessed via the “Crops4Futrue” project website.

Vegetative conservation of Plant Genetic Resources (PGR) that cannot be preserved as seeds, are maintained in the field (as shownhere for Allium), in vitro or by cryopreservation in the Federal Ex situ Gene Bank.

HIGHLIGHTS

2020

20 January
Dr. Martin Mascher is awarded the Günter and Anna Wricke Research Prize 2020 for his seminal contributions to the sequencing of cereal genomes. He is the second researcher at the Institute to receive this prestigious distinction, which is granted every three years.

19 February
Prof. Dr. Klaus Töpfer, former Federal Environment Minister and Executive Director of the United Nations Environment Programme, gives a lecture on "The Crisis of Parliamentary Democracy – Diagnosis and Therapy" at the IPK.

21 February
Robert Hoffie receives the Science Communication Award of the Section Plant Physiology and Molecular Biology of the German Botanical Society.

26 February
The joint project AVATARS, which aims to process the enormous amounts of data from science using virtual reality (VR) and thus support research and rape breeding, is launched officially with a kick-off meeting at IPK.

18 May
Start of the EU research project AGENT, coordinated by the IPK. The aim is to fully unlock the potential of biological material stored in gene banks around the globe by deveolping international standards and an open digital infrastructure for the management of Plant Genetic Resources.

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18 March
IPK scientists find the key to the comprehensive gene pool of rye. MDR, among others, reports on the results, which are published in the journal “Nature Genetics”.

11 June
Big data in plant breeding: IPK researchers double the accuracy of wheat yield predictions. An international research team led by the IPK Leibniz Institute has compiled, processed and analysed extensive data sets for this purpose. The results, which could herald a new era for plant breeding, have been published in the magazine “Science Advances”.

17 June
Prof. Dr. Nicolaus von Wirén is appointed a member of the Leopoldina. After Prof. Dr. Ingo Schubert and Prof. Dr. Andreas Graner, he is now the third current IPK scientist to become a member of the Leopoldina. Prof. Dr. Nicolaus von Wirén is appointed a member of the Leopoldina. Also, he had been ranked by the "Web of Science" among the most influential scientists in his field.

17 August
IPK researchers: spread of peppers is an early example of global trade. The work titled “Global range expansion history of pepper (Capsicum spp.) revealed by over 10,000 genebank accessions” was published in PNAS.

5 October
"Stem cell systems in cereals": IPK is partner in new DFG research group. The network officially will start in early next year and is scheduled for two times four years. Initially it will be funded with almost four million euros over the next four years.

30 July

The Investment and Marketing Corporation Saxony-Anhalt awards the "Green Gate Gatersleben" with the IPK Leibniz Institute as one of twelve so called “Places of the Future”.

3 September

Dr. Martin Mascher (34) and Dr. Stefan Heckmann (38) both receive a Starting Grant from the European Research Council (ERC). This means that the current research projects TRANSFER and MEIOBARMIX of the two heads of Independent Research Groups will each be funded with 1.5 million euros over the next five years.

7 October

Dr. Alevtina Ruban is awarded the Gatersleben Research Prize 2020 for her work on B chromosomes at the start of the Institutes Days. Dr. Dominic Knoch received the Beagle Award from the PhD Student Board, the representation of PhD students.

23 October

In a special issue on climate change, SPIEGEL also reports on the work of the IPK under the title "German researchers are working on the agriculture of the future".

25 November

An international team of researchers led by the IPK has reached a milestone on the way to the "virtual plant" barley. With the complete sequencing of 20 different genotypes, the scientists completed the first step towards decoding the genetic information of the entire species "barley" – the barley pan-genome. The results were published in the journal “Nature”.

2021

6 October

Lydia Kienbaum is awarded the Rudolf Mansfeld Prize at the start of the Institutes Days. Krishna Mohan Pathi received the Beagle Award from the PhD Student Board, the representation of IPK´s PhD students

22 October

Leopoldina Journalists' College is guest at the IPK. Among others, Prof. Dr. Thomas Altmann, Prof. Dr. Nicolaus von Wirén and Robert Hoffie take part in the discussions.

23 October

MDR publishes a major portrait of Prof. Dr. Andreas Houben entitled "Der Herr der Chromosomen" (The Lord of Chromosomes), which appears in the series "Mitteldeutschlands klügste Köpfe" (Central Germany's Smartest Minds).

23 November

In its podcast "Climate Report" The SPIEGEL magazine intervews Prof. Dr. Nicolaus von Wirén if modern genetic engineering can save the climate.

14/15 December

"Crops4Future," a project as part of the German government's “Year of Science – Bioeconomy”, brought researchers at IPK together with schoolchildren. Together, they developed concepts on how farming, food production, plant research and much more should become more environmentally and climate friendly.

DEPARTMENT
GENEBANK

GENEBANK

GENOMICS OF GENETIC RESOURCES (GGR)
Prof. Dr. Nils Stein

GENEBANK DOCUMENTATION (DOK)
Dr. Stephan Weise

RESOURCES GENETICS AND REPRODUCTION (RGR)
Prof. Dr. Andreas Börner

CRYO- UND STRESS BIOLOGY (CSB)
PD Dr. Manuela Nagel

SATELLITE COLLECTIONS NORTH (TEN)
Dr. Klaus Dehmer

EXPERIMENTAL TAXONOMY (ETX)
Dr. Frank Blattner

DOMESTICATION GENOMICS (DG)
Dr. Martin Mascher

DEPARTMENT GENEBANK

Head: Prof. Dr. Andreas Graner

MISSION

The preservation of Plant Genetic Resources (PGR) in the Federal *Ex situ* Gene Bank is a fundamental prerequisite to curb genetic erosion, study crop plant evolution and spark innovation for crop plant improvement. Modern PGR management requires the integration of the conservation of biological materials with information including molecular, phenotypic and environmental data. Understanding the interplay of the multitude of external factors and genetic mechanisms that drive speciation, genome evolution, and the relationship between genetic diversity and trait expression will benefit conservation and knowledge-driven utilisation of PGR. These issues are addressed by a research programme employing genomics approaches to study selected crop plant genomes at the structural and functional levels.

RESEARCH STATUS

Conservation Management

The Federal *Ex situ* Gene Bank is one of the world's largest collections, both in terms of botanical diversity and the size of its collection. As of July 2021, the holdings comprise 151,861 accessions from 93 plant families representing 761 genera and 2,901 species. 20,281 accessions remain to be taxonomically determined at the species level.

The collection is maintained in Gatersleben and the two external sites, Malchow (oil and fodder plants) and Groß Lüsewitz (potato assortment). For seed propagation, 11,030 accessions were cultivated in the field or greenhouse during the reporting period (July 1, 2019 – June 30, 2021). For seed quality control, about 40,000 germination tests were carried out.

In addition to its living collections, the Gene Bank has a herbarium with 469,767 specimens, 109,990 reference samples of seeds and fruits and 57,062 cereal spikes. In the last two years, 33,015 samples were distributed to researchers, plant breeders or other interested stakeholders. The distribution is based on the terms of the Standard Material Transfer Agreement (SMTA), ensuring that the relevant provisions of the International Treaty or the Nagoya Protocol are followed. Thus, since 1948, more than 1.1 million samples have been provided to users in Germany and abroad (Figure 1). Table 1 summarises the inventory.

In addition to the preservation of seed-borne accessions, the IPK houses one of the world's largest cryo-collections for vegetatively preserved plants. The collection comprises over 2,300 accessions, including 1,902 potato as well as 157 mint and 239 *Allium* samples. The safety collection in the Svalbard Global Seed Vault of the Crop Trust was increased to 59,518 accessions representing around 39% of the total collection.

To support the coordinated conservation of genetic resources at the national and international level, the Gene Bank works closely with the Federal Ministry of Food and Agriculture (BMEL) and Biodiversity International (European Cooperative Programme on Plant Genetic Resources, ECPGR). In this context, the Genebank Department is responsible for hosting and further advancing the European Search Catalogue for Plant Genetic Resources (EURISCO). All accessions housed at IPK have been linked to Digital Object Identifiers (DOIs) to improve the tracking and the documentation of material. Also, the extent of phenotypic information online available has been increased.

RESEARCH HIGHLIGHTS

Plant Genetic Resources are of central importance for research and the downstream breeding improvement of crops. The networking of biological material with digitised data, e.g. by providing sequence infor-

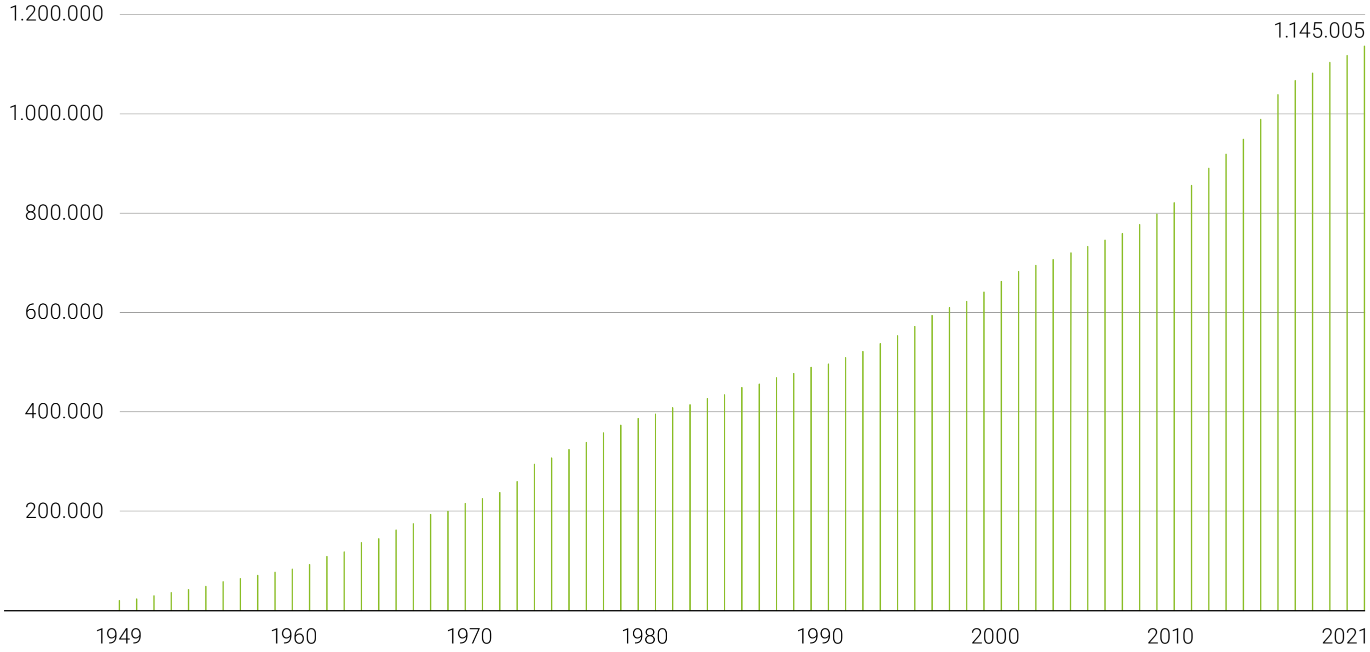


Figure 1: *Cumulated distribution of samples between 1949 and 2021*

mation for extensive partial collections, contributes to the further development of the Gene Bank as a research infrastructure. The scientific programme of the department delivers significant contributions to the two Research Themes, "Valorisation of Plant Genetic Resources" and "Genome Diversity and Evolution".

The department's research groups are assigned to three programmes: “Characterisation and Documentation”, “Conservation Management and Evaluation”, “Taxonomy and Evolution”. In 2021 the formerly independent research group on Domestication Genomics was integrated into the department to complement and strengthen the research programme in computational genomics. Vice versa, the research group Genome Diversity was closed down by the end of 2020. For more than 23 years, it has contributed to genome analysis in barley, including the development of mapping populations, genomics resources, and a reference sequence for the barley genome. A large number of agronomic traits and QTLs were mapped. In recent years, phenotypic analysis of vegetative growth parameters was advanced by putting into operation the first automated phenotyping platform at the institute. Since its inception in 1997, the research results of this group have been published in more than 170 reviewed papers.

The research programme "Conservation Management and Evaluation" includes the continuous evaluation of selected agronomic traits. A further focus is the improvement of conservation management. Here, studies on the genetics of seed longevity were continued. Concerning vegetatively propagated species, we continually expand the cryo-collections of potato and *Allium*. Research into biochemical and cell biological processes during the freezing treatment provides insights for understanding the physiological processes. Transcriptome analysis provided first insights regarding gene expression patterns linked to the cryopreservation process and provided hints to epigenetic alterations. Experiments on the cryopreservation of pollen cells have been continued to advance the use of genetic resources in hybrid wheat breeding.

The research programme "Taxonomy and Evolution" is mainly concerned with the phylogenetic classification and investigation of speciation within selected plant genera. Within the Triticeae tribe, the phylogeny of di- and polyploid species was investigated to help clarify the evolution of domesticated wheat and closely related *Aegilops* species. In a similar vein, the evolution of di- and tetraploid *Hordeum bulbosum*, the closest relative to domesticated barley (*Hordeum vulgare*), has been investigated.

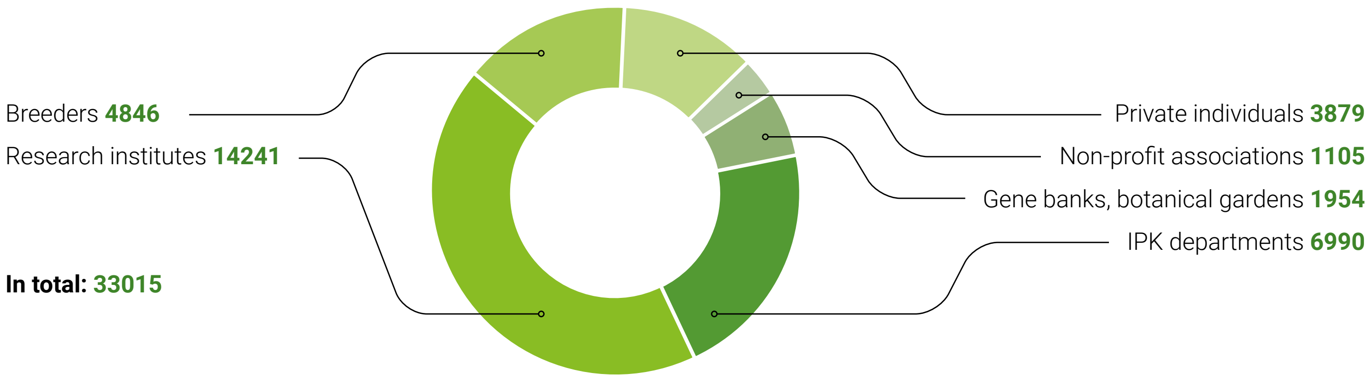


Figure 2: *Distribution of 33,015 samples of plant genetics resources to different user groups.*

Benefitting from an integrated approach combining long and short-range sequencing technologies, a first analysis of the pan-genome of *Hordeum vulgare* has been completed. The results revealed a hitherto unknown structural diversity challenging the tenet of an almost static genome structure within a given species.

The research programme "Characterisation and Documentation" focuses on the description of Gene Bank materials at the DNA level and the maintenance and further development of the data management system of the Gene Bank (GBIS). Special emphasis is being placed on the integration of passport data with phenotypic and molecular data to characterise the biological material. Experimental work focuses on the genetic mapping of qualitative and quantitative traits in barley, wheat and rye, and the isolation of genes encoding agronomic traits.

Many studies on trait mapping in wheat, barley and rye have benefited from the development of extensive genomics resources in recent years. Of particular note in this context are significant contributions to the development of high-quality reference sequences for the genomes of barley (*Hordeum vulgare*), bread wheat (*Triticum aestivum*) and rye (*Secale cereale*), to which research groups of the department contributed significantly. Based on the availability of the most recent sequencing technologies and protocols established in the sequencing platform run by the department, genomic sequencing activities have been expanded to study the pan-genomes of oat (*Avena sp.*) and the 21 diploid species of the genus *Hordeum*.

An important milestone in the further development of the Gene Bank into a bio digital Resource Centre was reached with the completion of the DNA fingerprinting of the entire barley collection comprising more than 23,000 accessions. In a subsequent step, resequencing of the IPK wheat collection has now been initiated.

FUTURE PRIORITIES

Building on the expertise accumulated over more than seven decades, the department stands for research-driven conservation of Plant Genetic Resources collections. It warrants the sustainable preservation of one of the largest *Ex situ* collections of the world and gives rise to innovations to improve its value as an infrastructure for research and crop plant improvement.

To further improve conservation management and better cover the research needs for forage plants and potatoes, the infrastructure advancement at the Gene Bank sites in Groß Lüsewitz and Malchow was initiated in 2021.

Technical progress in genome analysis and plant phenotyping will further accelerate the systematic characterisation of complete collections by DNA sequencing and trait analysis. It will allow for the comprehensive molecular characterisation of gene bank collections. Molecular characterisation of the extensive *Vicia faba* collection will be initiated in 2022 in collaboration with a newly established independent research group associated with the Genebank department and thus expand the research agenda to legume species.

The availability of sequence information will benefit the conservation of genetic resources in manifold ways. In this context, we will continue on the

Species groups	Accessions
cereals and grasses	**66213**
wheat	28283
barley	23761
oat	4858
rye	2471
triticale	1600
Aegilops	1526
millets	842
maize	1531
others	1341
legumes	**27857**
Phaseolus	9011
field beans	3056
soybeans	1493
other beans	616
pea	5364
chickpea	527
vetchling	515
vetches	1844
lupines	2761
lentils	461
clover	1934
others	275
Cucurbitaceae	**2660**
pumpkins	1055
melons	727
cucumbers	727
others	151
larger-grain oil, fibre and dye plants	**5472**
flax	2322
sunflower	679
dye plants	458
fibre plants	191
oil plants	551
others	1271
vegetables	**18455**
tomatoes	3823
pepper	1535
eggplants	113
beta beets	2401
raphanus	761
carrots	494
chicory	680
Allium	2591
Brassica	2185
lettuce	1156
spinach	215
celery	255
Quinoa	953
others	1293
medicinal and spice plants	**8210**
poppy	1135
tobacco	590
others	6485
mutants	**1699**
tomato mutants	743
soybean mutants	529
Antirrhinum mutants	427
potatoes	**6315**
small-grained oil and forage crops	**14980**
rapeseed and feeding kale	2566
grasses	11085
red clover and alfalfa	1329
Total	**151861**

Table 1: *Overview of collections from the Gene Bank by crop species*

path taken to further develop the Gene Bank into a bio digital Resource Centre by linking the relevant information with conventional passport data.

By laying the foundation stone to establish the Federal *Ex situ* Gene Bank for Agricultural and Horticultural Crop Plants at IPK in 2003, the introduction of a quality management system according to ISO standards in 2007, and by hosting the EURISCO database since 2014, the department has continued to set international standards for the conservation of genetic resources and cemented the value of the Gene Bank as an internationally visible and widely used research infrastructure. By its scientific focus on molecular genetics and genomics of Triticeae, the department has substantially contributed to implementing the IPK research programme. In the years to come, it will continue along these lines to help valorise Plant Genetic Resources and to further advance the research into genome diversity and evolution.

RESEARCH GROUP **GENOMICS OF GENETIC RESOURCES** (GGR)

Head: Prof. Dr. Nils Stein

MISSION

Our research goal is to use state-of-the-art high-throughput genomics to unlock the pan-genomes of barley, wheat and rye. This provides a new knowledge-base for discovery and display of global genomic diversity of these important crop species as captured in *ex situ* gene banks. The established approach of gene bank genomics is being adopted for further key species of IPK's Gene Bank. We are using this information to unravel the genetic basis of soil- and insect-borne virus disease in barley, barley morphology and architecture, cytoplasmic male sterility restoration and chloroplast differentiation and maturation.

To aid implementation of its research programme and to provide services at an institute wide level, the research group operates and continuously advances a next generation DNA-sequencing platform.

RESULTS

Pan-genomes for the Triticeae

The research group takes a leading role in sequencing and re-sequencing of the genomes of barley, wheat and rye. Based on established procedures of short-read de novo chromosome-scale genome assembly in Triticeae (Monat *et al.* 2019, Genome Biology), the group collaborated with the research groups Domestication Genomics and Bioinformatics at IPK and further international collaborators to produce first version pan-genomes in barley (Jayakodi *et al.* 2020) and wheat (Walkowiak *et al.* 2020). Two rye genome assemblies (Rabanus-Wallace *et al.* 2021, Li *et al.* 2021, both Nat Genet) are providing a start into rye pan genome analysis. This activity is expanded also to wild relatives, e.g. in collaboration with the research groups Domestication Genomics, Bioinformatics, Experimental Taxonomy, Chromosome Structure and Function and Applied Chromosome Biology in the *Hordeum bulbosum* IPK flagship project and as part of the pan-*Hordeum* initiative coordinated by Martin Mascher from Domestication Genomics.

Unlocking crop plant genetic resources

The research group has demonstrated in a large IPK-internal collaborative effort, including groups Resources Genetics and Reproduction, Genebank Documentation, Domestication Genomics, Bioinformatics, Genome Diversity and Quantitative Genetics (Milner *et al.* 2019, Nat Genet), the feasibility of genotyping entire crop collections of IPK Gene Bank – a research area we and others have coined "gene bank genomics" (Mascher *et al.* 2019, Nat Genet). Since then, part of the concept has been transferred to unlocking other important crop collections at IPK. In the BMBF funded project Genebank2.0 (phase I & II), coordinated by Quantitative Genetics, so far more than 13,000 wheat accessions were genotyped by reduced-representation sequencing. The effort in barley and wheat was taken by IPK now to the European level through coordination of the EU Horizon 2020 project AGENT; bringing together 19 gene bank and

Selected Publications

JAYAKODI, M. et al.: The barley pan-genome reveals the hidden legacy of mutation breeding. Nature 588 (2020) 284-289.

WALKOWIAK, S. et al.: Multiple wheat genomes reveal global variation in modern breeding. Nature 588 (2020) 277-283.

MASCHER, M. et al.: Long-read sequence assembly: a technical evaluation in barley. Plant Cell 33 (2021) 1888-1906.

RABANUS-WALLACE, M.T. et al.: Chromosome-scale genome assembly provides insights into rye biology, evolution and agronomic potential. Nat. Genet. 53 (2021) 564-573.

TRIPODI, P., M.T. RABANUS-WALLACE* et al.: Global range expansion history of pepper (Capsicum spp.) revealed by over 10,000 genebank accessions. Proc. Natl. Acad. Sci. U.S.A. 118 (2021) e2104315118. * joint first authorship*

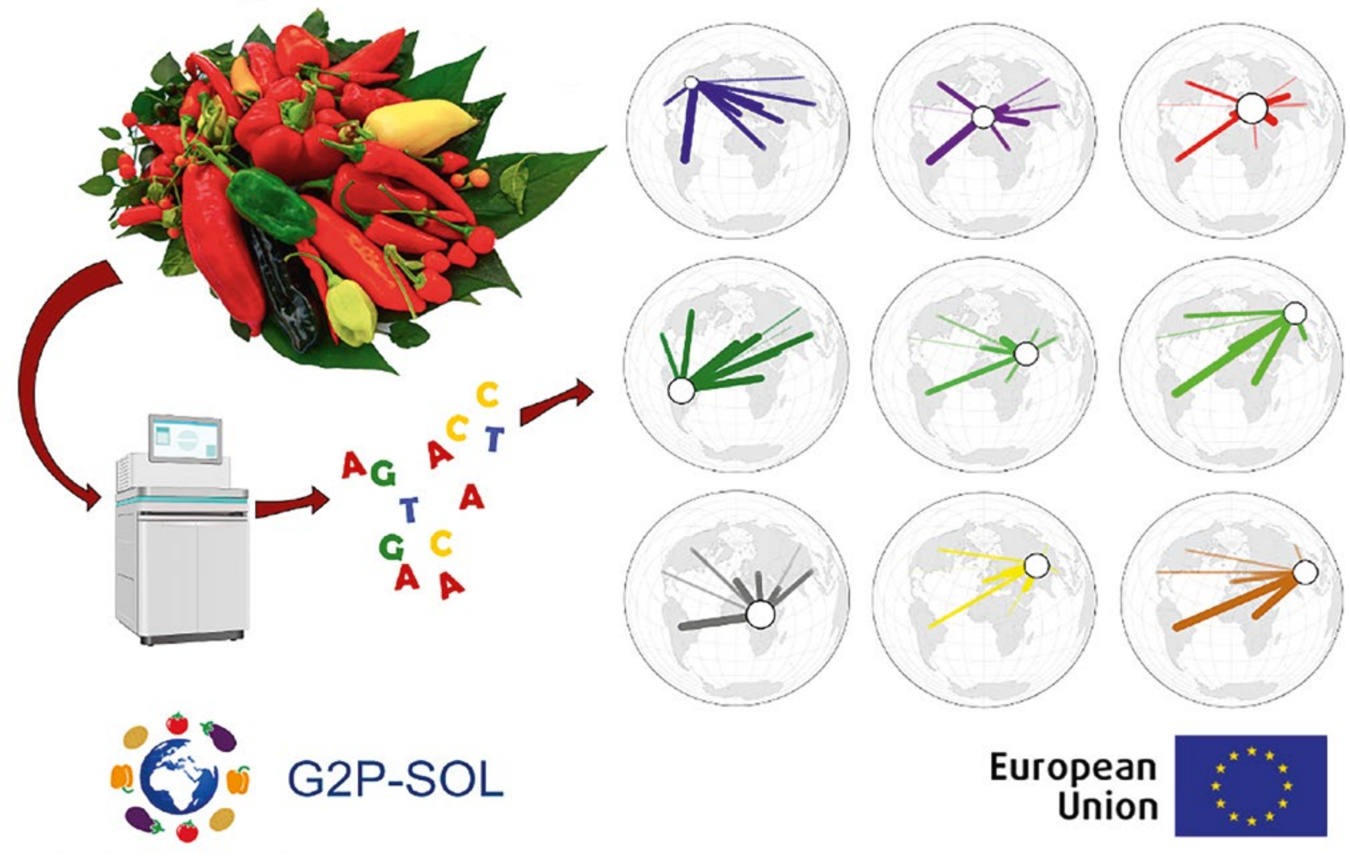


Figure. 1: *As part of the G2P-SOL consortium (www.g2p-sol.eu) the research group Genomics of Genetic Resources genotyped by sequencing >10,000 gene bank pepper samples. The data gave insight into the way the peppers grown in various regions of the globe overlap with each other, often as a result of their human trading and migrations (P. Tripodi & M.T. Rabanus-Wallace et al., PNAS, 2021, picture by: M. Timothy Rabanus-Wallace / IPK Leibniz Institute).*

gene bank-informatics partners from all-over Europe in a 5-year collaborative project with a total budget of 7 million EURO. The pepper (Capsicum spp.) collection of IPK is another example. In the EU Horizon 2020 project G2P-SOL 10,000 pepper accessions, including ~1,400 from IPK, were genotyped and the data revealed patterns of historic global distribution of pepper, following major trade and migration routes (P. Tripodi, M.T. Rabanus-Wallace *et al.* 2021, PNAS and Figure 1).

EMBEDDING IN IPK RESEARCH THEMES

The research group is contributing mainly to the Research Theme 1 “Valorisation 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.

OUTLOOK

The research group will continue its activity in structural genome and pan-genome analysis of the crop species barley, wheat, rye and wild relatives. This will cover the areas of structural variation, pan-epi-genomics, developmental and tissue specific 3D genome organisation, the systematic characterisation of globally available genomic diversity. Direct access to IPK`s Next Generation Sequencing (NGS) platform and its continued equipping with complementing innovative technology (PacBio Sequel IIe, Illumina NovaSeq6000, ONT Promethion etc.) is providing excellent opportunities for this kind of research and for international collaboration and networking.

More information: *www.ipk-gatersleben.de/en/genebank/genomics-of-genetic-resources/*

RESEARCH GROUP
GENEBANK DOCUMENTATION (DOK)

Head: Dr. Stephan Weise

MISSION

The activities of the research group cover a wide range of aspects of documentation of genetic resources and gene bank data handling. In particular, the research group develops and operates information systems for Plant Genetic Resources (PGR) with the aim of making information on PGR available to researchers, breeders and other users, and to support the workflows in the Gene Bank.

Therefore, a major focus is on the further development of the Genebank Information System (GBIS) with its core components GBIS/M (internal management system) and GBIS/I (online search and ordering system) as well as on the development of the European Search Catalogue for Plant Genetic Resources (EURISCO). These systems are designed to ensure the long-term availability of PGR-related data. The research group contributes to the development of international information networks on PGR and biodiversity informatics.

RESULTS

GBIS forms the central infrastructure of the institute to support all processes related to the maintenance of Gene Bank accessions. In order to assure the performance and efficiency of the system in the long term, it is essential to continuously develop its various components. An example is the extension of the necessary infrastructure to enable gene bank accessions to be provided with Digital Object Identifier (DOIs) for unique identification. In this way, all accessions of the active Gene Bank collection were provided with a DOI allowing their unequivocal identification. In addition, the research group is also responsible for assigning DOIs to research collections developed in and maintained at the institute.

The coordination of EURISCO was continued and strengthened further. The research group has already been responsible for hosting and advancing EURISCO since 2014, as well as for coordinating the underlying network. EURISCO is operated on behalf of the European Cooperative Programme for Plant Genetic Resources (ECPGR) and provides a central hub for information on more than two million *ex situ* accessions maintained in about 400 collections in 43 countries. In close cooperation with the International Treaty on Plant Genetic Resources for Food and Agriculture (ITPGRFA), EURISCO supports its data providers in registering their germplasm material for DOIs. Since 2020, the research group receives additional funding within the European Evaluation Network (ECPGR-EVA) to expand EURISCO with the necessary infrastructure for the EVA network. EURISCO is a vital component of the Global Information System (GLIS).

The research group has been involved in a number of EU Horizon 2020 research projects in the reporting period. EUCLEG focused on breeding forage and grain legumes to increase protein self-sufficiency in the EU and China. Farmer's Pride aimed at developing a network of European *in situ* sites and stakeholders. GenRes Bridge was a joint project of the three European plant, animal and forest genetic resources networks (ECPGR, ERFP and EUFORGEN). All these projects resulted in a strengthening of EURISCO.

Two more EU Horizon 2020 projects involving the Genebank Documentation group started in May 2020: AGENT and INCREASE. AGENT is a concerted effort to activate gene banks. It focuses primarily on wheat and barley and aims to facilitate access to genetic resources for breeders and farmers through standardised protocols for data generation, documentation and delivery to users. The research group is mainly involved in two work packages aimed at developing guidelines and formats for the generation, exchange and presentation of data and at developing the infrastructure for the management and analysis of genotypic and phenotypic data on genetic resources alongside the established EURISCO structures, respectively. The INCREASE project aims to advance the conservation of European Plant Genetic Resources of common bean, chickpea,

Selected Publications

BELLUCCI, E. et al.: The INCREASE project: Intelligent collections of food-legume genetic resources for European agrofood systems. Plant J. 108 (2021) 646-660.

CORTINOVIS, G. et al.: Towards the development, maintenance, and standardized phenotypic characterization of single-seed-descent genetic resources for common bean. Curr. Protoc. 1 (2021) e133.

JIANG, Y. et al.: Using genome-wide predictions to assess the phenotypic variation of a barley (Hordeum sp.) gene bank collection for important agronomic traits and passport information. Front. Plant Sci. 11 (2021) 604781.

WEISE, S. et al.: Document or lose it – on the importance of information management for genetic resources conservation in genebanks. Plants 9 (2020) 1050.

PAPOUTSOGLOU, E.A. et al.: Enabling reusability of plant phenomic datasets with MIAPPE 1.1. New Phytol. 227 (2020) 260-273.

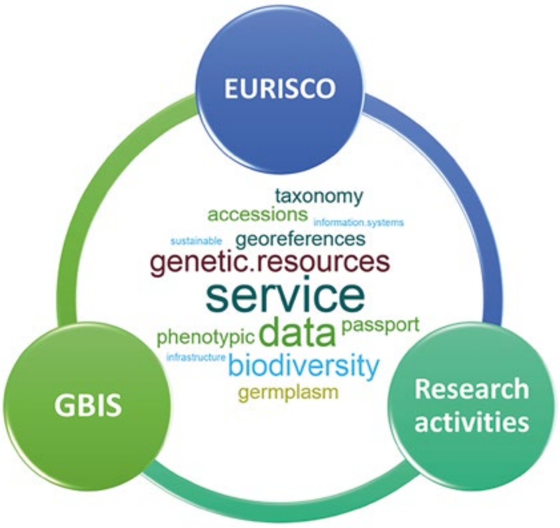


Figure. 1: *Thematic focus of the activities of the Gene Bank Documentation.*

lentil and lupin and to promote their use and valorisation. To this end, cutting-edge approaches in plant genetics and genomics are combined with phenotypic information from field evaluation but also from high-throughput phenotyping, including molecular phenotyping (e.g. transcriptomics and metabolomics). The results will be stored in a data portal that is easily accessible to the public to ensure informed selection of plant material. Conservation and evaluation of common beans will be tested for the first time using a citizen science approach. The research group is responsible for the work package to develop the data infrastructure and integrate the data, which forms the backbone of the project. Here, the working group can benefit from its dual character as experts for the documentation of genetic resources and IT specialists.

The continuous curation and analysis of data on gene bank accessions is one of the fundamental tasks of the research group (both historical and current data). Through this continuous improvement and extension of both passport and phenotypic data, the quality and quantity of available information on gene bank accessions has been and continues to be significantly increased. Since 2018, five papers have been published in this context in collaboration with the Quantitative Genetics research group. These dealt with the compilation and analysis of historical phenotypic data from the barley and wheat collections of IPK and, in particular, with the added value that even unbalanced data sets can offer.

The research group is involved in the (further) development of international standards, e.g. for phenotypic data and *in situ* data.

EMBEDDING IN IPK RESEARCH THEMES

The Genebank Information System forms the central infrastructure to support all processes related to the maintenance of gene bank accessions. During the reporting period, the research group processed and integrated accession-related data and made it available to various research projects. This will continue to be an important task within the framework of Research Theme 1 on the "Valorisation of Plant Genetic Resources". In cooperation with other bioinformatics groups of the institute, the activities of the research group are part of the strategy of transforming the Gene Bank into a bio digital Resource Centre.

OUTLOOK

The Genebank Documentation group will continue to operate and develop its well-established information systems, in particular GBIS and EURISCO, and strengthen cooperation within national and international information networks on PGR and biodiversity. The continuous curation and expansion of the Gene Bank's data sets is an ongoing task (incl. data stewardship) that is flanked by activities to measure data quality. A special focus will be on the work on the two EU Horizon 2020 projects AGENT and INCREASE as well as on the collaboration in the European Evaluation Network within the framework of ECPGR.

More information: *www.ipk-gatersleben.de/en/research/genebank/genebank-documentation*

RESEARCH GROUP **RESOURCES GENETICS AND REPRODUCTION** (RGR)

Head: Prof. Dr. Andreas Börner

MISSION

The research group is responsible for the management of the Gatersleben Gene Bank collection, which entails the long-term storage, multiplication and distribution of the germplasm comprising a wide spectrum of accessions representing most of temperate crop species. The major research focus concern seed longevity but also a comprehensive phenotypic 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 with the main focus on abiotic stress tolerance. In addition, material is used for various physiological and biochemical surveys in collaboration with partners within and outside of IPK.

RESULTS

The total number of accessions maintained at the Gatersleben site comprises 130,566 samples. Safety duplicates are available for 59,518 accessions (about 39% of the whole collection). They are kept at the Global Seed Vault, Svalbard, Norway. During the last 24 months 17,271 germination tests have been performed. The annual distribution comprises 12,471 (July 2019 – June 2020) and 17,217 (July 2020 – June 2021) accessions, excluding the External Branch. During the regeneration seasons 2019/2020 and 2020/2021 totals of 8,092 and 8,043 accessions, respectively, were cultivated including 481 and 609 samples grown for evaluation, demonstration and research only. Studies on the genetics of seed longevity were continued exploiting bi-parental mapping populations of durum wheat and tobacco. Examining seeds either untreated or after controlled deterioration quantitative trait loci were found for the traits under consideration which were distributed on several chromosomes. It was demonstrated that, as in many other species, germination-related traits are very complex and under polygenic control.

Research to improve the utilisation of gene bank collections is focused on agronomic and abiotic stress traits of cereals (wheat, barley, rye). A genetic analysis (GWAS) of post anthesis drought response of barley following chemical desiccation was performed using a panel of 183 accessions from 23 countries of the Gatersleben Gene Bank that were genotyped with a 9 K SNP chip. Plants were grown in the field in two consecutive years and post-anthesis drought stress was simulated by spraying 1% KI ten days after anthesis. The treatment caused a significant reduction in total biomass by 10.7%, in kernel number by 2.5%, in kernel weight per spike by 21.4% and in thousand kernel weight (TKW) by 16.7%. GWAS analysis revealed 97 significant MTAs associated with kernel number and kernel weight per spike and confirmed prominent regions such as 2H (18.9 cM), 6H (54.8 cM) and 7H (70.5-71.0 cM) for drought response. Drought tolerant barley accessions may be used as pre-breeding material to widen the genetic diversity of cultivated barley.

In collaboration with the research groups Assimilate Allocation and NMR, Structural Cell Biology and Gene and Genome Mapping the abiotic stress trait lodging was investigated exploiting the rye mutant ´Stabilstroh' ('stable straw') possessing an exceptional combination of high lodging resistance, tall posture, and high biomass production. Nuclear magnetic resonance imaging displayed the 3-dimensional assembly

Selected Publications

REHMAN ARIF, M.A. et al.: A SNP-based genetic dissection of versatile traits in bread wheat (Triticum aestivum L.). Plant J. 108 (2021) 960-976.

MUSZYNSKA, A. et al.: A mechanistic view on lodging resistance in rye and wheat: a multiscale comparative study. Plant Biotechnol. J. 19 (2021) 2646-2661.

RABANUS-WALLACE, M.T. et al.: Chromosome-scale genome assembly provides insights into rye biology, evolution and agronomic potential. Nat. Genet. 53 (2021) 564-573.

TIKHENKO, N. et al.: DEFECTIVE ENDOSPERM-D1 (Dee-D1) is crucial for endosperm development in hexaploid wheat. Commun. Biol. 3 (2020) 791.

TARAWNEH, R.A. et al.: Genome-wide association mapping reveals putative candidate genes for drought tolerance in barley. Environ. Exp. Bot. 180 (2020) 104237.

Additive QTLs

Trait	Nr of QTLs	Linkage groups
TG-C	3	6, 22, 24
TG-CD	2	1, 22
NG-C	2	7, 24
NG-CD	-	-
AUC-C	6	4, 12, 15, 18, 22, 24
AUC-CD	1	19
T50-C	6	4, 12, 15, 18, 22, 24
T50-CD	3	5,18,24

Epistatic QTLs

TG-C	4 pairs	3-3, 5-5,8-8, 24-24
TG-CD	1 pair	22-24

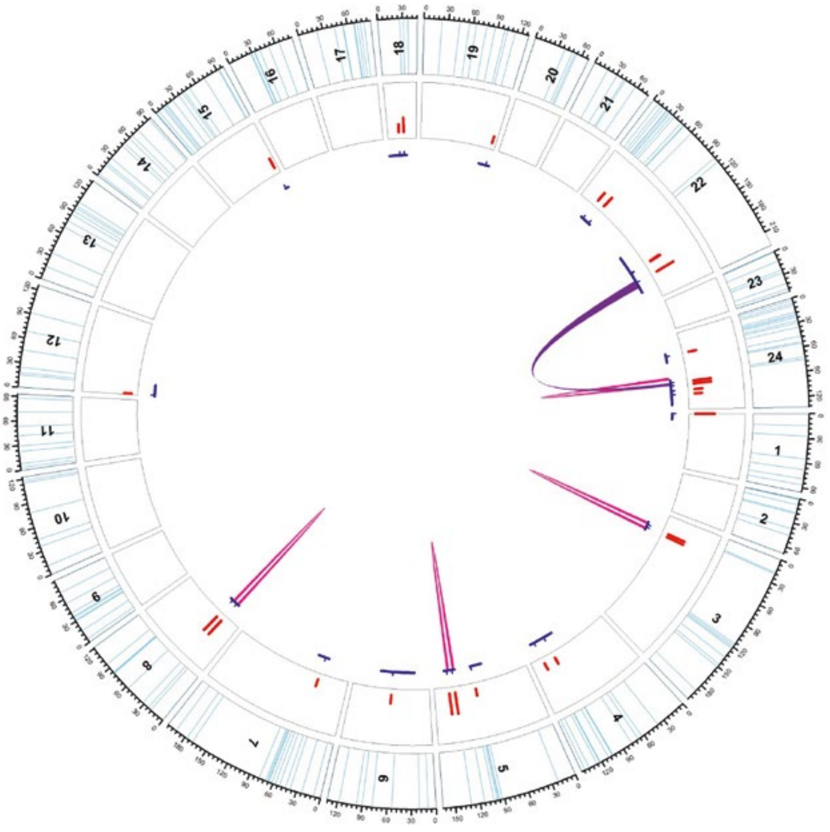


Figure. 1: *Distribution of additive (unconnected blue lines in the inner circle) and epistatic (connected blue lines in inner circle) QTLs. Skyblue lines in the outer track indicate the marker positions on each chromosome; red bars in the second circle indicate the LOD values of QTLs. The blue lines under the track circle indicate the confidence interval of QTLs with small vertical lines point to the peak position. The colored lines linked different biallelic epistasic QTLs (pink = TG-C; purple = TG-CD). Table on the left shows number of additive and epistatic QTLs detected. TG = total germination; NG = normal germination; AUC = area under the curve; T50 = time to reach 50% of TG; C = control; CD = controlled deterioration.*

of vascular bundles in stem. A higher number of vascular bundles and a higher degree of their incline were features of lodging-resistant versus lodging-prone lines. Histology and electron microscopy revealed that stems are fortified by a higher proportion of sclerenchyma and thickened cell walls, as well as some epidermal invaginations. Biochemical analysis using Fourier-transform infrared spectroscopy and inductively coupled plasma-optical emission spectrometry further identified elevated levels of lignin, xylan, zinc, and silicon as features associated with high lodging resistance.

EMBEDDING IN IPK RESEARCH THEMES

The research group is responsible for the management of the Gatersleben Gene Bank collection. This includes the long-term storage, multiplication, characterisation and distribution of the germplasm. The experimental work belongs to the IPK Research Theme 1 " Valorisation of Plant Genetic Resources ". In collaboration with other research groups within the Genebank department but also in other departments of the IPK we use Gene Bank accessions for phenotypic and genetic investigations.

OUTLOOK

Studies on seed storability will be the main focus of the research. In addition to genetic analyses, seed material will be also used for various physiological and biochemical surveys. Furthermore, we plan to continue the biophysical investigations to model the relationship between seed viability, vigour, dormancy and longevity with delayed luminescence utilising artificial aged and long-term stored seeds. In cereals (wheat, barley, rye) bi-parental mapping populations and association mapping panels have been established. They will be used for further genetic analyses of agronomic traits with major emphasis on abiotic stress tolerance (drought, pre-harvest sprouting, lodging).

More information: *www.ipk-gatersleben.de/en/research/genebank/resources-genetics-and-reproduction*

RESEARCH GROUP
CRYO AND STRESS BIOLOGY (CSB)

Head: PD Dr. Manuela Nagel

MISSION

The research group conserves part of the clonal collections of the Federal *Ex situ* Gene Bank and examines the effects of long-term storage and conservation procedures, especially for desiccation sensitive organs. Overall, 236 accessions of mint, Brassica, and antirrhinum are maintained/distributed as *in vitro* culture. In parallel, for long-term preservation, 1,902 potato, 157 mint and 239 *Allium* accessions are stored at 196°C and represent one of the world's largest cryocollections. To preserve high tissue quality and viability of unique resources, research includes studies on stress mechanisms following desiccation and ultra-low temperatures as well as the complex interaction with endophytic microorganisms.

RESULTS

Wheat pollen viability and storability

Wheat sheds tricellular pollen which loses viability rapidly. After storage for 60 min under 23°C and low relative humidity (R-L), pollen germination decreased to 1.1 ± 2.2% and lost around 94% of the initial water content including visual changes in the pollen ultrastructure. Compared to three other lines, TRI 9102 produced one of the most resistant pollen which accumulated highest amounts of hexanedioic acid, pipecolate and lysine. When this pollen was exposed to R-L for different durations, proline, leucine, GABA, glycerol, sucrose and glucose showed strongest increase. To test different hypothesis about the storage of desiccation sensitive pollen, and to get a deeper understanding about wheat pollen viability, we applied new concepts of fast- and slow-drying and -cooling. To evaluate different aspects of drying and freezing, we used Impedance-Flow-Cytometry (Pollen viability measurements), Differential Scanning Calorimetry (Heat flow measurements) and Video-cryomicroscopy (Cooling behaviour and ice crystallization). A final combination of fast drying, fast cooling and warming rates during video-cryomicroscopy resulted in less ice crystal formation, a reduction of the temperature for intracellular water crystallisation, and an increase in the temperature of intracellular ice melting (Figure 1). All three properties may favour the formation of intracellular glasses and could contribute to the development of technical solutions for wheat pollen preservation which are urgently needed in wheat hybrid breeding and for the preservation of wheat genetic resources.

Biochemical changes during cryopreservation of potato and garlic shoot tips

PVS3 droplet vitrification is used for all species cryopreserved at IPK and induces a series of complex stress response mechanisms that affect the regenerative capacity of shoot tips. In both, garlic and potato shoot tips, sucrose concentration gradually increases during the process of shoot excision, pre-culture and cryoprotection. In parallel, adenosine triphosphate (ATP) and the activity of antioxidant enzymes (APX, GR, CAT) gradually decrease. Transcriptional analysis of garlic shoots revealed that the number differentially expressed genes (DEGs) decreased in garlic shoot tips from 608 DEGs during pre-culture to 273 DEGs during cryoprotection. Once the shoot tips were rewarmed, rehydrated and recovered, 1,293 DEGs were observed, accounting for increased levels of DNA binding and transcription factor activities, and increased levels of ATP and antioxidative enzymes. To improve the success of cryopreservation of potato and garlic shoot tips, further analyses of genotype differences and the effects of environmental and microbial contamination are planned.

Transcriptional and posttranslational regulation after cryoprotection in Arabidopsis.

Transcriptome analysis of Arabidopsis shoot tips undergoing cryopreservation re-

Selected Publications

BAJERSKI, F., M. NAGEL* & J. OVERMANN: Microbial occurrence in liquid nitrogen storage tanks: a challenge for cryobanking? Appl. Microbiol. Biotechnol. 105 (2021) 7635-7650. * joint first authorship*

IMPE, D. et al.: Assessment of pollen viability for wheat. Front. Plant Sci. 10 (2020) 1588.

PANIS, B., M. NAGEL* & I. VAN DEN HOUWE*: Challenges and prospects for the conservation of crop genetic resources in field genebanks, in in vitro collections and/or in liquid nitrogen. Plants 9 (2020) 1634. * joint first authorship*

STOCK, J. et al.: The transcription factor WRKY22 is required during cryo-stress acclimation in Arabidopsis shoot tips. J. Exp. Bot. 71 (2020) 4993-5009.

WIEBACH, J. et al.: Age-dependent loss of seed viability is associated with increased lipid oxidation and hydrolysis. Plant Cell Environ. 43 (2020) 303-314.

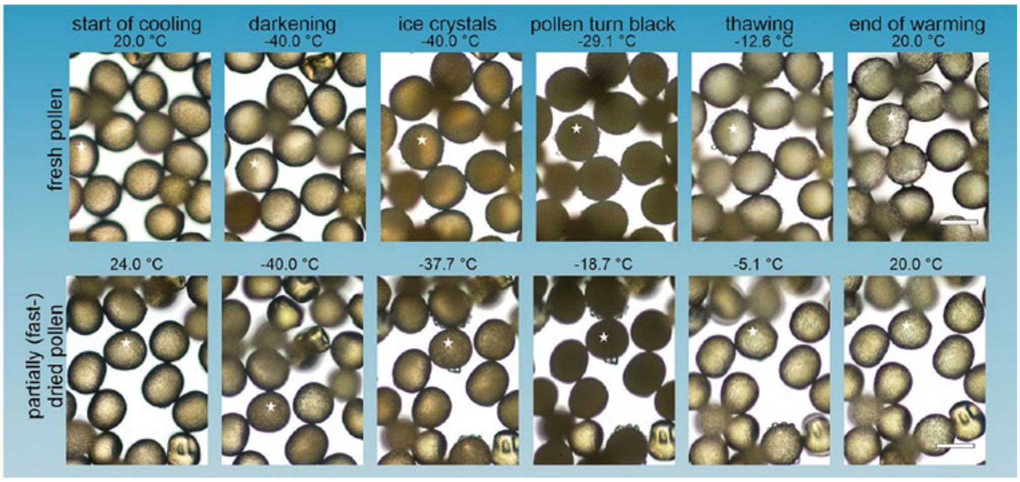


Figure 1. *Structural changes in wheat pollen that occur at different temperatures during fast cooling. Fresh pollen, pollen partially fast dried for 5 minutes and pollen air-dried to water contents below the unfrozen water content for 60 min were used. Due to movements in the Linkam chamber, for better orientation we marked the same pollen in each series (row) with a star. Scale bars indicate 50 µm, size and magnification were identical for all images. Source Impe et al. (2022). Plant Cell Reports. doi. org/10.21203/rs.3.rs-809031/v1*

vealed that the majority of changes appeared during the dehydration/cryoprotection step. The cryoprotectant induces changes in the primary metabolism, RNA processing and RNA methylation, which led to the degradation of meristematic cells. Here, transcription factors (TFs) of the AP2-EREBP family including DREBs/CBFs are up-regulated after dehydration/cryoprotection. The inactivation of CBF1 and CBF3 compromised the recovery of cryopreserved explants. Interestingly, about 29 RNA methyltransferases (out of 59 in total), that contain a CBF motif in the promotor sequence, are significantly up- or down-regulated in Arabidopsis Col-0 during cryoprotectant treatment. Therefore, the term 'RNA methylation' was found to be significantly represented in the GO analysis of DEGs during cryopreservation. Wienken *et al.* (2011) indicated that methylated regions of dsDNA and RNA affected the double strand hybridisation stability. The methylation lowers the melting temperature of RNA/DNA and may inhibit the ds formation. As dsRNA is immediately processed by the DICER enzyme followed by post-transcriptional gene silencing processes, methylation have an influence on RNA stability and translation. Therefore, we assume that DREBs/CBFs TFs are directly involved posttranslational regulation and stress response mechanisms after cryopreservation which will be further studied.

EMBEDDING IN IPK RESEARCH THEMES

The research group Cryo- and Stress Biology and Experimental Taxonomy evaluate garlic genetic resources within Research Theme 1 "Valorisation of Plant Genetic Resources". Studies on wheat pollen viability are in collaboration with the research group Plant Architecture and Quantitative Genetics in Research Theme 3 "Mechanism of Plant Reproduction". Cryo and Stress Biology contributes to the Research Theme 5 "Mechanisms of Resistance and Stress Tolerance" by investigating complex stresses during cryopreservation and collaborates with Applied Biochemistry, Structural Cell Biology, Heterosis, Phytoantibodies. Furthermore, Cryo and Stress Biology coordinates material exchange, field multiplication and data management to back-up and cryopreserve vegetatively propagated accessions within the Genebank department (Resources Genetics and Reproduction, Satellite Collections North, Experimental Taxonomy, Genebank Documentation) and is supported in LIMS data management by the research group Bioinformatics.

OUTLOOK

Cryopreservation is the only approach to conserve desiccation sensitive organs and clonal Plant Genetic Resources over extended periods of times. Challenges include maintaining high tissue viability, adapting protocols for relevant new organs, i.e. cereal pollen, and species such as *Allium*, *Lemna* and *Dioscorea* species and the unknown number of duplicate accessions. To support duplicate management decisions, genotyping-by-sequencing (GBS) has been initiated for 510 garlic and shallot accessions and the results will provide further potential for investigating metabolic pathways, evolutionary effects on seed development and breeding opportunities. In addition, the participation in COST action CA19125 "EpiCATCH" will support studies of the posttranslational regulations which will be further addressed for the model plant Arabidopsis, cereal pollen and cryopreserved tissues.

More information: *www.ipk-gatersleben.de/en/research/genebank/cryo-and-stress-biology*

RESEARCH GROUP
SATELLITE COLLECTIONS NORTH (TEN)

Head: Dr. Klaus J. Dehmer

MISSION

At IPK Gross Luesewitz and Malchow/Poel, we maintain Plant Genetic Resources of more than 21,000 accessions of potatoes, oil and forage crops. Our collection-based research focuses on the phenotypic and genotypic diversity encompassed in our Plant Genetic Resources (PGR), especially in relation to traits like nutrient efficiency. Furthermore, we analyse resistance/tolerance to drought and diseases, as well as the activation of recalcitrant seeds via cold plasma treatment – all in order to maximise the level of accession-specific information available.

RESULTS

Phenotyping in wild potatoes, fodder legumes and ryegrass

Analysing the data of 1,055 wild potato accessions for resistance to tuber late blight identified 68 entries with high and 311 with partial resistance. Besides in accessions of species well-known for it, resistance to tuber blight was also observed in previously less reported species like *S. fendleri*, *S. polytrichon*, and others.

Evaluations of pale cyst nematode resistance identified 78 out of 749 wild potato accessions as resistant. New/less reported sources of resistance were found in *S. brevicaule*, *S. demissum* and *S. microdontum*. In various accessions of different species, combined resistance to tuber late blight and *G. pallida* was observed.

Tuber starch content in wild potato accessions ranged from 7% to 36% of fresh weight. Promising wild species regarding elevated tuber starch contents were *S. chacoense*, *S. commersonii*, *S. jamesii*, and *S. pinnatisectum*. Several genotypes were identified as combining high tuber starch content and high N utilisation efficiency.

Phosphorus use efficiency was studied in 200 cultivated potatoes. Genotypes were identified combining high shoot and root biomass formation with high P uptake under both optimal and reduced P supply (Figure 1).

Triennial analyses of 41 ecotypic *Lolium* populations from an EU project identified nine populations with superior agronomic performance. Based on field phenotyping results, hierarchical clustering separated nine populations from northern Germany, Belgium and France from the others. The former combine low winter damage with strong vigour, large plant height, tussock size and a high amount of ear producing tillers. Vigour after planting, winter damage as well as aftermath heading revealed a strong relation to geographic origin/bioclimatic variables at the sampling sites.

F1 progenies of 14 *L. perenne* crossing populations (tolerant x tolerant and susceptible x tolerant) were evaluated for drought tolerance in the field and in rainout shelters for two years at two sites. An increasing differentiation became visible: while most crossing populations revealed a high share of weak or dead plants, the best still exhibited a high number of medium to very vital plants at the end of the trial. The most tolerant genotypes were selected, multiplied and added as new, drought tolerant accessions to the IPK collection.

Collection management and enhanced evaluations

At Gross Luesewitz, 6,315 potato accessions from 140 tuber bearing *Solanum* species are maintained. The collections at Malchow/Poel comprise 14,985 oil and fodder crop entries from18 genera and 132 species.

In 2020 and 2021, 3,327 accessions were provided to 202 users. Germination rates were determined for 13,390 seed lots, and 14,486 or 82% of the seed propagated accessions are saved at the Svalbard Global Seed Vault. 1,902 potato accessions are cryopreserved at IPK Gatersleben (cooperation with CSB).

7,455 of the accessions were multiplied and partially phenotyped. At Malchow, C&E data were collected for 1,150 entries. Evaluations of Gross Luesewitz potato acces-

Selected Publications

BACHMANN-PFABE, S. & K.J. DEHMER: Evaluation of wild potato germplasm for tuber starch content and nitrogen utilization efficiency. Plants 9 (2020) 833.

BLANCO-PASTOR, J.L. et al.: Canonical correlations reveal adaptive loci and phenotypic responses to climate in perennial ryegrass. Mol. Ecol. Resour. 21 (2021) 849-870.

KAVKA, M. et al.:: Potato root and leaf phosphatase activity in response to P deprivation. J. Plant Nutr. Soil Sci. 184 (2021) 668-677.

KEEP, T. et al.: To grow or survive: Which are the strategies of a perennial grass to face severe seasonal stress? Funct. Ecol. 35 (2021) 1145-1158.

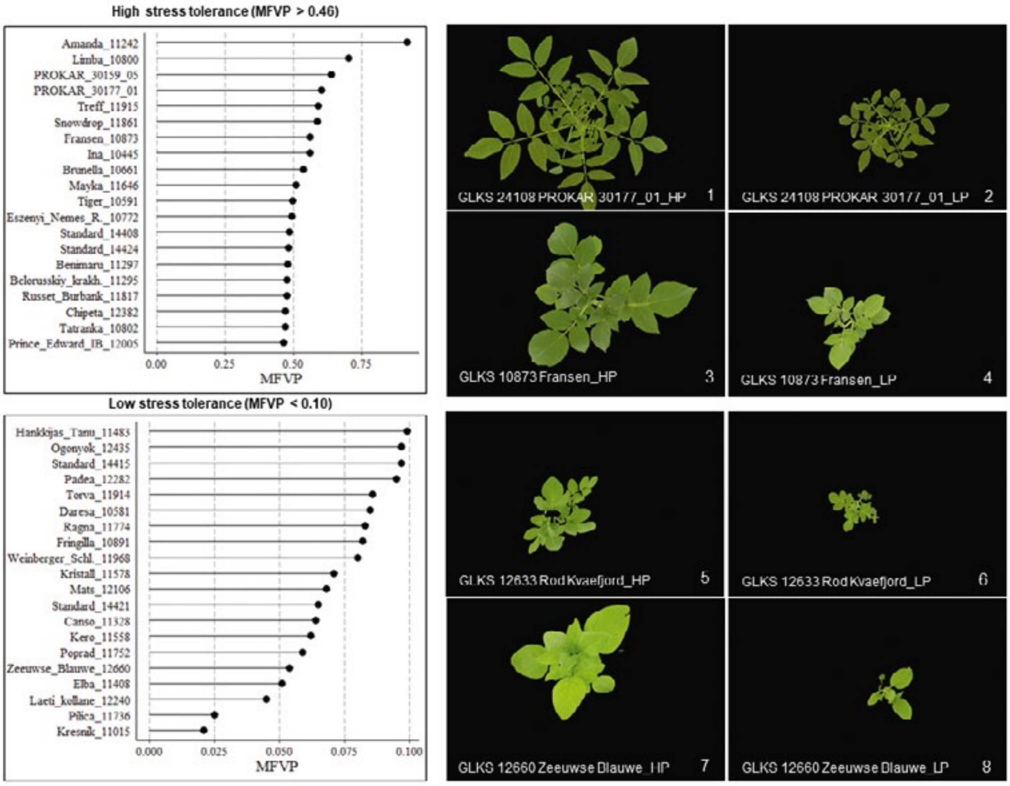


Figure 1: *Membership function value (MFVP) for P stress tolerance according to Chen et al., 2012 of the 20 best and 20 worst performing GLKS genotypes. Data are based on greenhouse screening under high P (HP) and low P (LP) conditions and on the differences in shoot and root dry weight, total dry weight and P uptake; top view pictures on the left depict two of the best (1-4) and two of the worst (5-8) performing genotypes under HP and LP. (Hazarika and Bachmann Pfabe, 2021)*

sions were performed for resistance to *Globodera pallida* (11 accs./55 genotypes; BioTestLabor Sagerheide) and to potato wart (127 accs.; JKI/A), as well as for tuber dormancy (248 accs.). Results are available upon request.

EMBEDDING IN IPK RESEARCH THEMES

By focusing on potatoes, oil and fodder crops, research at TEN integrates perfectly into IPK's Research Theme 1 "Valorisation of Plant Genetic Resources" and broadens the knowledge on the species studied. Via major contributions of C&E data to both GBIS and EURISCO and via constantly enhancing the information available on our germplasm, we strive to pheno- and genotype our accessions as comprehensively as possible, adding to the over-all goal of a bio digital Resource Centre.

OUTLOOK

In order to assess traits of increasing relevance in the future, we will phenotype our accessions for nutrient efficiency and drought tolerance. Special attention will be paid to the potato PGR, where we plan a comprehensive screening of the clonal entries for traits like tuber quality and biotic resistances.

TEN seed and *in vitro* management will continuously be improved. Here, cold plasma treatment should help to activate seed lots with low germination rates or improve early seedling vigour. In combination with the introduction of an image-based germination testing, this will further ensure the high quality of the seeds stored and distributed.

For a sustainable conservation management meeting international standards, activities are initiated to advance infrastructure and to increase staffing for TEN. This will not only warrant a continued high quality conservation of PGR, but also permit an intensified, application-oriented research.

More information: *www.ipk-gatersleben.de/en/research/genebank/satellite-collections-north*

RESEARCH GROUP
EXPERIMENTAL TAXONOMY (ETX)

Head: Dr. Frank R. Blattner

Selected Publications

BERNHARDT, N., J. BRASSAC* et al.: Genome-wide sequence information reveals recurrent hybridization among diploid wheat wild relatives. Plant J. 102 (2020) 493-506. * joint first authorship*

Merklinger, F.F. et al.: Population genomics of Tillandsia landbeckii reveals unbalanced genetic diversity and founder effects in the Atacama Desert. Global Planet. Change 184 (2020) 103076.

ŽERDONER ČALASAN, A. et al.: Pleistocene dynamics of the Eurasian steppe as a driving force of evolution: Phylogenetic history of the genus Capsella (Brassicaceae). Ecol. Evol. 11 (2021) 12697-12713.

RUBAN, A. et al.: Supernumerary B chromosomes of Aegilops speltoides undergo precise elimination in roots early in embryo development. Nat. Commun. 11 (2020) 2764.

SASSONE, A.B. et al.: Genomic, karyological, and morphological changes of South American garlics (Ipheion) provide insights into mechanisms of speciation in the Pampean region. Mol. Ecol. 30 (2021) 3716-3729.

MISSION

The group focuses on the phylogenetic classification and evolution of crops and their wild relatives and is therefore an important part of the Research Theme 2 “Genome Diversity and Evolution”, of the IPK research strategy. We use experimental studies to link molecular markers and phylogenetic data with ecological, cytogenetic 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.

RESULTS

Within a DFG project aiming at clarifying the phylogeny of di- and polyploid Triticeae we used hybridisation-captured gene sequences and genotyping-by-sequencing (GBS) data to infer the evolution of wheat (*Triticum*) and closely related genera (*Aegilops*, *Amblyopyrum*). Phylogenetic analyses and estimations of inter-species gene flow (hybridisation, introgression) arrived at the hypothesis that hybridisation of early members of the Triticum and *Amblyopyrum* lineages gave rise to all diploid *Aegilops* species with the exception of *Ae. speltoides* that seems to be an old but independent lineage. Our analysis implies that throughout wheat wild relatives – even at the diploid level – the genomes of most taxa must consist of a mixture of genome parts, which are shared among several today (mostly) independent species.

In *Hordeum* we currently clarify the evolution of *Hordeum bulbosum*, the closest relative of *H. vulgare*. Collections of the populations thriving in the Mediterranean were conducted during the last years. Genome size analyses showed that in Greece diploid (West Mediterranean) and autotetraploid (East Mediterranean, Levant and West Asia) cytotypes of the species are in contact. GBS-based phylogeographic analyses shows that the species originated most probably in the area of todays southernmost Italy/adjacent North Africa from where it spread to the eastern coast of the Adriatic Sea and through Sicily into the western Mediterranean. The tetraploid cytotype originated in Greece and colonised from there the Aegean Archipelago and South-West Asia. The materials we collected are now used to obtain a reference-quality genome of *H. bulbosum* (together with the research groups Domestication Genomics, Genomics of Genetic Resources and Chromosome Structure and Function).

Within a DFG-funded project we were able to uncover the evolution of saffron (*Crocus sativus*), as a segmental allopolyploid that originated within *C. cartwrightianus*, a crocus species from Greece and the Aegean Islands. Analyses of metabolites (together with the research group Applied Biochemistry) and transcriptomes showed that the wild populations in Attica are most similar to cultivated saffron regarding carotenoid content and gene expression. Based on a new resolved multi-locus phylogeny of all

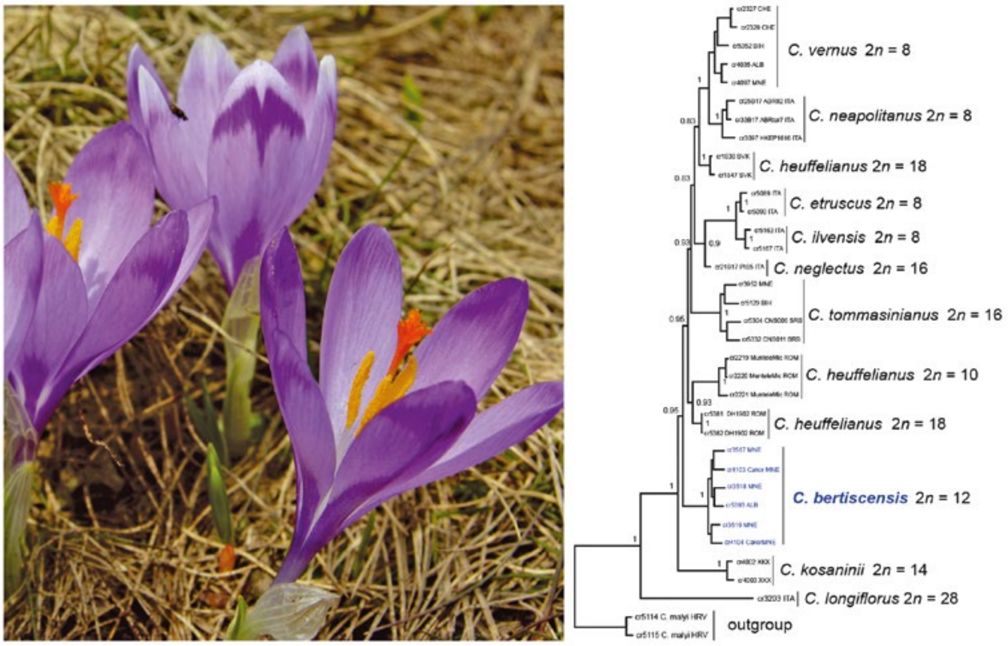


Figure 1: *The newly discovered species Crocus bertiscensis from Montenegro and northern Albania (left) and a GBS-derived phylogenetic tree (right) of the species of Crocus series Vernus that indicate the relationships of the new species to its closest relatives. The name of the species refers to Berticus, an ancient Greek term for the mountain system where the species occurs. Photo: L. Shuka.*

crocuses we now work to finally arrive at a new systematic treatment of the genus that will reflect the evolutionary history of the taxa much better than the artificial system still in use.

The Eurasian steppe belt is the largest area on Earth with steppe vegetation. To understand the evolution of this vegetation unit in space and time we analysed together with groups in Osnabruck, Vienna and Barnaul multiple key species of the steppe. We use population genomic analyses to infer migration routes, cold- vs. warm-period refugia, ages of the taxa and their colonisation routes. Our results indicate that for many species, populations mirror the extension of the steppe habitat from east to west indicating migration with the Pliocene westward expansion of the steppe climate. However, there are also species, which used relatively recently the newly formed steppe belt as a "highway" for their very fast expansion eastwards.

The herbarium of the IPK currently holds a collection of about 450,000 specimen copies, with additional 109,000 samples in the seed and fruit collection and 56,000 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 were included. Thus, the herbarium is an integral part for documenting biodiversity-related research within the IPK. Specimens of crops and wild plants of the IPK herbarium have been digitised and are online accessible 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 IPK RESEARCH THEMES

Our work is mostly connected to Research Theme 2 "Genome Diversity and Evolution". Here we contribute to the IPK flagship project on the evolution of *Hordeum bulbosum*, the pan-*Hordeum* project, and the ERC project on phylogenomics of the genus *Hordeum*.

OUTLOOK

We contribute with our experience in phylogeographic analysis in an DFG Collaborative Research Centre of the universities of Cologne and Bonn dealing with organismic evolution at the dry limit, mostly conducted in the Atacama desert (DFG-SFB 1211). In addition, we will establish certain groups of crocuses as model for the study of disploidy and karyotype evolution (DFG funding was just approved). This topic will also be approached by Agostina Sassone (a Humboldt Fellow) who studies *Nothoscordum* species (American relatives of *Allium*), which show highly dynamic karyotypes. We plan to start taxonomic research in Apiaceae, where many crops are used for multiple purposes, like seed, tuber and leaf consumption. An initial project on coriander domestication is currently drafted with Israeli colleagues.

More information: *www.ipk-gatersleben.de/en/research/genebank/experimental-taxonomy*

RESEARCH GROUP
DOMESTICATION GENOMICS (DG)

Head: Dr. Martin Mascher

MISSION

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. Key research goals are: (i) elucidating the relationship between crops and their extant wild relatives and progenitors; (ii) tracing the demographic development and adaptation of cereal crops as they expanded their range from the initial site of domestication into Europe; (iii) understanding the molecular consequences of domestication on patterns of nucleotide diversity, gene expression and gene regulation. Towards these aims, we apply methods of population genetics and genome informatics. We are also involved in the development of genomic infrastructures for several crops and their wild relatives.

RESULTS

Our on-going gene bank genomics work has laid the basis for the informed selection of the most representative germplasm for pan-genomic studies. Pan-genome sequence assembly in barley and wheat was done with a computational pipeline developed by the research group. Combining several tools and workflows developed over the past five years, we have developed TRITEX, an open-source computational pipeline for constructing chromosome-scale sequence assemblies of Triticeae genomes. The first application of the TRITEX pipeline was the assembly of a much-improved genome sequence for the barley reference cultivar Morex. Subsequently, we applied TRITEX to assemble genomes of 20 diverse barley genotypes to develop the first-generation pan-genome of barley in close collaboration with research groups Genomics of Genetic Resources and Bioinformatics and several national and international partners. As a complement to genome assembly, we have used chromosome conformation capture sequencing (Hi-C) to discover polymorphic inversions in a panel of 69 barley genotypes. In frame of international consortia, we are applying our TRITEX pipeline to assemble the genomes of cereal crops and their wild relatives. These include rye (Secale cereale), oat (Avena spp.), and wild taxa in the genera Hordeum, Triticum and Aegilops.

In 2020, we reworked the TRITEX pipeline to include accurate long-reads (PacBio HiFi). HiFi reads greatly increased the contiguity of the assemblies and improved their representation of intergenic space. At same time, cost and effort required for genome assembly decreased. The long-read sequencing approach is now routinely applied in wheat and barley. In the second phase of the barley pan-genome project, we are currently assembling 40+ genomes of wild and domesticated barley.

Together with the research group Chromosome Structure and Function and international partners at the Institute of Experimental Botany in Olomouc (Czech Republic), we are currently analysing the three-dimensional conformation of barley chromosomes along the cell cycle based on chromosome conformation capture sequencing (Hi-C) and fluorescence *in situ* hybridisation (FISH). This research is supported by the bi-national DFG-GACR project 'MITOCHROM'. The barley reference genome enabled the design of oligonucleotide probes that can label long contiguous stretches of chromatin. FISH results confirmed a high-level organisation of chromatin into helical turns comprising ~30 Mb of sequence, as suggested by Hi-C analyses. Biophysical models based on polymer simulations enabled the development of a uniform conceptual framework to harmonise microscopic observations and Hi-C contact matrices. This modelling approach was used to propose a simple model for the condensation of mitotic chromosomes in holocentric species.

Selected Publications

JAYAKODI, M. et al.: The barley pan-genome reveals the hidden legacy of mutation breeding. Nature 588 (2020) 284-289.

MASCHER, M. et al.: Long-read sequence assembly: a technical evaluation in barley. Plant Cell 33 (2021) 1888-1906.

CÂMARA, A.S. et al.: A simple model explains the cell cycle-dependent assembly of centromeric nucleosomes in holocentric species. Nucleic Acids Res. 49 (2021) 9053–9065.

HAAS, M. et al.: The contribution of cis- and trans-acting variants to gene regulation in wild and domesticated barley under cold stress and control conditions. J. Exp. Bot. 71 (2020) 2573-2584.

WALKOWIAK, S. et al.: Multiple wheat genomes reveal global variation in modern breeding. Nature 588 (2020) 277-283.

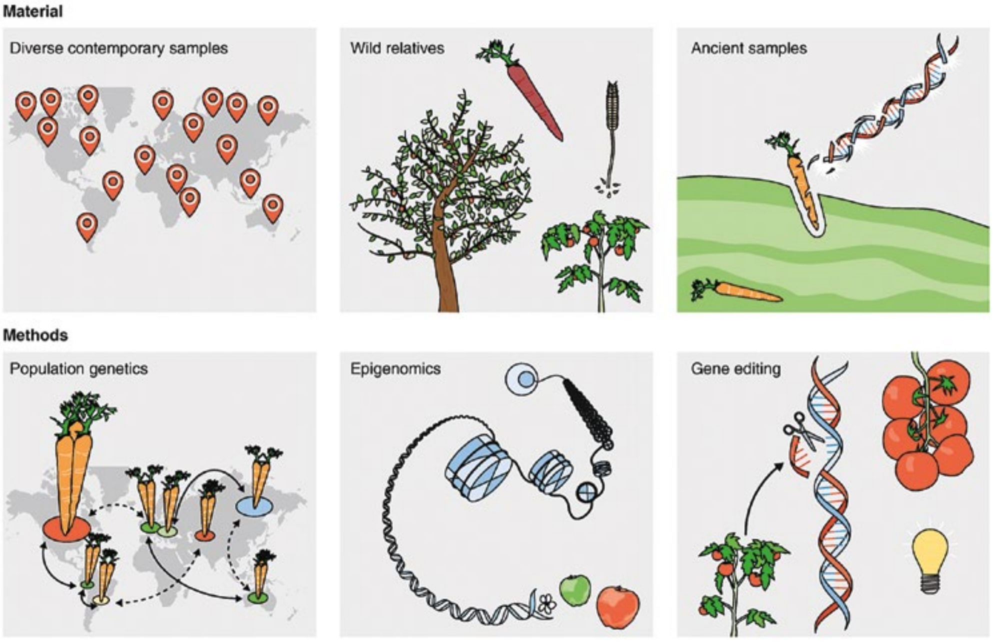


Figure 1: *Topics in domestication genomics. The study of crop evolution will continue to rely on the population genetic analysis of diversity panels comprising domesticates and their wild relatives. If well-preserved archaeobotanical remains are available, ancient samples can serve as a time-capsule informing about past demography of a crop. Moreover, new approaches such as epigenomics and gene editing complement the toolbox of domestication research.*

EMBEDDING IN IPK RESEARCH THEMES

Our research on population genomics of cereal crops and their wild relative in context of IPK's Gene Bank collection contributes to Research Theme 2 "Genome Diversity and Evolution" and Research Theme 1 "Valorisation of Plant Genetic Resources". We contribute to in-depth molecular characterisation of Plant Genetic Resources and to developing means for leveraging genotypic passport for gene bank management. The research group Domestication Genomics is coordinating the IPK flagship project on establishing genomic resources in *Hordeum bulbosum*, the closest wild relative of barley.

OUTLOOK

We will conduct species-wide population genomics of wild and domesticated barley and wheat using sequence assemblies and resequencing data. A PhD student is currently running demographic analyses to understand the historic relationships between barley populations and to assess the relative strengths of bottlenecks as barley moved out of the Fertile Crescent. In cooperation with the Plant Architecture group and Israeli partners, we will study crop-wild hybrids focusing on six-rowed wild-growing barley from Israel and Central Asia, which likely arose by spontaneous hybridisation between wild and domesticated genotypes.

We will extend our genomic methodology to minor crops and wild relatives and participate in international sequencing consortia for rye, oats and wild wheat. This research is currently supported by (i) an IPK flagship project on the genomics of *Hordeum bulbosum*, the closest wild relative of barley, and (ii) an ERC Starting Grant to explore the prospects of genomic-assisted mobilization of the tertiary genepool of barley. Building on our existing network of the barley and cereal research community, we have initiated the Pan-Hordeum consortium to construct a genus-wide pangenome of *Hordeum* from annotated chromosome-scale assemblies of all 21 diploid species in the genus.

We have also initiated PanOat, a pan-genome project of oat (*Avena* spp.) with the goals (i) to study genome evolution in this genus comprising both diploid, tetraploid and hexaploid taxa, and (ii) to provide a genomic research infrastructure to the oat community on a par with those of wheat and barley. At the time of writing, ~25 of a project of 32 Avena assemblies have been completed.

More information: *www.ipk-gatersleben.de/en/research/genebank/domestication-genomics*

DEPARTMENT BREEDING RESEARCH

BREEDING
RESEARCH

QUANTITATIVE GENETICS (QD)

Prof. Dr. Jochen C. Reif

BIOINFORMATICS AND INFORMATION TECHNOLOGY (BIT)

Dr. Uwe Scholz

CHROMOSOME STRUCTURE AND FUNCTION (CSF)

Prof. Dr. Andreas Houben

KINETOCHORE BIOLOGY (KB)

Dr. Inna Lermontova

BIOTROPHY AND IMMUNITY (BIM)

Dr. Dimitar Douchkov

GENE AND GENOME MAPPING (GGK)

Dr. Marion Röder

SENIOR GUEST GROUP (EMERITUS GROUP): KARYOTYPE EVOLUTION (KTE)

Prof. Dr. Ingo Schubert

DEPARTMENT BREEDING RESEARCH

Head: Prof. Dr. Jochen Reif

MISSION

Plant 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 creation of genetic variation, through the identification of parental material to the selection of superior genotypes and maintenance breeding. This is done with a focus on breeding informatics, chromosome biology, and genome analysis.

RESEARCH STATUS

The research activities of the department of Breeding Research ranged from work in chromosome biology, e.g. on the development of a model for the cell cycle-dependent assembly of centromeric nucleosomes in holo- and monocentric species or on the deeper understanding of factors involved in chromosome elimination, to pioneering work on the use of Big Data in plant breeding and the development of bioinformatics methods for the implementation of FAIR data management. The Breeding Research department contributes with its work to all five interdepartmental Research Themes of the IPK. According to the research activities, the research groups are divided into the three programmes Breeding Informatics, Chromosome Biology, and Genome Analysis.

There were several personnel and structural changes during the reporting period. The head of the research group Biotrophy and Immunity, Dr. Armin Djamei, accepted an appointment to a professorship at the University of Bonn on 01.10.2020. Interim head is Dr. Dimitar Douchkov. Dr. Marion Röder retired at the end of March 2021 and the research group Gene and Genome Mapping was suspended. On February 01, 2020, the research group Kinetochore-Biology was established by Dr. Inna Lermontova.

RESEARCH HIGHLIGHTS

The following scientific achievements
are considered as highlights in 2020/2021:

Programmed elimination of chromosomes exists in plants

Not all cells of an organism necessarily contain identical genomes. Some eukaryotes show dramatic differences between cells of different organs due to programmed elimination of chromosomes. In cooperation between the research groups Chromosome Structure and Function, Bioinformatics and Information Technology and other groups of the IPK, the first analysis of programmed chromosome elimination was presented in plants. Using the goatgrass *Aegilops speltoides* as a model, it was demonstrated that the elimination of supernumerary B chromosomes is a strictly controlled and highly efficient root-specific process (Figure 1). At the onset of embryo differentiation, B chromosomes undergo elimination in proto-root cells. Independent of centromere activity, B chromosomes undergo nondisjunction of chromatids and anaphase lagging, leading to micronucleation. The degradation of micronucleated DNA is the final step of B chromosome elimination. This process might allow root tissues to survive the detrimental expression or overexpression of B chromosome-located root-specific genes. Future understanding of the molecular mechanism behind tissue and chromosome type-specific cohesion dysfunction may provide clues about the process of chromosome nondisjunction, which is a major cause of genetic diseases across species, but also could result in novel biotechnological applications.

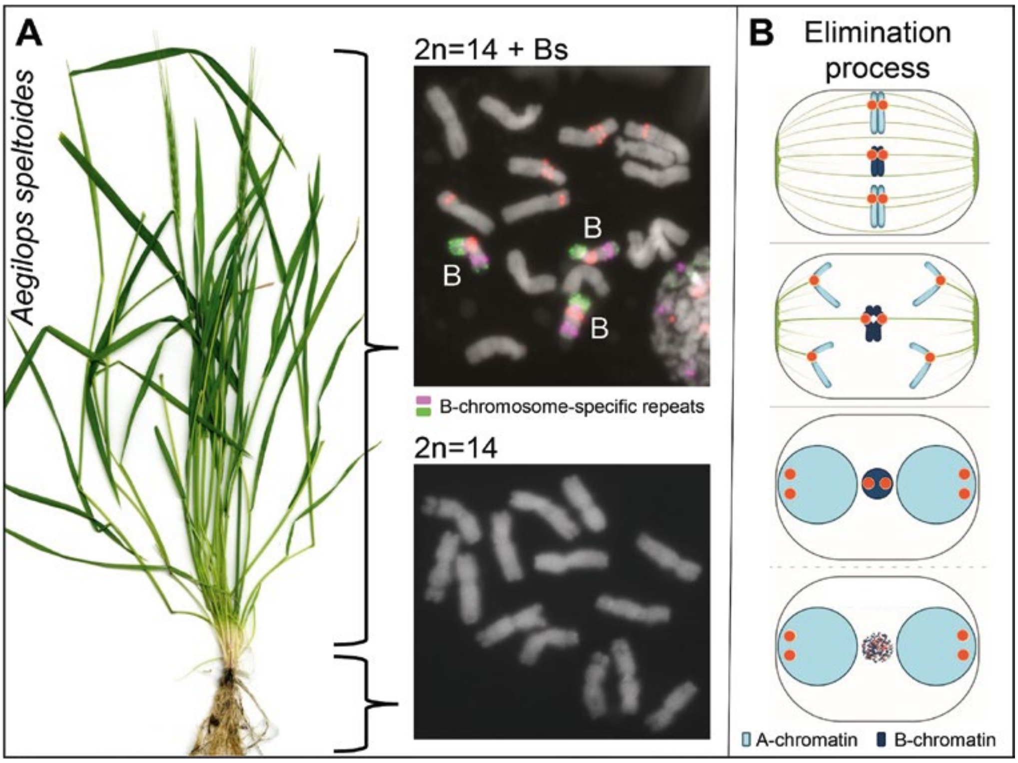


Figure 1: *Aegilops speltoides performs programmed chromosome elimination during early embryogenesis. (A) It may carry up to eight supernumerary B chromosomes which are absent in the roots but stably present in the plant parts above ground in the same individual. B chromosomes are labelled by FISH using B-specific probes. (B) The step-wise process of B chromosome elimination. B chromosomes fail to separate their chromatids and linger at the cell equator during mitotic divisions at the early stage of embryo development. At anaphase, in contrast to the separated A chromatids, the chromatids of B chromosomes remain cohesive, likely due to a delayed release of sister chromatid cohesion. Finally, lagging B chromosomes form micronuclei and undergo complete elimination (Ruban et al. 2020).*

Publication of sequencing data in international repositories with maximal FAIRness enables a reuse

In many central research projects of the IPK, extensive sequence resources, so-called Next-Generation Sequencing data (NGS), are generated and analysed. The raw sequence data must be made accessible in public databases such as EMBL-ENA. The basic requirement for this is a detailed description with metadata that must be recorded during the sequence generation. Together with colleagues from the German Network for Bioinformatics Infrastructure (de.NBI) from various life science areas, different data management services were evaluated in form of self-assessments using the FAIR criteria and published in the journal "Briefings in Bioinformatics", see https://dx.doi.org/10.1093/bib/bbab010. Here, the NGS data flow process executed at IPK was evaluated regarding FAIRness and described in three steps: sequencing in the laboratory (step 1), transfer into the IPK Laboratory Information Management Systems (LIMS) as a generic data backend (step 2), and feeding into the EMBL-ENA repository (step 3). Using this pipeline, the BIT group registered sequencing projects for 10 different IPK research groups and external partners in ENA. The number of projects in ENA has increased from 58 in 2020 to 84 in 2021. A total of 27 terabytes of raw read files and 84 gigabytes assembly data have been submitted in 2020. In 2021 submitted data volumes were increased (43 terabytes raw data and 90 gigabytes for 59 assemblies' project) illustrating a persisting use (see summarised in Figure 2).

Unlocking the potential of Big Data for hybrid wheat breeding

Hybrid wheat breeding is a promising way to increase yield and yield stability. A major bottleneck in the successful implementation of hybrid breeding is the lack of efficient methods to predict the best crosses. Genome-wide selection is a promising tool to achieve this, but requires large populations to train predictive models that accurately predict the performance of hybrids with a low degree of relatedness to the training population. Therefore medium-sized hybrid wheat datasets generated over more than a

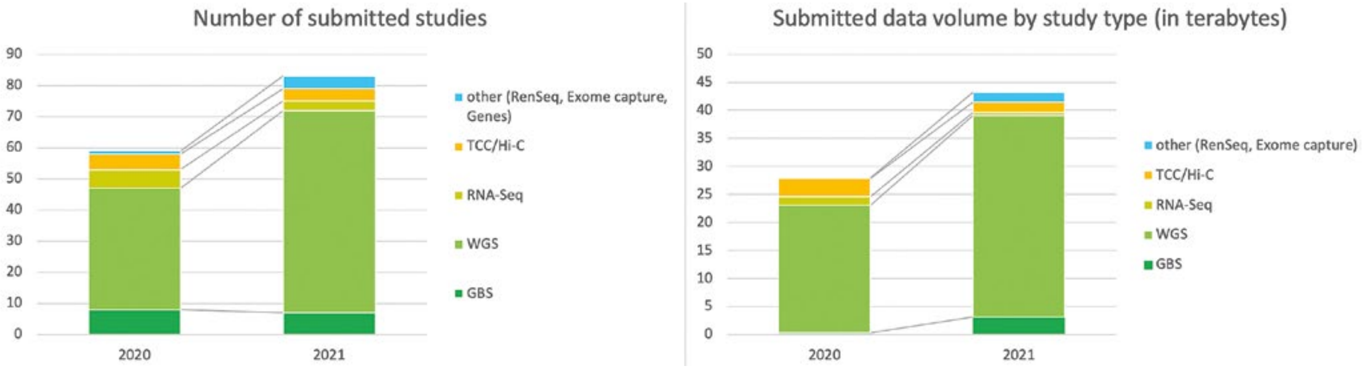


Figure 2: *Overview about the submitted studies and data volume to EMBL-ENA*

decade of public-private research collaborations were curated and approaches developed that enable integrated data analyses of the cumulative Big Data set. This largest public hybrid wheat dataset in the world to date enabled a doubling of predictive accuracy compared to individual datasets (Figure 3) reflecting currently available population sizes for individual hybrid wheat breeding programmes.

FUTURE PRIORITIES

The department's research work and the knowledge gained will be used to develop innovative approaches to unlocking the genetic diversity of crops in breeding. To this end, research will continue in the three areas of chromosome biology, genome analysis and breeding informatics.

In the field of chromosome biology, the aim is to better understand the mechanisms of chromosome segregation and elimination as well as centromere regulation in order to be able to specifically influence them. This includes, for example, the induction of haploids as a basis for increasing efficiency in the production of double-haploid lines. In addition, the internationally leading role in research on the drive and evolution of supernumerary chromosomes is to be further expanded. Research work in the field of chromosome biology benefits from high-performance microscopy. Of particular note is the super-resolution microscope Elyra PS.1, which has been successfully used in the department since 2012. In the coming years, acquisition of the advanced of super-resolution microscope system Elyra 7 will further improve the research in chromosome biology, via enabling live observations through dramatically accelerated image acquisition technology and a further increased resolution.

Understanding the genetic architecture of important agronomic traits is key to implementing knowledge-based plant breeding. The department will intensify its research on understanding important agronomic traits. In addition to work on biotic stress, a new focus on grain yield components will be developed. The goal is to increase wheat yield potential through improved ear morphology.

In the area of breeding informatics, the potential of Big Data for plant breeding and genetics will be further explored. In this context, one focus of the work is on the development and implementation of federated research data infrastructures. In addition, powerful prediction models from the field of artificial intelligence are developed and evaluated on the basis of Big Data. In doing so, the department can draw on extensive data from public-private partnerships as well as extensive historical data from genetic resources. This enables the department to make a significant contribution to the institute-wide Research Theme 1 “Valorisation of Plant Genetic Resources”.

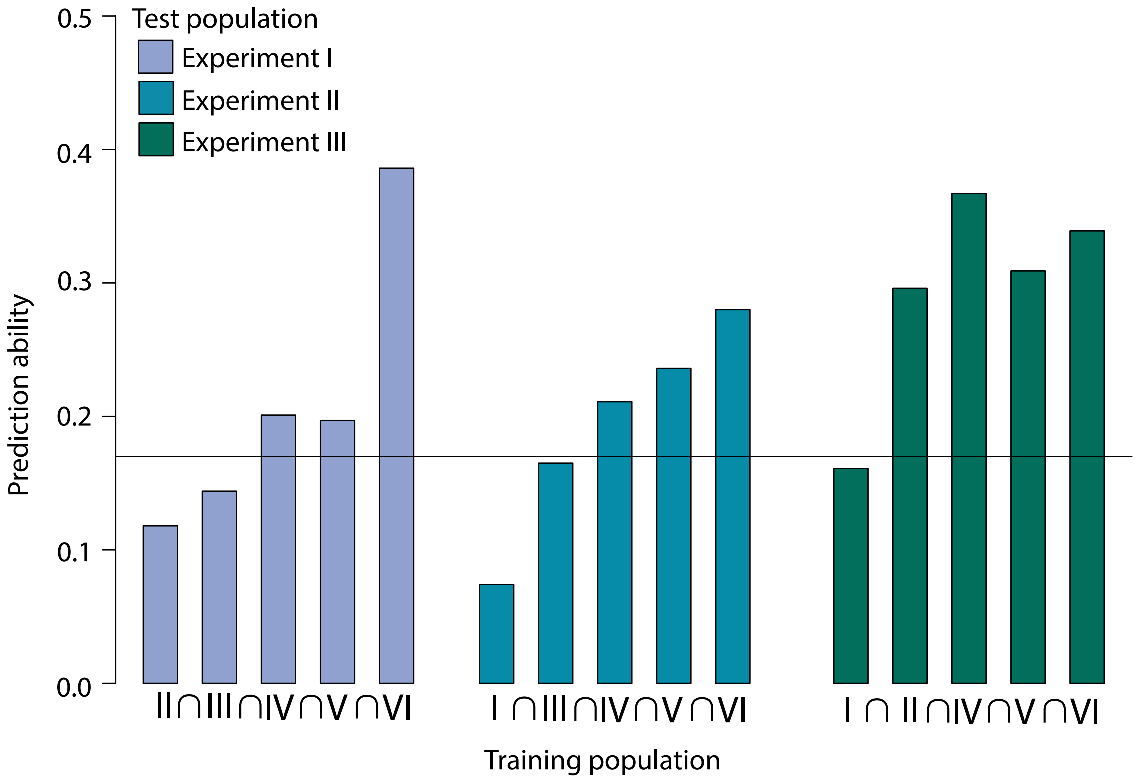


Figure 3: *Increase in prediction ability of the hybrid grain yield performance of three test populations combining incrementally data across experimental series (Experiment I – VI). The horizontal line reflects the average prediction ability between single experiments.*

RESEARCH GROUP
QUANTITATIVE GENETICS (QG)

Head: Prof. Dr. Jochen C. Reif

MISSION

The Quantitative Genetics research group focuses on the development, implementation and evaluation of "omics"-based breeding strategies to increase selection gain in (pre)breeding programmes. Our research goals are (1) to redesign the use of genetic resources for breeding, (2) to enable hybrid breeding in selfing species, and (3) to expand the toolbox of statistical genomics. The model crop is wheat, but research activities also include barley, soybean, common bean, German chamomile, licorice, *Arabidopsis thaliana*, and canola.

RESULTS

The best parents: Genetically as divergent as possible with similar preferences.

For decades, plant breeding has been taking advantage of the phenomenon of heterosis: parents that are as genetically different as possible are crossed to produce offspring that perform better on average than their parents. So-called hybrid breeding is used very successfully in corn, sugar beet, rye or sunflowers. The maximum genetic distance between parents that produces the best hybrid performance has not yet been clarified. Two studies from the 1960s came to contradictory results. While one assumed that the genetic distance between parents should be maximised, the other indicated that the increase in performance of the offspring decreases again after a certain point of diversity. A public-private partnership coordinated by the Quantitative Genetics research group created a unique germplasm comprising three sets of hybrid wheat that differed in the degree of divergence between the parents (Boeven *et al.* 2020). As part of the research collaboration, a genetic distance measure was developed that weights heterotic loci by considering their contribution to phenotypic variance. Use of this new measure showed that heterosis in all 1903 hybrids increased steadily with heterotic genetic distance (Figure 1). However, midparent heterosis was significantly lower in hybrids containing crosses between elite lines and exotic lines than in crosses between elite lines. Analysis of the genetic architecture of heterosis revealed that this was due to a higher proportion of negative dominance and dominance-by-dominance epistasis effects. Overall, these results expand our understanding of heterosis in crops, an important pillar of global food security.

Unlocking big data doubled the accuracy in predicting the grain yield in hybrid wheat.

The potential of Big Data to help businesses has been demonstrated in financial services, manufacturing, and telecommunications. To usher in a new era of data in plant breeding as well, the Quantitative Genetics group has compiled genomic and phenotypic information from approximately 13,000 wheat genotypes representing 6,575 single hybrids and 6,283 inbred lines (Zhao et al. 2021). The wheat genotypes were evaluated for grain yield in six series of field trials involving ~125,000 plots. Integration of the data resulted in a two-fold increase in genome-wide prediction ability compared to cases where hybrid performance was predicted using individual trial series. The results suggest that combining data from different breeding programmes is a particularly appropriate strategy for harnessing the potential of Big Data for predictive plant breeding. This paradigm shift can help increase yield and resilience, which is necessary to feed the world's growing population.

Using genome-wide predictions to assess the phenotypic variation of gene bank collection for important agronomic traits and passport information.

Genome-wide predictions are a promising tool for (pre)breeding. Against this back-

Selected Publications

BOEVEN, P.H.G. et al.: Negative dominance and dominance-by-dominance epistatic effects reduce grain-yield heterosis in wide crosses in wheat. Sci. Adv. 6 (2020) eaay4897.

JIANG, Y. et al.: Using genome-wide predictions to assess the phenotypic variation of a barley (Hordeum sp.) gene bank collection for important agronomic traits and passport information. Front. Plant Sci. 11 (2021) 604781.

ZHANG, J. et al.: On the use of GBLUP and its extension for GWAS with additive and epistatic effects. G3 Genes Genom. Genet. 11 (2021) jkab122.

ZHAO, Y. et al.: Unlocking big data doubled the accuracy in predicting the grain yield in hybrid wheat. Sci. Adv. 7 (2021) eabf9106.

LIU, F. et al.: Exome association analysis sheds light onto leaf rust (Puccinia triticina) resistance genes currently used in wheat breeding (Triticum aestivum L.). Plant Biotechnol. J. 18 (2020) 1396-1408.

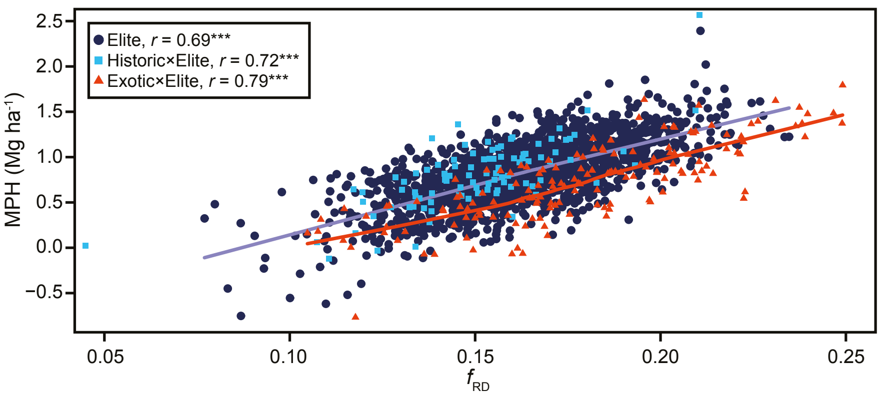


Figure 1: *Association between midparent heterosis and heterotic genetic distance (fRD). The coloured trendlines are locally weighted regression lines for the "Elite" (blue) and "Exotic × Elite" sets (red).*

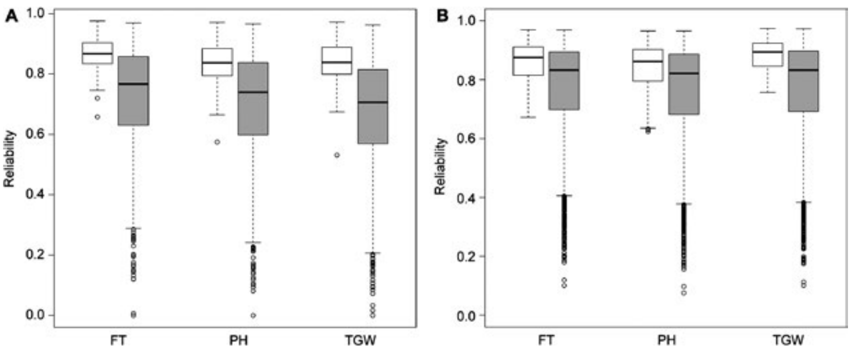


Figure 2: *The distribution of reliabilities for the predicted genetic values of (A) winter and (B) spring barley accessions. Reliabilities for the phenotyped and non-phenotyped accessions were separately presented in white and grey boxes. FT: flowering time; PH: plant height; TGW: thousand grain weight.*

drop, the objective of a research study was to evaluate the potential and limitations of genome-wide predictions to inform the IPK barley collection with phenotypic data on complex traits such as flowering time, plant height, thousand grain weight, and growth habit and row type (Jiang et al. 2021). Previously published sequence data were used, including information on 306,049 high-quality SNPs for 20,454 barley accessions. The prediction ability of the two unordered categorical traits row type and growth type, as well as the quantitative traits flowering time, plant height, and thousand grain weight, was examined using different cross-validation scenarios. The results showed that the disordered categorical traits can be predicted with high precision. In this way, genome-wide prediction can be routinely used to provide information on the taxonomic status of gene bank accessions. In addition, the three quantitative traits were also predicted with high accuracy (Figure 2), increasing the amount of information available for genotyped but not phenotyped accessions. Deeply phenotyped core collections, such as the 1,000 core set of barley from IPK Gatersleben, are a promising training population for calibrating genome-wide prediction models. Consequently, genome-wide predictions can significantly contribute to increasing the attractiveness of gene bank collections and developing gene banks into centres for bio digital resources.

EMBEDDING IN IPK RESEARCH THEMES

The research of the research group Quantitative Genetics contributes mainly to the Research Theme 1 "Valorisation of Plant Genetic Resources".

OUTLOOK

The goal is to increase the international visibility with innovations in research on (pre)breeding methodology and theoretical and applied quantitative genetics in wheat. Emphasis continues to be on (1) hybrid breeding methodology in selfing species, (2) redesigning the use of wheat genetic resources, and (3) expanding the toolbox of statistical genomics with a focus on Big Data analysis in the context of quantitative genetics.

More information: *www.ipk-gatersleben.de/en/research/breeding-research/quantitative-genetics*

RESEARCH GROUP **BIOINFORMATICS AND INFORMATION TECHNOLOGY** (BIT)

Head: Dr. Uwe Scholz

MISSION

The group is responsible for data management infrastructure. This comprises services to offer databases, compute & storage infrastructures and activities to implement FAIR principles for activating multi-domain research data of genetic resources. Major focus is standardised, machine actionable and long-term committed data sharing. This is featured by a LIMS to implement a harmonised data capture process. Furthermore, services for reproducible data analysis workflows using GALAXY were provided and cloud ready data & software containers were developed. To enable a sustainable operation and outreach, the group is actively involved in (inter-)national programmes and communities. The Figure 1 summarises these activities.

RESULTS

Results within the FAIR digital resource centre are DOI assignment services for research data and IPK Gene Bank accessions, standardised publication and sharing frameworks. One example is the Plant Genomics & Phenomics Research Data Repository (e!DAL-PGP), which shows an increased number of users and downloads (December 2021: 176,000 unique IP addresses; total download volume: 758 TB). An overview about the usage and downloads is available at this address: https://edal-pgp.ipk-gatersleben.de/.

In cooperation with the Julius Kühn Institute a mobile app to record phenotypic observations from the field or greenhouse was developed and a corresponding LIMS user interface for data import/export is being set up. In collaboration with the research group Genebank Documentation, the mobile app is extended towards an application for IPK Gene Bank to record field observation.

In addition, BIT has been involved in geno- and phenotyping projects for *Hordeum* (https://bridge.ipk-gatersleben.de/), *Triticum* and *Phaseolus* and has taken responsibility for FAIR-compliant storage of research data and metadata within the IPK LIMS and provides reusable tools for data analysation and visualisation (e.g. http://divbrowse.ipk-gatersleben.de/).

In the area of FAIR data sharing, BIT contributes to the Horizon 2020 projects AGENT, INCREASE, CAPITALISE and to projects generating pan-genomes, e.g. of barley within the SHAPE-II project. Results of the pan-genome projects are accessible to users via a GALAXY infrastructure (https://galaxy-web.ipk-gatersleben.de/).

The BIT group contributes to the AVATARS project ("Advanced Virtual and Augmented Reality Approaches in Seeds to Seeds") for developing novel approaches for data handling and visualisation based on heterogeneous data of *Brassica napus*. For this, the group is responsible for methods and services for harmonised data management and integrated data stewardship using the digital twin concept.

In the context of the political debate surrounding digital sequence information (DSI) from genetic resources under the CBD and the Nagoya Protocol, the group is involved in the BMBF funded WiLDSI project. A web portal has been developed to facilitate discussions on quantitative monitoring of sequence data from genetic resources in relation to their citations in the literature (https://wildsi.ipk-gatersleben.de/).

As partner in de.NBI & ELIXIR, the group coordinates the GCBN service center as a

Selected Publications

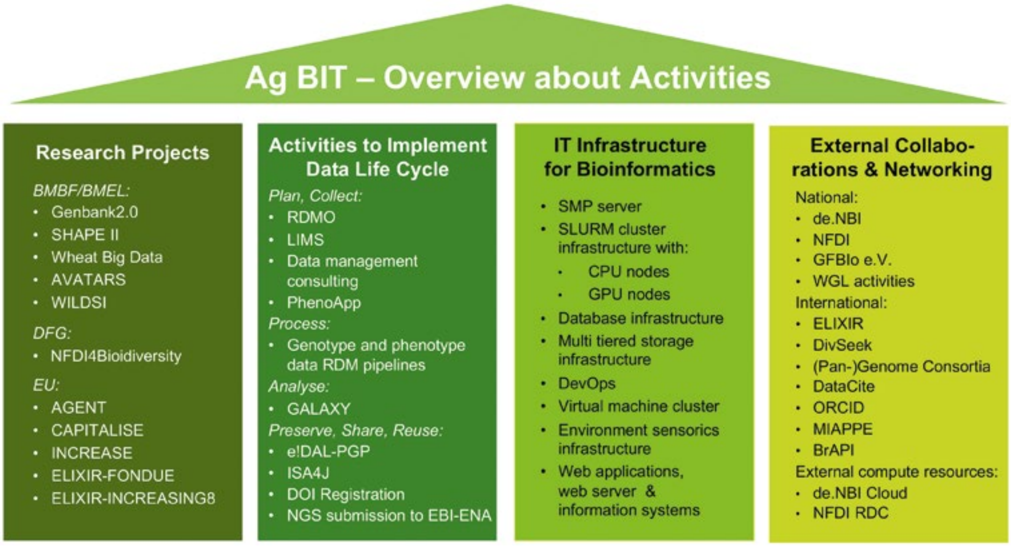
AREND, D. et al.: The on-premise data sharing infrastructure e!DAL: Foster FAIR data for faster data acquisition. Gigascience 9 (2020) giaa107.

KÖNIG, P. et al.: BRIDGE – a visual analytics web tool for barley genebank genomics. Front. Plant Sci. 11 (2020) 701.

MAYER, G. et al.: Implementing FAIR data management within the German Network for Bioinformatics Infrastructure (de.NBI) exemplified by selected use cases. Brief. Bioinform. 22 (2021) bbab010.

LANGE, M. et al.: Quantitative monitoring of nucleotide sequence data from genetic resources in context of their citation in the scientific literature. GigaScience 10 (2021) giab084.

PAPOUTSOGLOU, E.A. et al.: Enabling reusability of plant phenomic datasets with MIAPPE 1.1. New Phytol. 227 (2020) 260-273.



Ag BIT – Overview about Activities

Research Projects

BMBF/BMEL:
- Genbank2.0
- SHAPE II
- Wheat Big Data
- AVATARS
- WILDSI

DFG:
- NFDI4Biodiversity

EU:
- AGENT
- CAPITALISE
- INCREASE
- ELIXIR-FONDUE
- ELIXIR-INCREASING8

Activities to Implement Data Life Cycle

Plan, Collect:
- RDMO
- LIMS
- Data management consulting
- PhenoApp

Process:
- Genotype and phenotype data RDM pipelines

Analyse:
- GALAXY

Preserve, Share, Reuse:
- e!DAL-PGP
- ISA4J
- DOI Registration
- NGS submission to EBI-ENA

IT Infrastructure for Bioinformatics

- SMP server
- SLURM cluster infrastructure with:
  - CPU nodes
  - GPU nodes
- Database infrastructure
- Multi tiered storage infrastructure
- DevOps
- Virtual machine cluster
- Environment sensorics infrastructure
- Web applications, web server & information systems

External Collaborations & Networking

National:
- de.NBI
- NFDI
- GFBIo e.V.
- WGL activities

International:
- ELIXIR
- DivSeek
- (Pan-)Genome Consortia
- DataCite
- ORCID
- MIAPPE
- BrAPI

External compute resources:
- de.NBI Cloud
- NFDI RDC

Figure 1: *The four pillars of the BIT activities. We contribute to a lot of IPK research projects in the field of data management by providing services, powerful bioinformatics infrastructures and participating in network activities as well as communities.*

national plant service unit. In addition, the BIT leads the ELIXIR implementation study "FONDUE – FAIR-ification of Plant Genotyping Data and its linking to Phenotyping using ELIXIR Platforms" and participates in "Increasing Plant data findability and reuse beyond ELIXIR".

Within the National Research Data Infrastructure (NFDI) the group is actively represented in the funded NFDI4BioDiversity consortium and in the FAIRAgro consortium, which is currently under evaluation. However, through connections established in de.NBI and ELIXIR, there are also links to the already funded DataPLANT consortium.

EMBEDDING IN IPK RESEARCH THEMES

The group contributes to the Research Themes 1 “Valorisation of Plant Genetic Resources” and 2 “Genome Diversity and Evolution”. BIT is also involved in the other three Research Themes through excellent cooperation with almost all IPK groups. With its experiences in FAIR-compliant research data management, the group has been able to contribute to collaborative projects and had the leading role in the assigning process for Digital Objects Identifier (DOIs) of the 200.000 accession stored in the IPK Gene Bank.

OUTLOOK

The main goal of our future activities is the development of the IPK into a bio digital Resource Centre. Specifically, work will be done on:

- A comprehensive material management based on the digital twin concept
- Data collection and provision for applications from automated sensor networks
- Improving the FAIRness of data by semi-automatic conversion into community agreed standards (e.g. MIAPPE)
- Automatic submission of sequencing data to EMBL-ENA
- Establishment of long-term data stewardship concept
- Evolving the IPK publication process by integrating infrastructure like ORCID or ROR

In order to exploit synergies and benefit from ongoing initiatives, active participation in (inter) national networks and infrastructures will be further expanded.

More information: *www.ipk-gatersleben.de/en/research/breeding-research/bioinformatics-and-information-technology*

RESEARCH GROUP **CHROMOSOME STRUCTURE AND FUNCTION** (CSF)

Head: Prof. Dr. Andreas Houben

Selected Publications

CÂMARA, A.S. et al.: A simple model explains the cell cycle-dependent assembly of centromeric nucleosomes in holocentric species. Nucleic Acids Res. 49 (2021) 9053–9065.

DREISSIG, S. et al.: Quantification of recombination rate and segregation distortion by genotyping and sequencing of single pollen nuclei. In: PRADILLO, M. & S. HECKMANN (Eds.): Plant Meiosis: methods and protocols. (Series: Methods in molecular biology, Vol. 2061) New York, NY: Humana Press (2020) 281-300.

ISHII, T. et al.: Unequal contribution of two paralogous CENH3 variants in cowpea centromere function. Commun. Biol. 3 (2020) 775.

MUNICIO, C. et al.: The Arabidopsis condensin CAP-D subunits arrange interphase chromatin. New Phytol. 230 (2021) 972-987.

RUBAN, A. et al.: Supernumerary B chromosomes of Aegilops speltoides undergo precise elimination in roots early in embryo development. Nat. Commun. 11 (2020) 2764.

MISSION

The research group deciphers the regulation, organisation, segregation and evolution of mitotic, meiotic and interphase chromosomes intending to unravel basic mechanisms of chromosome biology in model, wild, and crop species. The gained knowledge will be used to accelerate and optimise the breeding process of crop plants and to develop novel chromosome analysis and manipulation tools. A combination of different DNA-, RNA- and protein-based methods interlinked with bioinformatics, optical and transgenic tools is employed to reach the goals.

RESULTS

Helical metaphase chromatid coiling is conserved

The dense compaction of chromatin into metaphase chromosomes is the prerequisite to segregate chromosomes correctly into daughter cells during cell division. To decipher the long-lasting question of how metaphase chromosomes are arranged at the higher-order organisation level a combination of state-of-art methods was was used in cooperation with The Institute of Experimental Botany (Olomouc, Czech Republic) and several IPK research groups.. All data provide cumulative evidence for the presence of a helically arranged 400 nm chromatin fibre representing the so-called chromonema within the chromatids of barley (Figure 1). The number of turns is positively correlated with the arm length. Based on plant and non-plant species, it is concluded that the helical turning of metaphase chromatid arms is a conserved feature of large eukaryotic (>12 Mb) chromosomes.

Modelling of holo- and monocentromeres

Holocentric species occur in both plant and animal taxa. One of the fascinating features is their cell-cycle dependent restructuring of centromeres. In contrast to monocentric species, where no obvious dispersion of the centromeres occurs during interphase, the organisation of holocentromeres differs between interphase and mitotic metaphase. During interphase, holocentromeres are dispersed into a large number of CENH3-positive nucleosome clusters. With the onset of chromosome condensation, the centromeric nucleosomes join and form line-like holocentromeres. Using polymer simulations, in collaboration with the research group Domestication Genomics, we propose a mechanism relying on the interaction between centromeric nucleosomes and loop extruders corresponding to Structural Maintenance of Chromosomes (SMC) proteins. Similar mechanisms may also organise a monocentric chromosome constriction.

Unequal contribution of paralogous CENH3 variants in centromere function

In most diploids, the centromere-specific histone H3 (CENH3), the assembly site of active centromeres, is encoded by a single-copy gene. Persistence of two CENH3 paralogs in diploid species raises the possibility of subfunctionalisation. Phylogenetic analysis suggests that gene duplication of CENH3 occurred independently during the speciation of the cowpea *Vigna unguiculata*. Both *CENH3* variants are transcribed, and the corresponding proteins are intermingled in subdomains of different types of centromere sequences in a tissue-specific manner together with the kinetochore protein CENPC. CRISPR/Cas9-based inactivation of *CENH3.1* resulted in delayed vegetative growth and sterility, indicating that this variant is needed for plant development and reproduction. By contrast, *CENH3.2* knockout individuals did not show obvious defects during vegetative and reproductive development. Hence, *CENH3.2* of cowpea is likely at an early stage of pseudogenisation and less likely undergoing subfunctionalisation.

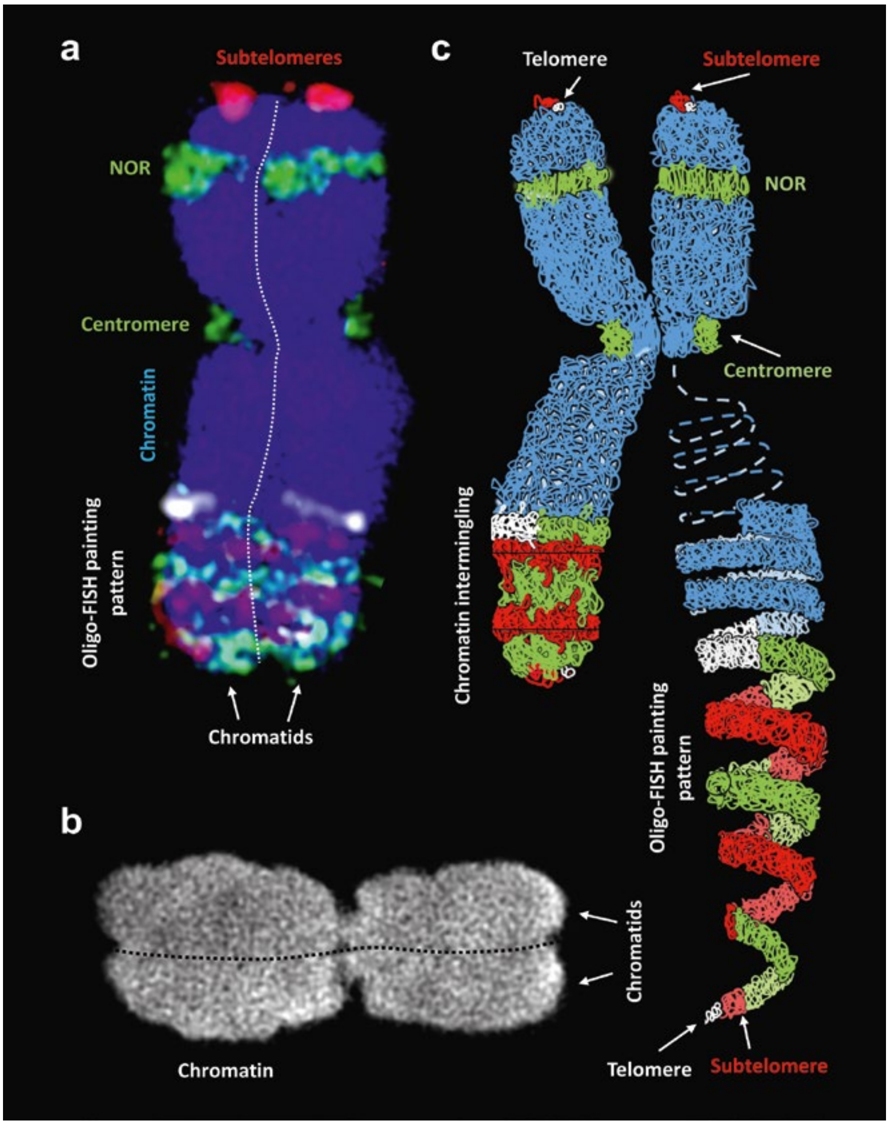


Figure 1: *Metaphase chromatids are helically organised. Oligo-FISH (fluorescence in situ hybridisation) of a barley chromosome (a) indicates that the densely compacted chromatin within metaphase chromosomes (B) is arranged as helix within each chromatid as shown in the model (c).*

Condensin I and II are present in Arabidopsis and their CAP-D subunits arrange interphase chromatin

Condensins are best known for their role in shaping chromosomes. To elucidate the specific composition of condensin complexes and the expression of CAP-D2 (condensin I) and CAP-D3 (condensin II) analyses were performed in *Arabidopsis thaliana. In silico* and pull-down experiments indicate that both CAP-D proteins interact with the other condensin I and II subunits. A model for the function of CAP-D3 during interphase is proposed, in which CAP-D3 localises in euchromatin loops to stiffen them, and consequently separates centromeric regions and 45S rDNA repeats.

EMBEDDING IN IPK RESEARCH THEMES

The projects of the research group Chromosome Structure and Function are part of the IPK Research Themes 3 “Mechanisms of Plant Reproduction” and 2 “Genome Diversity and Evolution”.

OUTLOOK

A CENH3-degradation based haploidisation method will be developed. Candidate genes involved in the regulation of chromosome drive and elimination comparative will be functionally tested. The evolution and organisation of holocentromeres will be determined using closely related species with a contrasting organisation of centromeres.

More information: *www.ipk-gatersleben.de/en/research/breeding-research/chromosome-structure-and-function*

RESEARCH GROUP
KINETOCHORE BIOLOGY (KB)

Head: Dr. Inna Lermontova

MISSION

The research group Kinetochore Biology is interested in studying the organisation, establishment, and maintenance of the kinetochore complex in plants. Our main research goals are (1) to elucidate the mechanism of kinetochore assembly and function (2) to establish an efficient haploid induction approach based on the manipulation of kinetochore proteins, (3) to analyse the effect of environmental factors on the kinetochore assembly.

RESULTS

The kinetochore is a large protein complex that assembles at specialised chromosomal domains, the centromeres, during cell divisions. The main function of this complex is to ensure the proper segregation of chromosomes during mitosis and meiosis and, consequently, genome stability.

The centromere-specific histone H3-variant CENH3 is essential for kinetochore formation and centromere function. Its deposition at centromeres depends on CENH3 assembly factors, chaperones, transcription of the centromeric repeats, and the epigenetic status of centromeric chromatin.

KINETOCHORE NULL 2 (KNL2) is involved in licensing centromeres for CENH3 recruitment. The *knl2* mutant functions as a haploid inducer when crossed with the wild type and its haploid induction efficiency can be increased after exposure to high temperatures.

Performing evolutionary analysis of the KNL2 gene in plants, we showed that it underwent three independent ancient duplications in ferns, grasses, and eudicots. Additionally, we demonstrated that KNL2 genes could be divided into two clades αKNL2 and βKNL2 in eudicots and γKNL2 and δKNL2 in grasses, respectively. All clades encode the conserved SANTA domain, but only the αKNL2 and γKNL2 groups additionally encode the CENPC-k motif. We showed that despite the absence of a centromere-targeting CENPC-k motif, βKNL2 localises to the centromeres of *Arabidopsis* root tip nuclei.

To investigate the interactors of KNL2 in *Arabidopsis* and to find out in which regulatory and functional pathways KNL2 is involved, Immunoprecipitation combined Mass Spectrometry (IP-MS) and yeast-two hybrid (Y2H) analyses were performed. From the IP-MS assay, we identified 399 proteins precipitated with the N-terminal part of KNL2 and 392 proteins with the C-terminal part of KNL2. As a result of the Y2H library screening, 38 proteins containing potential direct interactors were found for full-length KNL2, 54 proteins for KNL2-N, and 76 proteins for KNL2-C, respectively (Figure 1). The interaction network analysis revealed that KNL2 could be involved in a variety of regulatory pathways, including ubiquitination, SUMOylating, and G2/M phase transition pathways. Based on the generated protein-protein interaction network, we decided to focus first on the ubiquitination and cell cycle regulation pathways.

Previously, we showed that KNL2 knockout in *Arabidopsis* resulted in reduced DNA methylation in selected marker regions. To check how the DNA methylation in *knl2* changes in general, a global methylome analysis was performed in collaboration with Claude Becker (GMI, Vienna). It was found that the methylation level of the *knl2* mutant was reduced in all contexts compared to wild type Col0. Comparison of RNAseq data (Boudichevskaia *et al.* 2019) with methylome data showed that transposable elements upregulated in *knl2* are hypomethylated. Interestingly, most differentially methylated regions were concentrated around centromeres.

In cooperation with Prof. Karel Riha (CEITEC, Brno, Czech Republic), we identified and characterised a new *cenh3-4* mutant of *Arabidopsis* (Capitao *et al.* 2021). However, despite low levels of CENH3 and other kinetochore proteins (Figure 2), this mutant was very inefficient haploid inducer under standard growth conditions, indicating that

Selected Publications

CAPITAO, C. et al.: A CENH3 mutation promotes meiotic exit and restores fertility in SMG7-deficient Arabidopsis. PLoS Genet. 17 (2021) e1009779.

HOUBEN, A. et al.: Generation of haploids based on mutation of SAD2. (Patent), Veröffentlichung: 24.03.2021, IPK-Nr. 2018/06. EP3794939. (2021).

LE GOFF, S. et al.: The H3 histone chaperone NASPSIM3 escorts CenH3 in Arabidopsis. Plant J. 101 (2020) 71-86.

MUNICIO, C. et al.: The Arabidopsis condensin CAP-D subunits arrange interphase chromatin. New Phytol. 230 (2021) 972-987.

SORGE, E. et al.: Engineered degradation of EYFP-tagged CENH3 via the 26S proteasome pathway in plants. PLoS One 16 (2021) e0247015.

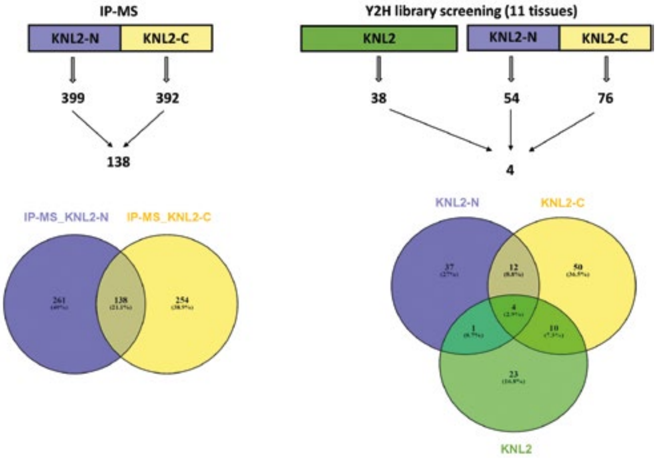


Figure 1: *Schematic illustration of the identification of KNL2 interacting proteins using IP-MS and Y2H approaches and Venn diagrams of their comparative analysis. To identify proteins interacting with KNL2, IP-MS and Y2H experiments were performed separately with the N-terminal part of KNL2 containing the conserved SANTA domain, or with the C-terminal part possessing the conserved centromere targeting motif CENPC-k.*

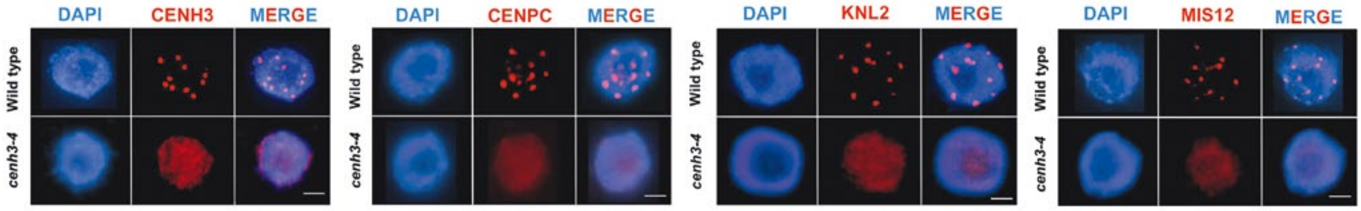


Figure 2: *The cenh3-4 mutation shows reduced CENH3 and kinetochore proteins deposition. The immunolocalisation of CENH3, CENP-C, KNL2 and MIS12 proteins on meristematic root tip nuclei in wild-type and cenh3-4 plants. The decreased level of CENH3 and other kinetochore proteins signals at centromeres have been observed in cenh3-4 mutants compared to wild-type. Scale bars correspond to 5 µm.*

differences in centromere size are not a key determinants of centromere-mediate genome elimination.

We have shown that the haploid induction efficiency of *knl2* and *cenh3-2* mutants increase after exposure to high temperature from 1 to 10 and from 0.2 to 4%, respectively. In order to transfer the KNL2-based haploid induction method from *Arabidopsis* to the crop species such as rapeseed and radish we established a collaboration with breeding companies such as KWS and Enza Zaaden. In the frame of the project supported by KWS and in a collaboration with research group Chromosome Structure and Function, we focus on transferring the *KNL2* and *CENH3*-based haploid induction methods to the rapeseed plants, while the project supported by Enza Zaaden is focusing on radish.

In collaboration with the research groups Phytoantibodies and Chromosome Structure and Function, we successfully recruited the 26S proteasome pathway to directly degrade Yellow Fluorescent Protein-tagged CENH3 (Sorge *et al.* 2021). The uniparental degradation of CENH3 resulted in haploid A. *thaliana* plants. This success was achieved via the replacement of the interaction domain of the E3 ligase adaptor protein SPOP (Speckle-type POZ adapter protein) with a specific anti-Green Fluorescent Protein nanobody.

EMBEDDING IN IPK RESEARCH THEMES

The projects of the Kinetochore Biology group are part of the IPK Research Themes 3 “Mechanisms of Plant Reproduction” and 2 “Genome Diversity and Evolution”.

OUTLOOK

The Kinetochore Biology group plans to continue to focus on the detailed functional characterisation of known kinetochore proteins and the identification and functional characterisation of new components of the kinetochore complex in *Arabidopsis* and crop plants. The obtained knowledge will help us better understand the mechanism of assembly and function of the kinetochore complex in mitosis and meiosis and will enable us to regulate these processes in order to obtain efficient haploid inducers in different crop species. In addition to rapeseed and radish, we plan to apply the KNL2-based haploid induction approach to pennycress (Thlaspi arvense), barley, and maize. We will also study how the application of different abiotic stress conditions affects kinetochore assembly, chromatin structure, and haploid induction efficiency. Furthermore, we are aiming to establish new collaborations with international and national partners.

More information: *www.ipk-gatersleben.de/en/research/breeding-research/kinetochore-biology*

RESEARCH GROUP
BIOTROPHY AND IMMUNITY (BIM)

Interim Head: Dr. Dimitar Douchkov

MISSION

The Biotrophy and Immunity research group aims to discover and utilise novel disease resistance genes and mechanisms, focusing on broad-spectrum immunity as a tool for achieving robust and durable natural plant protection against existing and oncoming diseases. Furthermore, we aim to develop models for disease prevention and risk assessment based on evaluating the nonhost-resistance status of the plants using an innovative micro-phenotyping approach.

RESULTS

Powdery mildew resistance screen of over ten thousand wheat genotypes of the Federal *Ex situ* Gene Bank in Gatersleben

The Genebank 2.0 project aims to elevate the value of wheat genetic resources stored in the IPK Gene Bank by complementing them with genomics and phenomics information for developing a comprehensive breeding and research resource. In the frame of this project, over ten thousand wheat genotypes were phenotyped for powdery mildew (PM) resistance in two biological replications. The screen revealed over 50 PM-resistance associated loci in the wheat genome, where 11 were not present in the modern breeding material. Furthermore, the genomic analysis of the discovered loci revealed several resistance gene candidates, which are now in the process of functional and genetic validation.

Priming of disease resistance by soil bacteria. Establishing of *Bipolaris sorokiniana* pathosystem

The "Primed" state of the plant is a unique physiological situation caused by specific biotic and abiotic factors. The primed plants respond more rapidly and/or effectively when re-exposed to biotic or abiotic stress. As a result, priming is often associated with enhanced disease resistance. In the second phase of the PrimedPlant project, we investigate the priming response promoted by the symbiotic root bacteria *Ensifer meliloti* in a diverse collection of barley genotypes challenged by different pathogens. Besides the powdery mildew, we have established a new pathosystem for the hemibiotrophic fungus *Bipolaris sorokiniana*, the causal agent of some of the most severe foliar diseases as leaf spot blotch, root rot, head blight, and black point of wheat and barley. *B. sorokiniana* is an emerging pathogen of global concern. We have developed a high-throughput screening system for phenotyping *B. sorokiniana* resistance and applied it in a screeing for priming capacity of 200 diverse barley genotypes, which is in progress.

Selected Publications

BZIUK, N. et al.: Tillage shapes the soil and rhizosphere microbiome of barley – but not its susceptibility towards Blumeria graminis f. sp. hordei. FEMS Microbiol. Ecol. 97 (2021) fiab018.

KARKI, S.J. et al.: A small secreted protein from Zymoseptoria tritici interacts with a wheat E3 ubiquitin to promote disease. J. Exp. Bot. 72 (2021) 733–746.

LUECK, S. et al.: "Macrobot" – an automated segmentation-based system for powdery mildew disease quantification. Plant Phenomics 2020 (2020) ID 5839856.

POGODA, M. et al.: Identification of novel genetic factors underlying the host-pathogen interaction between barley (Hordeum vulgare L.) and powdery mildew (Blumeria graminis f. sp. hordei). PLoS One 15 (2020) e0235565.

SŁOMIŃSKA-DURDASIAK, K.M. et al.: Association mapping of wheat Fusarium head blight resistance-related regions using a candidate-gene approach and their verification in a biparental population. Theor. Appl. Genet. 133 (2020) 341–351.

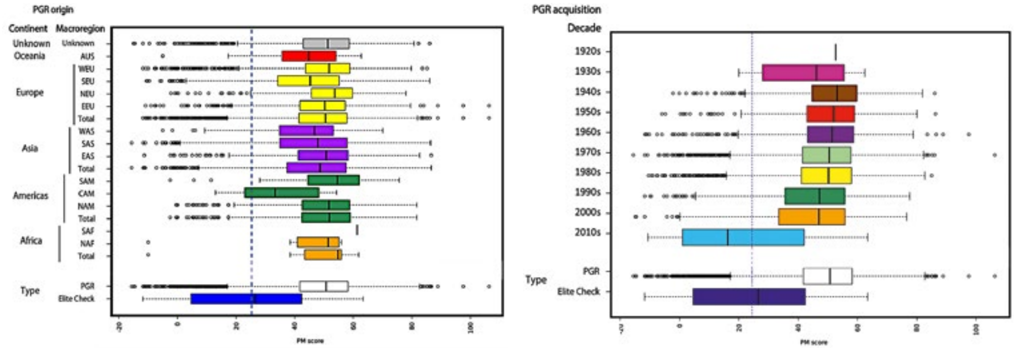


Fig.: *Spatial and temporal distribution of the PM resistance in 8236 winter wheat accessions (Hinterberger et al. 2022). Left panel – the genotypes are grouped by geographical region. Right panel – the genotypes are grouped by year of acquisition in the Genebank. Note: the Central Amerika's (CAM) and 1920s-1930s accessions are underrepresented, and the statistical data is unreliable.*

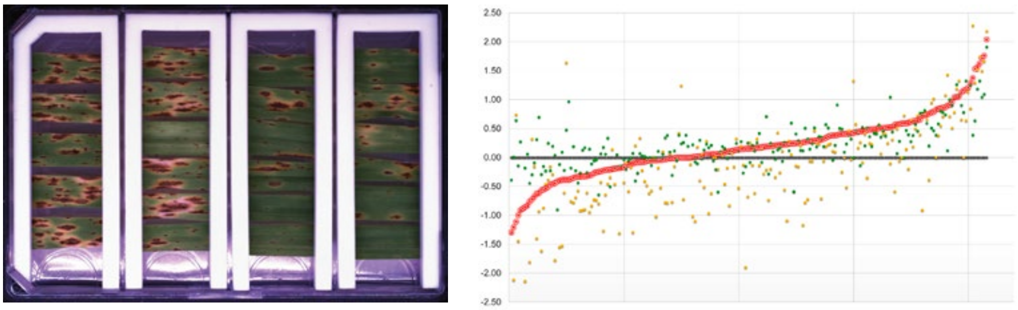


Fig.: *Priming of disease resistance against Bipolaris sorokiniana. Left – a plate with detached leaf segments from primed and control plants inoculated with B. sorokiniana. Right – distribution of the phenotypes (means from three independent experiments, normalized to the Mock control). Red dots – priming with high ALH producing strain 1, green dots – priming with high ALH producing strain 2; yellow – priming with low AHL producing strain; grey – Mock control.*

Microphenomics

Microphenomics combines high-throughput automated microscopy and deep-learning image analysis tools for extracting microscopic phenotypes. We have developed a microphenomics platform for plant-pathogen interactions that enable the study of the early and most crucial stages of pathogen infection. Combined with the comprehensive genomics information available for several plant species, micro-phenotyping allows the discovery of novel resistance genes and mechanisms and a better understanding of plant immunity. The established Microphenomics platform significantly expands IPK research capabilities and infrastructure as well as opportunities for collaborations.

Discovery of genetic determinants of the nonhost resistance

The high throughput and sensitivity of the new Microphenomics system allow approaching rare microscopic phenotypes in a large sample size. One of these phenotypes is the cryptic infection of non-adapted pathogens, marking the hidden transition stages of pathogen adaptation and breaking the nonhost barrier. We have applied this approach in a pilot study with 200 diverse barley genotypes challenged with a non-adapted pathogen (wheat powdery mildew) and revealed genetic determinants of the nonhost resistance to this fungus. The preliminary results show the high potential of the system to enable genetics and genomics research on this most robust and durable form for disease resistance.

EMBEDDING IN IPK RESEARCH THEMES

The research of the research group Biotrophy and Immunity contributes to Research Theme 5 "Mechanisms of Resistance and Stress Tolerance," and Research Theme 1 "Valorisation of Plant Genetic Resources".

OUTLOOK

Our research aims to become a leading lab for a high-throughput micro-phenomics of fungal disease and apply the accumulated knowledge and expertise for advanced genomics of disease resistance, focusing on broad-spectrum and nonhost resistance. Furthermore, we will work towards developing a micro-phenomics-based risk assessment and early warning system for preventing outbreaks of new diseases.

More information: *www.ipk-gatersleben.de/en/research/breeding-research/biotrophy-and-immunity*

FORMER RESEARCH GROUP
GENE AND GENOME MAPPING (GGK)

Head: Dr. Marion Röder

MISSION

Most traits in wheat and other crops are quantitative, i.e. they are inherited in a polygenic fashion. Our goal is to identify quantitative trait loci (QTL) for agronomically important traits in wheat and other cereals by exploiting the naturally available genetic diversity. By using novel genomic resources, we aim to identify the genes underlying the significant QTL and to describe the impact on inheritance of specific functional alleles.

RESULTS

Genetic architecture and genome-wide prediction of grain protein content, grain starch content and grain hardness in European winter wheat varieties

Grain quality traits determine the classification of registered wheat (*Triticum aestivum* L.) varieties. Although environmental factors and crop management practices exert a considerable influence on wheat quality traits, a significant proportion of the variance is attributed to the genetic factors. To identify the underlying genetic factors of wheat quality parameters viz., grain protein content (GPC), starch content (GSC), and hardness (GH), we evaluated 372 diverse European wheat varieties in replicated field trials in up to eight environments. Our association analyses based on 26,694 high-quality single nucleotide polymorphic markers revealed a strong quantitative genetic nature of GPC and GSC with associations on groups 2, 3, and 6 chromosomes. Based on wheat's reference and pan-genome sequences, the physical characterisation of two loci viz., *QGpc.ipk-2B* and *QGpc.ipk-6A* facilitated the identification of the candidate genes for GPC.

Linkage mapping identifies a non-synonymous mutation in FLOWERING LOCUS T (FT-B1) increasing spikelet number per spike

Total spikelet number per spike (TSN) is a major component of spike architecture in wheat (*Triticum aestivum* L.). A major and consistent quantitative trait locus (QTL) was discovered for TSN in a doubled haploid spring wheat population grown in the field over four years. The QTL on chromosome 7B explained up to 20.5% of phenotypic variance. In its physical interval (7B: 6.37 to 21.67 Mb) the gene *FLOWERING LOCUS T* (*FT-B1*) emerged as candidate for the observed effect. In the parental lines, FT-B1 carried a non-synonymous substitution on position 19 of the coding sequence modifying an aspartic acid (D) into a histidine (H). The mutation was observed with a frequency of ca. 68% in a set of 135 hexaploid wheat varieties and landraces, while it was not found in other plant species. Individuals carrying the FT-B1 allele with amino acid histidine had on average a higher number of spikelets (15.1) than individuals with the aspartic acid allele (14.3) independent of their *VRN-A1* allele. Therefore, the effect of TSN is not mainly related to flowering time, but the duration of pre-anthesis phases may play a major role.

A Major Facilitator Superfamily Transporter is a putative candidate gene for nutrient mineral accumulation in wheat grains

A multilocus genome-wide association study of a panel of 369 diverse wheat (*Triticum aestivum*) genotypes was carried out in order to examine the genetic basis of variations in nutrient mineral concentrations in the grains. The panel was grown under field conditions for three consecutive years and the concentrations of Ca, K, Mg, Mn, P, and S were determined in collaboration with the research group Plant Nutrition. Genetic association analysis detected 86 significant marker–trait associations (MTAs) underlying the natural variations in mineral concentrations in grains. The major MTA was detected on the long arm of chromosome 5A and showed a pleiotropic effect on Ca, K, Mg, Mn, and S. Further significant MTAs were distributed among the whole genome except for chromosomes 3D and 6D. We identified putative candidate genes that are

Selected Publications

ALOMARI, D.Z. et al.: Toward identification of a putative candidate gene for nutrient mineral accumulation in wheat grains for human nutrition purposes. J. Exp. Bot. 72 (2021) 6305-6318.

BRASSAC, J. et al.: Linkage mapping identifies a non-synonymous mutation in FLOWERING LOCUS T (FT-B1) increasing spikelet number per spike. Sci. Rep. 11 (2021) 1585.

DRAZ, I.S. et al.: Quantitative trait loci for yellow rust resistance in spring wheat doubled haploid populations derived from the German Federal Ex situ Gene Bank genetic resources. Plant Genome 14 (2021) e20142.

MUQADDASI, Q.H. et al.: Prospects of GWAS and predictive breeding for European winter wheat's grain protein content, grain starch content, and grain hardness. Sci. Rep. 10 (2020) 12541.

TIKHENKO, N. et al.: DEFECTIVE ENDOSPERM-D1 (Dee-D1) is crucial for endosperm development in hexaploid wheat. Commun. Biol. 3 (2020) 791.

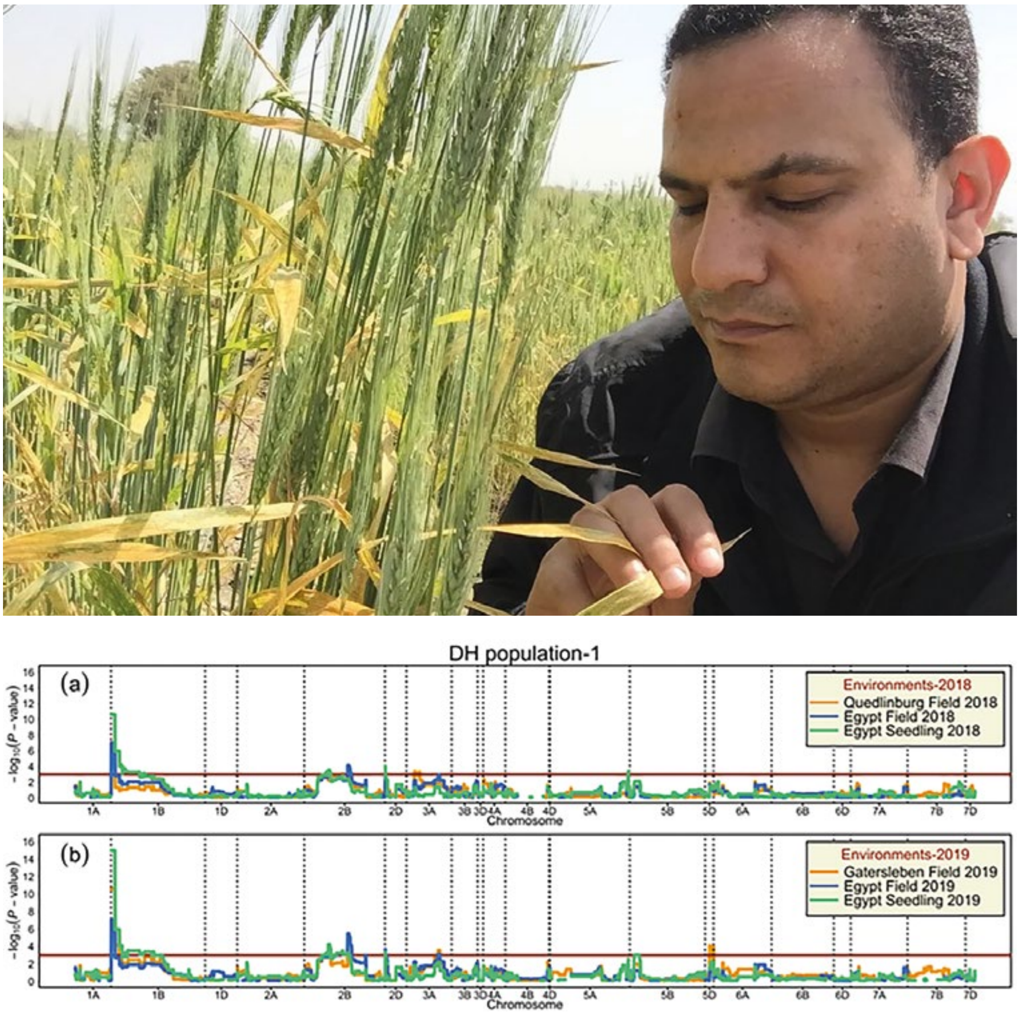


Figure 1: *A. Evaluation of wheat lines derived from genetic ressources of the IPK Genebank for yellow rust in Egypt by I. Draz. B. A major QTL for yellow rust resistance was detected in environments in Germany and Egypt rendering resistance against race ‚Warrior'.*

potentially involved in metal uptake, transport, and assimilation, including *TraesCS5A02G542600* on chromosome 5A, which was annotated as a Major Facilitator and was highly expressed in seed coat.

QTL analysis of yellow rust in two doubled haploid wheat populations derived from genetic resources

In a collaborative effort among IPK, JKI Quedlinburg (Albrecht Serfling) and ARC in Egypt (Ibrahim Draz) resistance to yellow rust was studied in two doubled haploid spring wheat populations derived from genetic resources of the Gene Bank of IPK. Two major resistance loci on chromosomes 1B and 6B were discovered which rendered resistance to Egyptian and German isolates including the race „Warrior".

EMBEDDING IN IPK RESEARCH THEMES

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 "Valorisation of Plant Genetic Resour¬ces".

OUTLOOK

The research group Gene and Genome Mapping was closed in March 2021 because of the retirement of the group leader Marion Röder.

More information: *www.ipk-gatersleben.de/en/research/former-workgroups/gene-and-genome-mapping*

SENIOR GUEST GROUP (EMERITUS GROUP): **KARYOTYPE EVOLUTION** (KTE)

Head: Prof. Dr. Ingo Schubert

Selected Publications

PALFALVI, G. et al.: Genomes of the Venus flytrap and close relatives unveil the roots of plant carnivory. Curr. Biol. 30 (2020) 2312-2320.

HOANG, P.T.N. et al.: Chromosome-scale genome assembly for the duckweed Spirodela intermedia, integrating cytogenetic maps, PacBio and Oxford Nanopore libraries. Sci. Rep. 10 (2020) 19230.

HOANG, P.T.N. et al.: Limitation of current probe design for oligo-cross-FISH, exemplified by chromosome evolution studies in duckweeds. Chromosoma 130 (2021) 15-25.

ACOSTA, K. et al.: Return of the Lemnaceae: Duckweed as a model plant system in the genomics and post-genomics era. Plant Cell 33 (2021) 3207-3234.

SCHUBERT, I.: Boon and bane of DNA double-strand breaks. Int. J. Mol. Sci. 22 (2021) 5171.

MISSION

Traditionally our focus is on evolution of genomes and karyotypes of related plant groups with varying genome sizes and chromosome numbers. We study reasons and consequences of genome size variability by testing for whole genome duplications and chromosome rearrangements, e.g. among the 36 species of the five duckweed genera. We quantify the outcome of DNA double-strand break (DSB) repair at the sequence and the chromosome level to elucidate its impact on evolutionary stability versus dynamics of small versus large genomes.

RESULTS

Evolutionary studies on duckweed genomes and chromosomes: After the genomes of the two species of the phylogenetically basic duckweed genus Spirodela have been assembled at chromosome scale (Hoang *et al.* 2018; 2020), cross-FISH (fluorescence *in situ* hybridisation) with mapped S. polyrhiza BACs could not reveal karyotype evolution across the duckweed family (Hoang 2019), while a similar approach worked well in Brassicaceae. Therefore, we generated oligo-FISH probes for chromosomes of both *Spirodela* species. These probes cross-hybridized well within the genus, but again failed to yield chromosome-specific signals in other duckweed genera (Figure). We could show that dispersed signals were caused by minisatellite sequences among the oligos which were abundant in some target genomes. The lack of chromosome-specific signals was obviously due to a too low density of similar (>75%) sequences in the target genomes. We developed a new strategy for future oligo-FISH in non-assembled genomes (Hoang *et al.* 2021). Together with international duckweed experts, an invited review (Plant Cell) on duckweed research in the past and in the future has been published. The concept phase of a BMBF project ('Euroduckweed') to establish a 'core of excellence' for duckweed research in Ukraine started at 01.12.2021.

DSB repair modes and genome evolution: We search for a master student to work on DSB repair mechanism(s) in hexaploid wheat (versus diploid barley) in collaboration with the groups Plant Reproductive Biology and Plant Architecture. A theoretical paper on "Boon and bane of DNA double-strand breaks" has been published (Schubert 2021).

EMBEDDING IN IPK RESEARCH THEMES

The cytogenomic work of the senior guest group fits well into IPK's Research Theme 2 "Genome Diversity and Evolution".

OUTLOOK

Our expertise could contribute i) to further elucidation of genome and karyotype evolution within the emerging crop plant family of duckweeds, ii) to organise duckweed research in the international context, iii) to resolve pathways and consequences of erroneous DSB repair, particularly in polyploid plant genomes, and iv) to interpret the evolution of the large diploid genome of Vicia faba (13 Gbp/1C).

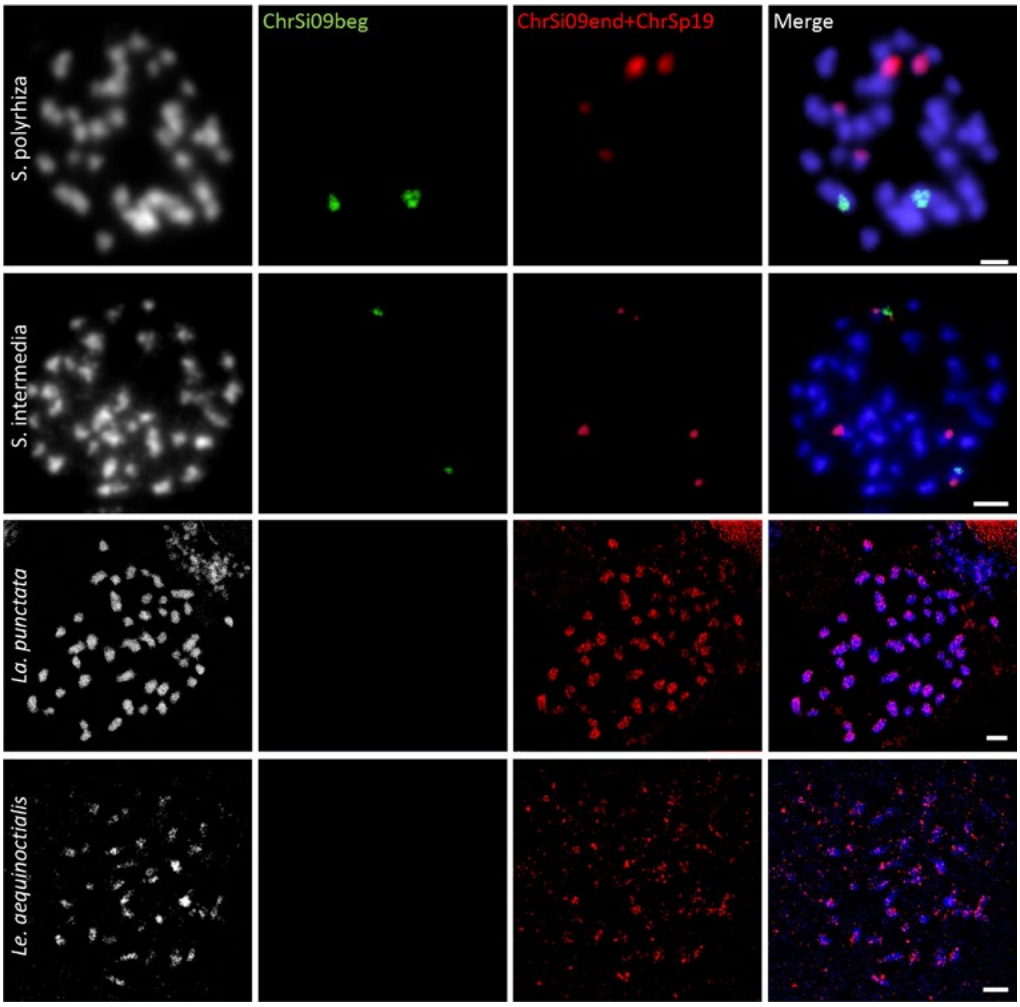


Figure 1: *FISH with oligo-probes derived from chromosome 19 of the Greater Duckweed, Spirodela polyrhiza (red) and from chromosome 9 of S. intermedia (green and red, respectively) labelled, as expected, 3 chromosome pairs in S. polyrhiza and two pairs of S. intermedia (upper two panels). However, on Landoltia punctata and Lemna aequinoctialis (lower two panels) the green probe labelled none and the red probes all chromosomes. Thus, oligo-FISH probes cross-hybridize well within, but not across duckweed genera. (images: PTN Hoang).*

More information:
www.ipk-gatersleben.de/en/research/breeding-research/senior-guest-group-karyotype-evolution-kte-emeritus-group

DEPARTMENT MOLECULAR GENETICS

HETEROSIS (HET)

Prof. Dr. Thomas Altmann

AUTOMATED PLANT PHENOTYPING (APP)

Dr. Kerstin Neumann

IMAGE ANALYSIS (BA)

Dr. Evgeny Gladilin

METABOLIC DIVERSITY (MD)

Dr. John D‘Auria

SEED DEVELOPMENT (SE)

Dr. Jozefus H. M. Schippers

ASSIMILATE ALLOCATION AND NMR (AAN)

PD Dr. Ljudmilla Borisjuk

NETWORK ANALYSIS AND MODELLING (NAM)

Dr. Jedrzej Jakub Szymanski

YOUNG INVESTIGATORS GROUP “INTEGRATED MECHANISTIC MODELS” (IMM)

Dr. Mary-Ann Blätke

DEPARTMENT MOLECULAR GENETICS

Head: Dr. Thomas Altmann

MISSION

Sustainable production of food and feed, as well as renewable raw materials and energy sources of adequate quantity and quality present great challenges in a world facing population growth and environmental changes. Therefore, the major aim of the Molecular Genetics (MOG) department is the gain of detailed information on the molecular processes that determine plant performance. The investigations focus on the dynamics of vegetative growth and metabolism, as well as development and filling of seeds. Molecular-genetic identification and characterisation of determining factors, elucidation of the affected molecular processes, and development of genetic solutions for crop improvement are the major research goals.

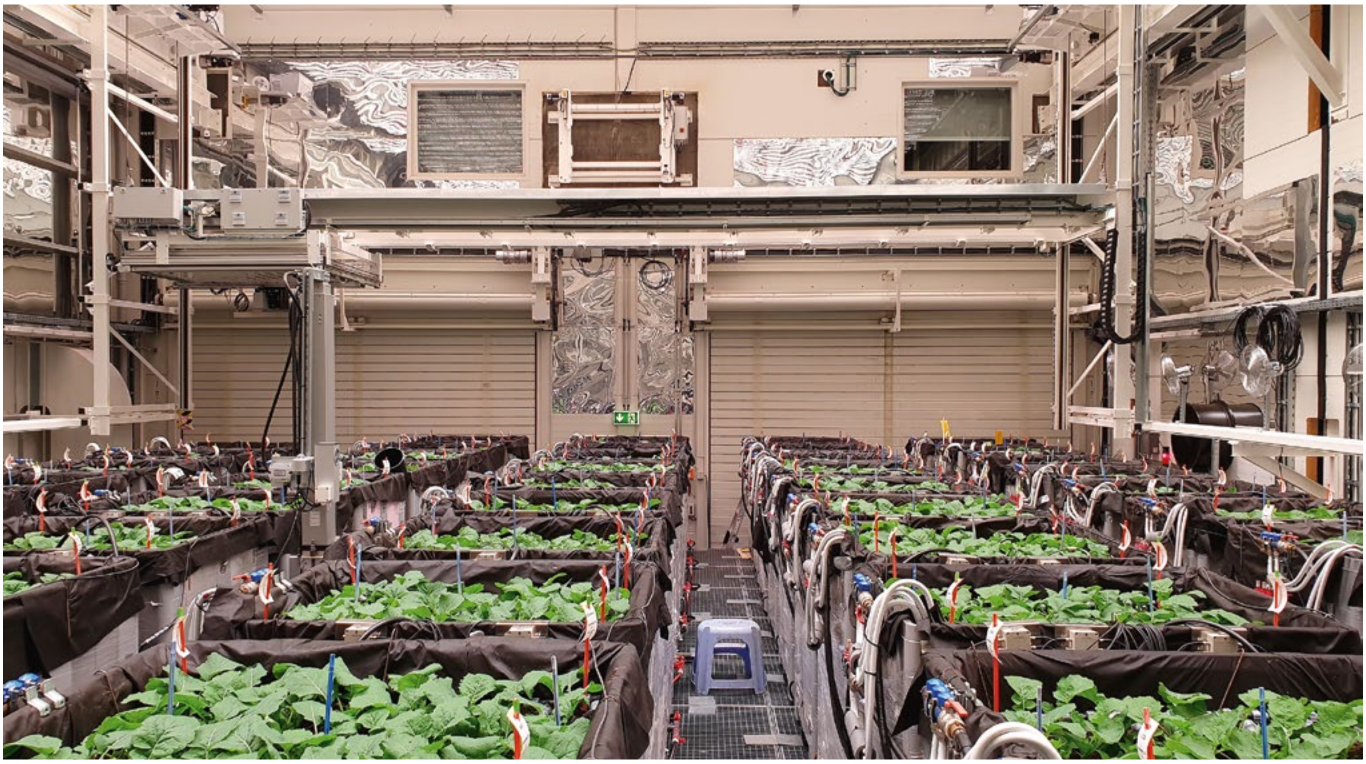
RESEARCH STATUS

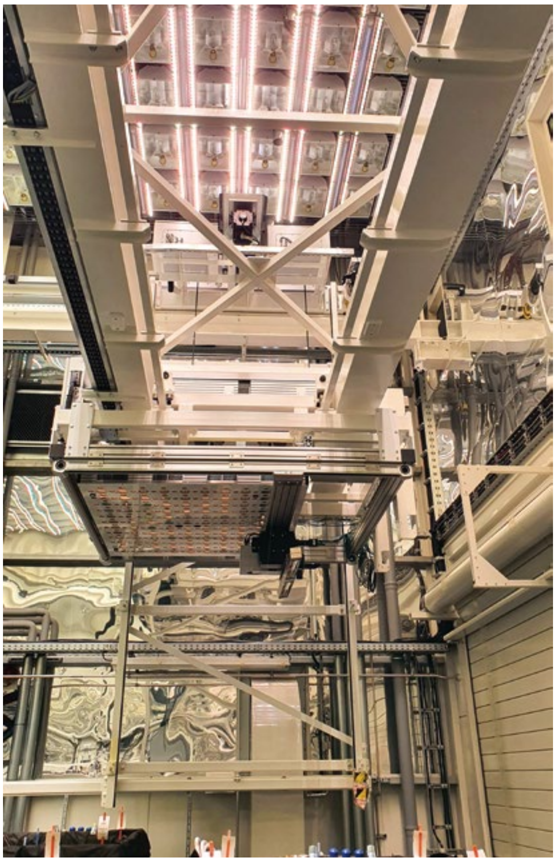
The research programme of the Molecular Genetics department aims at the elucidation of molecular processes that govern the expression of plant performance traits and at the use of the acquired knowledge to devise and test genetic and epigenetic strategies for targeted improvement of the crop performance potential. The focus is on the investigation and modulation of plant performance manifested in biomass accumulation and in seed production capacity. Following the philosophy that „Nothing in (plant) biology makes sense, except in the light of space and time and condition”, the main research approaches involve cultivation of suitable plant populations under appropriate controlled conditions simulating field-like dynamic environments, non-invasive phenotyping involving optical or NMR-based techniques, temporally and spatial resolved molecular/biochemical ‘omics’ analyses, and computational systems analyses and modelling. Relevant factors and regulators identified in this way will be modified using biotechnological approaches or natural variants to improve the performance capacity of crop plants.

Contributing predominantly to IPKs Research Themes 4, “Growth and Metabolism”, and 5, “Mechanisms of Resistance and Stress Tolerance”, MOG addresses the central strategic IPK goals to uncover fundamental processes of plant adaptation and performance and to help tailoring crop plants to improve traits and sustainability. Using its core competences, the research department supports the IPK-wide research expertise and infrastructure by the coordination of IPKs Plant Phenotyping Platform management and use as well as of the Bioinformatics Area of “Systems Analyses and Modelling”.

After completion of a thorough organisational transformation process which involved a substantial personnel turnover at the research group leader level and which lead to a gain in scientific expertise and to a thematic focusing, the MOG department is now fully enabled to address its goals and to carry out its major tasks. The department is composed of seven research groups and a Young Investigators Group (*Integrated Mechanistic Models – IMM*), which was established in the beginning of 2021. Furthermore, the independent research group on *Metabolic Systems Interactions* (*MSI*) is associated with the MOG department and supported through its resources.

The scientific expertise and the technical competences of the eight research groups of the MOG department provide the basis to persue three tightly interlinked research areas, which emerged from selected fields of previous research:





- Growth Dynamics during vegetative development and under the influence of dynamically changing, field-like conditions.
- Seed Biology, addressing developmental and metabolic processes in seeds, which control and regulate cell, tissue, and organ formation as well as seed filling and maturation and
- Systems Genetics to elucidate molecular-genetic mechanisms (including heterosis) and to elaborate improvement strategies through dynamic multi-omic QTL detection, functional network analysis, and modelling of regulatory and metabolic processes.

RESEARCH HIGHLIGHTS

Major highlights of the MOG research work performed in 2020 and 2021 relate to important scientific advances addressing plant performance-related processes, improvements and use of phenotyping facilities, and the development of novel research tools:

Scientific research highlights
include the identification of candidate *Arabidopsis* genes for multiple dynamic growth QTLs that are involved in hormone signalling, cell wall biogenesis,

Newly installed `PhenoCrane´ System in IPK PhenoSphere. The xyz-positioning system carries illumination and imaging devices for RGB and hyperspectral imaging, 3D laser scanning, and kinetic chlorophyll fluorescence imaging of plants. 4-week-old rapeseed (Brassica napus) plants grow in the large cultivation containers (fotos: 05.10.2021).

Flowering winter oilseed rape (Brassica napus) plants of five different lines cultivated under strictly controlled simulated field-like aerial and soil conditions in large containers in compartment 1 of IPK´s PhenoSphere. After indoors pre-cultivation from September to October 2020 in the same compartment, they were hibernated outdoors in a rolling greenhouse and further cultivated in the PhenoSphere from the end of March 2021 (fotos: 23.04.2021).

and regulation of transcription. Inclusion of transcriptome data in addition to genomic data significantly increased accuracies of rapeseed hybrid performance prediction models.

Analysis of the PS II operating efficiency in a spring wheat mapping panel revealed a steady increase through breeding during the last century, eventually compensating the decrease in photosynthetic area (decrease in plant height) by an increase in source productivity. A similar trend was observed for winter wheat elite lines developed during a period between 1960 and 2010.

A barley spike expression atlas was established though laser capture microdissection coupled with RNA sequencing. Transgenic knock-downs of histidine kinase 1, an element of a two-component signalling system, demonstrated its role in endosperm transfer cells formation and its importance for grain size.

Despite RNAi-mediated knock-down of the major storage proteins napins and cruciferins in rapeseed, storage of carbon and nitrogen reserves as well as seed morphology and viability were maintained through cellular plasticity and increased synthesis of oleosins. Using MRI and molecular analyses, it was demonstrated *in planta* and *in vitro*, that mechanical constraints during seed development induce and accelerate maturation of rapeseed embryos.

Trehalose-6-phosphate (T6P) was shown in transgenic peas to promote seed filling through induction of auxin biosynthesis.

With respect to secondary metabolites, all steps of tropane alkaloid biosynthesis in Erythroxylaceae were elucidated and two novel enzymes involved in removing phytotoxic steroidal glycoalkaloids in tomato during fruit ripening were identified using a multi-omics approach and phenotyping on a population of 580 backcrossed, inbred lines of *Solanum lycopersicum* x *S. pennellii*.

Research infrastructure advances
were achieved for IPK´s plant phenotyping facilities, which are continuously improved and used in collaborative projects. In addition to improved data management, storage, and distribution, installation of the PhenoCrane sensor platform in the Plant Cultivation Hall was completed, providing a fully functional phenotyping system for the Container-based Cultivation Platform designed to simulate field-like environments. Furthermore, a first large phenotyping experiment was performed in the *Rhizotron* facility to survey root development in 17 different monocot and dicot species.

Research tool development
involved efficient, KI-based segmentation of plant structures in multi-modal images from high-throughput plant phenotyping resulted in tools for (semi)-automated, quantitative analysis of shoot data, especially noisy root images, and other plant organs, such as spikes of wheat, which are difficult to recognise within almost identically coloured leaves. In flux balance analysis of metabolic models' concepts were developed to integrate machine learning algorithms, kinetic models and formal graphical languages to pave the way for an integrated interpretation of omics data in their physiological contexts.

FUTURE PRIORITIES

The MOG department is dedicated to make key conceptual and tangible contributions to the future long-term goal of enabling genome sequence variation-based prediction of crop plant performance in certain environmental scenarios. This will depend on biological knowledge of the molecular mechanisms that govern important performance-related regulatory and metabolic processes in plants and on the involved genes to estimate the consequences of sequence variation. Thus, major priority will be given to the gain of the necessary knowledge base through integration of spatially and temporally resolved phenotype and molecular omics analyses under specifically designed environmental conditions and by combining them with genetic mapping (systems mapping), network analyses, and process modelling. Integral is the experimental testing and validation of the predictions from mathematical modelling as well as machine learning / artificial intelligence approaches on performance characteristics of certain sets of defined genotypes exposed to relevant and informative environmental regimes. To enable this, MOG will further support the use of IPKs innovative HTP plant phenotyping facilities such as the *Rhizotron* and the PhenoCrane/Container systems in the Plant Cultivation Hall and a SuperWide Bore NMR facility for whole plant MRI analyses. Furthermore, it will persue central joint projects that establish mechanistic links between genomic sequence variation, environmental factors, and phenotypic expression of plant performance-related traits. A prominent example is the AVATARS project, that strives for *The Virtual Seed* by using Augmented Reality and Advanced Virtuality (AR / AV) for interactive data visualisation and exploration and assessing genetic and environmental factors affecting seed quality (germination ability).

RESEARCH GROUP
HETEROSIS (HET)

Head: Prof. Dr. Thomas Altmann

MISSION

The research group Heterosis (HET) studies plant performance, primarily in the crops maize, rapeseed and barley, and in the model *Arabidopsis*. Major aims are the identification and characterisation of genetic and epigenetic factors that influence and control vegetative plant growth performance and heterosis in relevant dynamic environmental conditions, and the elucidation of the affected molecular and physiological mechanisms. Systems biology approaches are combined with high-throughput non-invasive phenotyping techniques applied to plants cultivated in sophisticated controlled environment facilities to detect pertinent genes with emphasis on loci contributing to growth dynamics and biomass heterosis.

RESULTS

In 2020-2021, further important advances were made in the identification of genes/QTL controlling vegetative plant growth and the affected molecular/physiological processes:

Multiple QTL for projected leaf area and relative growth rate in *Arabidopsis* could be grouped according to their temporal expression patterns, emphasising that temporal variation of QTL action occurs during the vegetative growth phase (Meyer *et al.* 2021). Candidate genes are involved in hormone signalling, cell wall biogenesis or transcription regulation.

Molecular analyses of adaptive growth patterns associated with limited nitrate availability revealed genotype-specific differences in the expression of a candidate gene involved in epigenetic regulation (Kuhlmann *et al.* 2020). Three candidate genes for dynamic growth and metabolic QTL in canola (Knoch *et al.* 2020) have *Arabidopsis* homologs identified as candidate genes for biomass heterosis and nitrogen use efficiency (Kuhlmann *et al.* 2020). High-throughput phenotyping allowed a quantitative assessment of dynamic growth and architectural patterns during drought across vegetative maize development (Dodig *et al.* 2021). Several traits were identified as reference indicators for the selection of drought-adaptive genotypes. A similar analysis in spring barley distinguished features for which effects of drought were highly correlated with drought effects for spike traits and thousand grain weight (Mikołajczak *et al.* 2020).

Genomic prediction of hybrid performance in canola was augmented using different omics profiles (SNPs, metabolites, transcripts) and prediction methods (Knoch *et al.* 2021). Models incorporating transcriptome data yielded significantly higher prediction accuracies, indicating that transcripts carry important information beyond genomic data. Reproducing kernel Hilbert space regression significantly outperformed gBLUP models, demonstrating its potential for future canola breeding.

A quantitative analysis of nonoxidized and oxidized lipids in wheat seeds dry-aged for 5–40 years and varying in germination revealed that oxidized variants and hydrolysed products such as mono-/diacylglycerols, lysophospholipids, and fatty acids accumulated as viability decreased (Wiebach *et al.* 2020). The results link reactive oxygen species with lipid oxidation, structural damage, and death in long-term aged seeds.

Jointly with the ADP/APP and Image Analysis (BA) groups, important expansions of IPK’s plant phenotyping infrastructure were achieved (Langstroff *et al.* 2021):

A large validation experiment in the PKH *Rhizotron* platform surveyed root growth in 17 different plant species (mono- and dicots) and demonstrated the ability to detect substantial variation in root system architecture. The PKH Container system housed a first cultivation experiment of 5 diverse winter rapeseed lines grown and scored under field-like conditions (AVATARS project) to assess processes influenc-

Selected Publications

KNOCH, D. et al.: Multi-omics-based prediction of hybrid performance in canola. Theor. Appl. Genet. 134 (2021) 1147–1165.

MEYER, R.C. et al.: Temporal dynamics of QTL effects on vegetative growth in Arabidopsis thaliana. J. Exp. Bot. 72 (2021) 476–490.

DODIG, D. et al.: Dynamics of maize vegetative growth and drought adaptability using image-based phenotyping under controlled conditions. Front. Plant Sci. 12 (2021) 652116.

KUHLMANN, M. et al.: Epigenetic variation at a genomic locus affecting biomass accumulation under low nitrogen in Arabidopsis thaliana. Agronomy 10 (2020) 636.

WIEBACH, J. Age-dependent loss of seed viability is associated with increased lipid oxidation and hydrolysis. Plant Cell Environ. 43 (2020) 303-314.

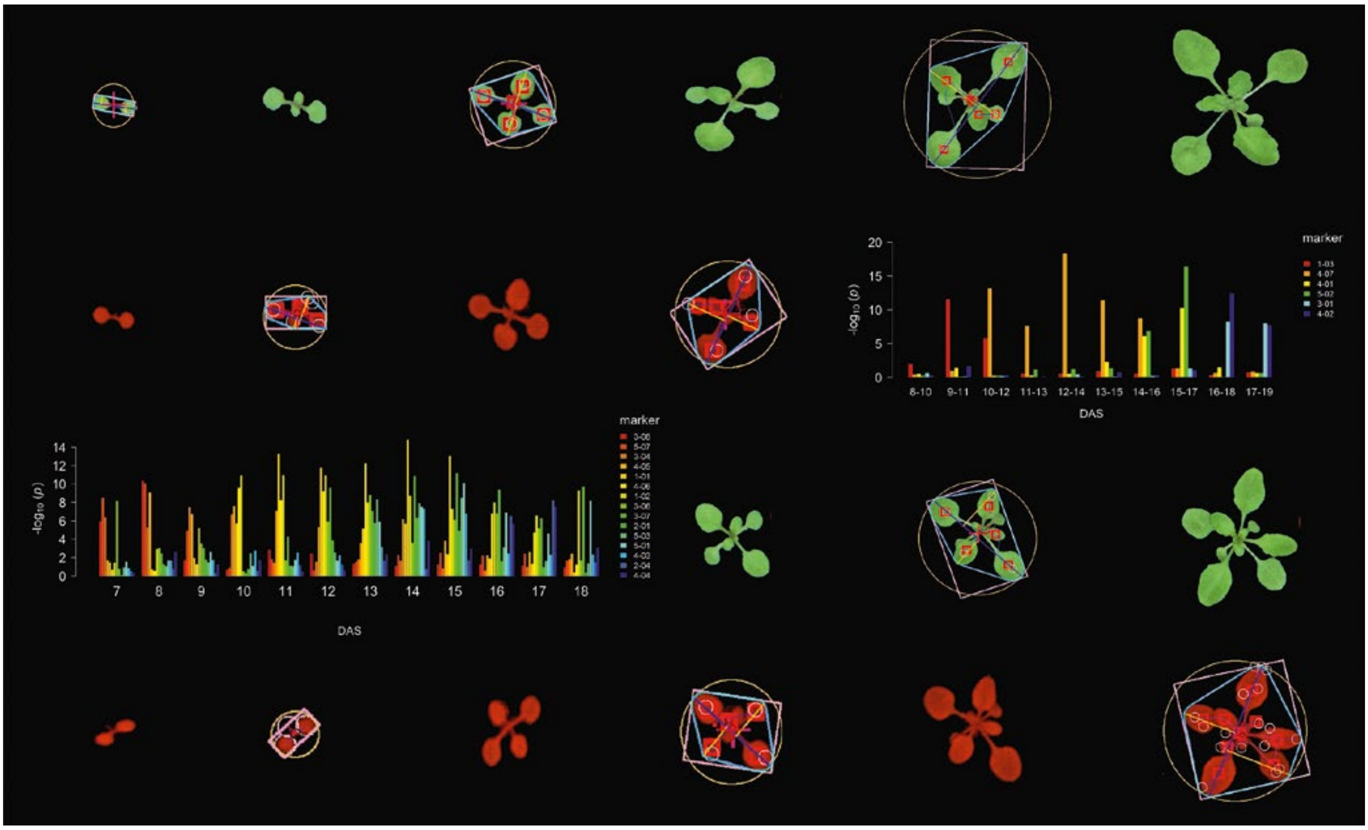


Figure 1: *Steps of a dynamic growth QTL analysis in Arabidopsis thaliana. Plant images were taken using visible (green) and fluorescence (red) light during vegetative plant growth, 7 to 18 days after sowing (DAS). Raw images were processed with the image analysis software IAP. Barplots showing QTL for the time-resolved traits projected leaf area (left) and relative growth rate (right), illustrate the temporal dynamics of QTL effects on rosette growth in Arabidopsis: QTL are only significant during restricted periods ranging from 2 days to 9 days. Each colour represents a different associated marker.*

ing seed quality using multi-omics data. Tools were developed for automated quantitative analysis of root images using a pre-trained convolutional neural network model (Narisetti *et al.* 2021), and for efficient (semi)automated segmentation (Henke *et al.* 2020; Henke *et al.* 2021).

EMBEDDING IN IPK RESEARCH THEMES

The research group Heterosis predominantly addressed the *Systems Genetics* research area of the Molecular Genetics (MOG) department focussing on vegetative development. Via the large transdisciplinary research project AVATARS, the research group also contributed to the departmental research area *Seed Biology*. The projects are embedded in the IPK Research Theme 4 “Growth and Metabolism”, 5 “Mechanisms of Resistance and Stress Tolerance”, and 1 “Valorisation of Plant Genetic Resources”; the research group co-ordinates jointly with the research group Automated Plant Phenotyping (former research group Acclimation Dynamics and Phenotyping) the IPK-wide plant phenotyping efforts and the corresponding research infrastructure built-up and use.

OUTLOOK

Investigating *Arabidopsis*, maize, rapeseed, and barley, the research group Heterosis will (i) identify and characterise genetic loci that determine the extent of biomass production and seed yield and quality under relevant dynamic environmental conditions, and also integrate spatial dynamics at the organ level (shoot in interaction with the root) (ii) analyse epigenetic effects on growth, biomass heterosis and stress tolerance, (iii) perform time-resolved systems analyses of growth dynamics in inbreds and hybrids, (iv) conduct systems mapping of hybrid-performance related processes in dynamic environments, (v) evaluate genetic and biological predictors of yield / hybrid-performance parameters.

More information: *www.ipk-gatersleben.de/en/research/molecular-genetics/heterosis*

RESEARCH GROUP **AUTOMATED PLANT PHENOTYPING** (APP)

Head: Dr. Kerstin Neumann
(since 01.01.2021)

Selected Publications

CORTINOVIS, G. et al.: Towards the development, maintenance, and standardized phenotypic characterization of single-seed-descent genetic resources for common bean. Curr. Protoc. 1 (2021) e133.

DODIG, D. et al.: Dynamics of maize vegetative growth and drought adaptability using image-based phenotyping under controlled conditions. Front. Plant Sci. 12 (2021) 652116.

HENKE, M. et al.: Semi-automated ground truth segmentation and phenotyping of plant structures using k-means clustering of eigen-colors (kmSeg). Agriculture 11 (2021) 1098.

HENKE, M. et al.: A two-step registration-classification approach to automated segmentation of multimodal images for high-throughput greenhouse plant phenotyping. Plant Methods 16 (2020) 95.

FADOUL, H. E. et al.: Comparative molecular and metabolic profiling of two contrasting wheat cultivars under drought stress. Int. J. Mol. Sci. 22 (2021) 13287.

Until 31.12.2020 this group was named Acclimation Dynamics and Phenotyping and lead by Dr. Astrid Junker

MISSION

Optimising crop performance is a main task in ensuring future crop yields under the two major challenges growing world population and ongoing climate change. The research group is managing key plant phenotyping facilities at IPK (whole plant phenotyping platforms in climatised glass houses, a phytochamber, and the novel Plant Cultivation Hall). The research focus is on employing plant phenomics to gain understanding of plant growth and performance under optimal and abiotic stress conditions, such as drought and heat. By combining relevant mapping panels and genome-wide information, the genetic architecture of complex traits with temporal dynamics such as biomass formation or drought tolerance is elucidated.

RESULTS

In the Whealbi-spring wheat panel, the negative impact of drought on biomass was clearly visible, while the relative growth rate increased after re-watering. The PSII efficiency in steady-state conditions (QY.H) and in the transition to low light (QY.L) was assessed. Both were strongly reduced and slowly recovered to the level of well-watered plants. During the recovery phase, we observed a correlation of QY.H and QY.L to the final biomass in drought treatment. We conclude that PSII efficiency is a limiting factor for growth under increased sink demand, which was not the case in control treatment. Breeding lead to a reduction of biomass/height but increasing QY.H (Figure 1A). Supporting the Whealbi findings, also in winter wheat lines (1960ies to 2010s) from the BRIWECS project, we observed similar breeding trends. Moreover, a correlation of QY.H to field grain yield (Fig. 1B) suggests that breeding improved yield at least partially by optimising photosynthesis.

The obtained drought severity threshold (Dhanagond *et al.* 2019) enabled us to mimic a slowly progressing and intensifying drought until maturity. For the first time ever, non-invasive phenotyping covered the complete life cycle. We investigated Israelian wheat cultivars and their corresponding near isogenic lines that carry a QTL for improved grain yield under drought. Our setup could reproduce the improved grain yield under drought in the field and shed light on the underlying factors. A manuscript on the results is currently being developed. Additionally, two contrasting wheat cultivars have been investigated (Fadoul et al. 2021). The tolerant cultivar upregulated regulatory genes, and produced more sugars, organic acids and important amino acids to maintain its superior growth under drought. The research group Automated Plant Phenotyping is furthermore involved in the management of the IPK phenomics facilities (jointly with research group Heterosis), coordination of collaborative access to phenotyping facilities and the implementation/improvement of the data management system for the standardised documentation, sustainable storage and dissemination of phenomics datasets according to FAIR principles (with research group Bioinformatics and Information Technology). In the frame of EPPN2020, seven collaborative projects have been conducted in 2020 and 2021. In 2021, the installation work of the PhenoCrane was completed, now having a fully functional Plant Cultivation Hall.

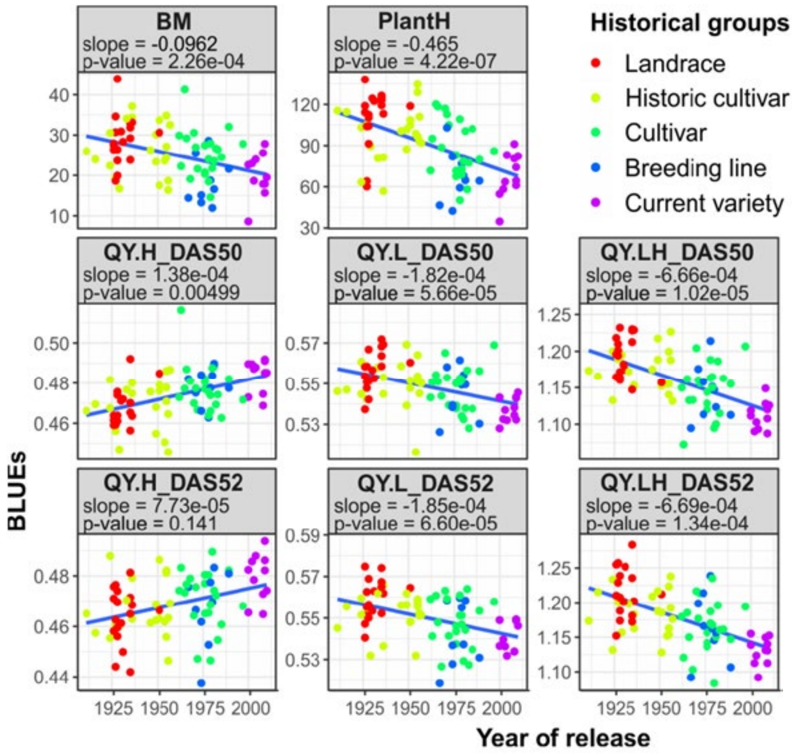


Figure 1A: *Breeding impact in Whealbi spring wheat panel on traits from well-watered conditions. BM – final plant biomass, PlantH – final plant height, QY.LH – ratio of QY.L to QY.H.*

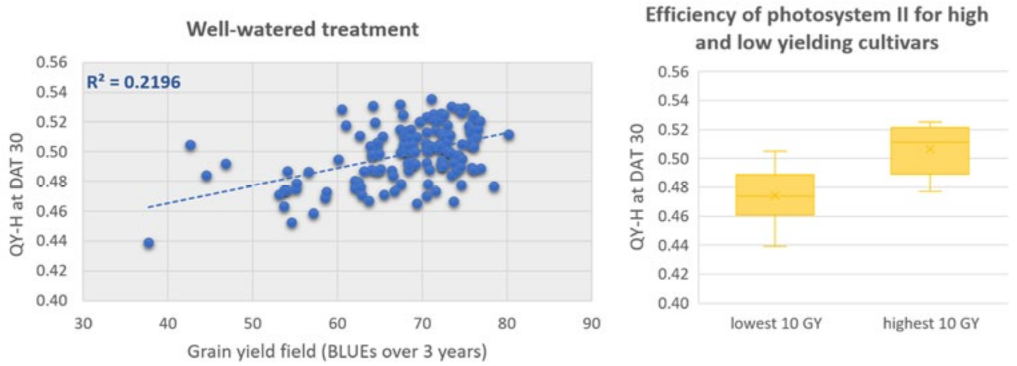


Figure 1B: *Correlation between QY.H in the tillering stage measured on the platform and field grain yield (GY) from in the BRIWECS winter wheat panel.*

EMBEDDING IN IPK RESEARCH THEMES

The research focus of the research group Automated Plant Phenotyping is deeply embedded into IPK Research Themes 4 “Growth and Metabolism”, 5 “Mechanisms of Resistance and Stress Tolerance” and 1 “Valorisation of Plant Genetic Resources”. In barley, wheat and chickpea Plant Genetic Resources are characterised for their growth characteristics and abiotic stress tolerance in combination with *omic*-approaches to reveal the underlying mechanisms. Within the INCREASE project, we are involved in the valorisation of bean, chickpea, lentil and lupin Plant Genetic Resources.

OUTLOOK

The research group Automated Plant Phenotyping is expanding the spectrum of crops to chickpea in the frame of the INCREASE project. It will deepen its research on drought and heat tolerance effects in wheat in a DFG research group building up on the BRIWECS results. Moreover, the focus is extended to root growth and architecture. We are further deepening the information gained by phenomics by adding -omics to gain a holistic understanding of the involved processes. The future work will also involve the novel plant phenotyping infrastructures in the Plant Cultivation Hall. The network of local, national and international collaborators will be strengthened, for example by DPPN access projects and by the Stargate project.

More information: *www.ipk-gatersleben.de/en/research/molecular-genetics/automated-plant-phenotyping*

RESEARCH GROUP
IMAGE ANALYSIS (BA)

Head: Dr. Evgeny Gladilin

MISSION

The research group Image Analysis focuses on development of algorithms and integrative software solutions for quantitative characterisation (phenotyping) of morphological, developmental and physiological plant traits using multimodal and multidimensional data such as visible light, fluorescence, near-infrared, 3D and microscopic images. The tasks of image analysis include image enhancement, segmentation, registration, classification and modelling of relevant plant structures (e.g., shoots, roots, leaves, spikes, barbs, seeds, cells, etc.) as well as design of software tools including algorithmic pipelines and user-interfaces for automated and semi-automated image processing.

RESULTS

In 2020-2021, the research group Image Analysis continued its major line of research including development of algorithmic pipelines and software tools for computational analysis of large multimodal image data acquired by plant phenotyping experiments. The particular research focus of the group was on development of two major groups of applications for semi- and fully-automated root and shoot image analysis.

For automated analysis of a large amount of heterogeneous image of permanently developing and optically changing plant structures, advanced machine and deep learning methods are required. For training advanced image segmentation and classification models, a large amount of representative ground truth (i.e. manually annotated) images is needed. To speed up the generation of reliable ground truth data, special tools for semi-automated image segmentation were developed. For example, the kmSeg tool was designed to enable even unskilled users an efficient segmentation of greenhouse shoot images into fore- and background structures. Based on representative sets of ground truth data for different plant types, imaging modalities, screening platforms and camera views, algorithmic pipelines for automated shoot image registration, classification and phenotyping were established.

For analysis of structurally complex and noisy soil-root images acquired with the recently established *Rhizotron* phenotyping facility, deep learning segmentation methods were applied.

To cover large variability in shape, size and structures of root structures in different species and experimental conditions, large amount of manually annotated images was generated. Using such semi-automatically annotated images, a U-net and GUI based tools for fully automated root image segmentation and phenotyping were developed.

Further research activities of the research group Image Analysis include investigation and development of methods for detection and quantitative analysis of special plant organs such as wheat spikes. The fundamental challenge of detecting plant parts that have a similar colour fingerprint as the remaining plant biomass was addressed by generating reliable reference data followed by training deep learning neural network models. In addition to peer-reviewed journal publications, the results of our work were presented at meetings as the “GCB 2021” and the “GPZ 2021”.

In 2020-2021, the Image Analysis group launched the R&D activities within the scope of the BMBF funded AVATARS project including development of methods for normalisation and statistical modelling of 3D seed structures as well as computational modelling of the early stages of embryonic seed growth.

Selected Publications

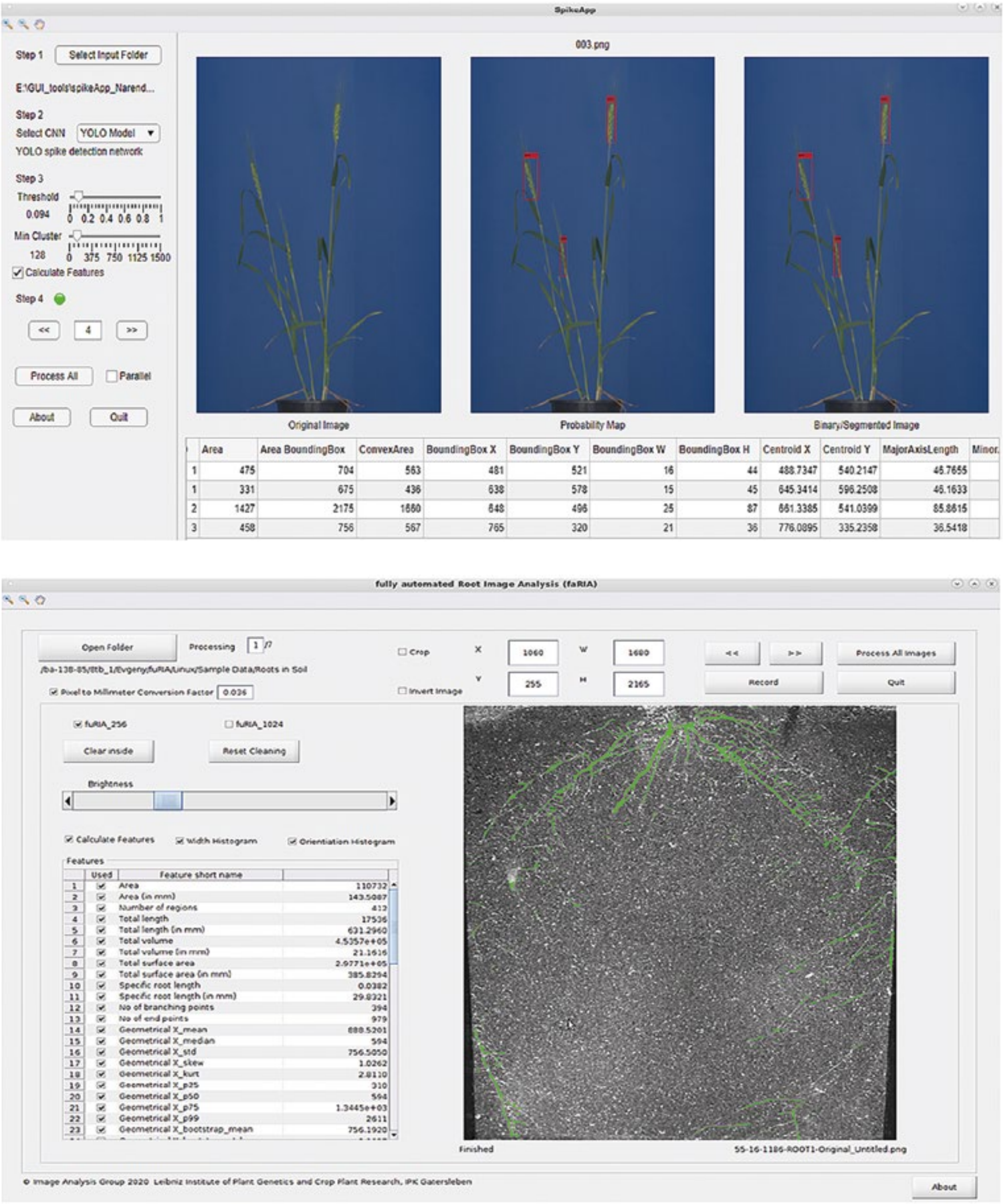
HENKE, M. et al.: Semi-automated ground truth segmentation and phenotyping of plant structures using k-means clustering of eigen-colors (kmSeg). Agriculture 11 (2021) 1098.

HENKE, M. et al.: A two-step registration-classification approach to automated segmentation of multimodal images for high-throughput greenhouse plant phenotyping. Plant Methods 16 (2020) 95.

NARISETTI, N. et al.: Fully-automated root image analysis (faRIA). Sci. Rep. 11 (2021) 16047.

NARISETTI, N. et al.: Automated spike detection in diverse European wheat plants using textural features and the Frangi filter in 2D greenhouse images. Front. Plant Sci. 11 (2020) 666.

ULLAH, S. et al.: Towards automated analysis of grain spikes in greenhouse images using neural network approaches: a comparative investigation of six methods. Sensors 21 (2021) 7441.



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Step 2
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YOLO spike detection network
Step 3
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	Area	Area BoundingBox	ConvexArea	BoundingBox X	BoundingBox Y	BoundingBox W	BoundingBox H	Centroid X	Centroid Y	MajorAxisLength	Minor.
1	475	704	563	481	521	16	44	488.7347	540.2147	46.7655	
1	331	675	436	638	578	15	45	645.3414	596.2508	46.1633	
2	1427	2175	1660	648	496	25	87	661.3385	541.0399	85.8615	
3	458	756	567	765	320	21	36	776.0895	335.2358	36.5418	

Processing 1 /7
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☐ Invert Image
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Y 255
W 1680
H 2165
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☐ fuRIA_1024
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☑ Orientation Histogram

Features

	Used	Feature short name	
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4	☑	Total length	17536
5	☑	Total length (in mm)	631.2960
6	☑	Total volume	4.5357e+05
7	☑	Total volume (in mm)	21.1616
8	☑	Total surface area	2.9771e+05
9	☑	Total surface area (in mm)	385.8294
10	☑	Specific root length	0.0382
11	☑	Specific root length (in mm)	29.8321
12	☑	No of branching points	394
13	☑	No of end points	979
14	☑	Geometrical X_mean	888.5201
15	☑	Geometrical X_median	594
16	☑	Geometrical X_std	756.5050
17	☑	Geometrical X_skew	1.0262
18	☑	Geometrical X_kurt	2.8110
19	☑	Geometrical X_p25	310
20	☑	Geometrical X_p50	594
21	☑	Geometrical X_p75	1.3445e+03
22	☑	Geometrical X_p99	2611
23	☑	Geometrical X_bootstrap_mean	756.1920

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Figure 1: *Screenshot of software solutions for automated detection of grain spikes (top) and root image segmentation (bottom) using pretrained deep learning models.*

EMBEDDING IN IPK RESEARCH THEMES

The research group Image Analysis contributes to the IPK Research Theme 4 "Growth and Metabolism" and 5 "Mechanisms of Resistance and Stress Tolerance" and cooperates closely with the IPK research groups Heterosis, Automated Plant Phenotyping, Assimilate Allocation and NMR, and Bioinformatics on quantitative plant image analysis and phenotyping. Furthermore, the group contributes to analysis of microscopic image data acquired by the research group Chromosome Structure and Function.

OUTLOOK

Future plans of the Image Analysis group include further development of advanced methods for plant image segmentation, registration, classification, phenotypic characterisation and modelling. The group will continue investigation and development of deep learning methods for automated detection and classification of plant structures in complex optical scenes from high-throughput phenotyping platforms. Furthermore, the spectrum of image analysis applications is going to be extended to segmentation and phenotyping of special plant organs such as root systems, leaves, spikes, barbs, seeds that are in focus of investigations of IPK and external partner groups.

More information: *www.ipk-gatersleben.de/en/research/molecular-genetics/image-analysis*

RESEARCH GROUP
METABOLIC DIVERSITY (MD)

Head: Dr. John D’Auria

MISSION

The overarching goal of the Metabolic Diversity group is to utilise modern biochemical, chemical analytical, and genetic techniques to study the production and utilisation of plant-derived metabolites in important agricultural species. Projects within the MD group not only study why plants make such a diverse range of compounds, but also why chemical profiles differ so drastically across all taxonomic levels. The integrative analyses performed by the group focuses on parameters (growth rates, vitality, seed viability and yield) necessary to provide the further development of hypotheses related to understanding the interplay of genetics and metabolism in cultivated plants.

RESULTS

Several main research themes within the auspices of the Metabolic Diversity research objectives have been of particular focus: (i) Elucidation of all biochemical steps used for the production of tropane alkaloids in members of the Erythroxylaceae and their demonstration via synthetic biology platforms (ii) Establishing genetic and biochemical resources for the study of napthodianthrone production in multiple plant families including the Hypericaceae and Polygonaceae (iii) Identification of metabolites and their biosynthetic pathways in the Poaceae involved in multiple abiotic and biotic stress interactions.

An important aspect of the future development of tools used in the group is synthetic biology. The ability to manipulate genes and their enzymes in multiple organisms enables the use of very powerful techniques to identify critical traits in plants for future agricultural purposes. In close collaboration with Dr. Christina Smolke of Stanford University, we have used the multiplicative power of synthetic biology in yeast to identify and characterise the remaining ‘black boxes’ existing in tropane alkaloid biosynthesis. It should be stressed that the tools developed in the group are not only for the study of alkaloids, but are also being used for what is considered more IPK relevant species such as barley and rye.

The Metabolic Diversity group continues to work on the genetics of hypericin production and apomixis in *Hypericum perforatum* (St. John´s wort) and related species. To this end, our group has prepared and submitted several grant applications this year regarding transcript profiling of *Hypericum*. In addition, we have been able to expand our collaboration with members of the Leibniz Institute of Plant Biochemistry (IPB) in Halle to further top researchers in the field of hypericin biosynthesis from the University of Braunschweig and the University of Hannover. Internal flagship funding for SpaceEx, a project for visualising mRNA transcripts on tissue sections continues with

Selected Publications

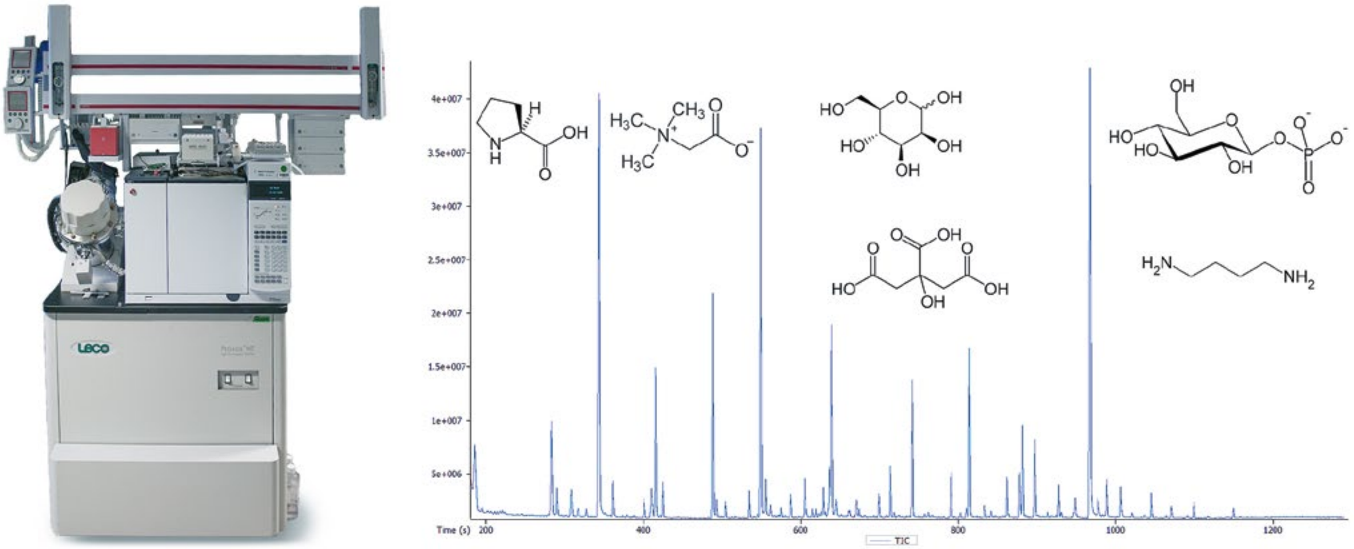
ALSEEKH, S. et al.: Mass spectrometry-based metabolomics: a guide for annotation, quantification and best reporting practices. Nat. Methods 18 (2021) 747-756.

IRFAN, M. et al.: Evolution-aided engineering of plant specialized metabolism. aBIOTECH 2 (2021) 240-263.

RIZZO, P. et al.: The biochemical and genetic basis for the biosynthesis of bioactive compounds in Hypericum perforatum L., one of the largest medicinal crops in Europe. Genes 11 (2020) E1210.

KIM, N. et al.: Structure and function of enzymes involved in the biosynthesis of tropane alkaloids. In: SRIVASTAVA, V., S. MEHROTRA & S. MISHRA (Eds.): Tropane alkaloids – pathways, potential and biotechnological applications. Singapore: Springer Nature (2021) 21-50.

STARK, P. et al.: PSYCHE – a valuable experiment in plant NMR-metabolomics. Molecules 25 (2020) 5125.



promising preliminary results and will continue development. Other proposals connected to *Hypericum* research that are embedded in the afore mentioned research network are currently in progress.

The Metabolic Diversity research group collaborations from within the institute include projects such as the ‘Stabilstroh‘ project, alfalfa and cowpea drought tolerance metabolism and barley secondary metabolites related to drought tolerance and allelopathy. From within Germany, the group is pursuing grants and projects regarding enzyme diversity in lipids and secondary metabolites with members of the Max Planck Institute of Molecular Plant Physiology (MPI-MP) in Potsdam, as well as members of the Pharmacy school at the University of Braunschweig. More than six European partners are collaborating with the research group within the framework of the EPPN2020 transnational access programme in order to assess metabolite changes occurring in multiple agronomically important species as a result of either abiotic (drought) or biotic (fungal infection) stress treatments.

Figure 1: *A representative polar/semi-polar analysis of plant metabolites using GC-TOF instrumentation. This non-targeted analysis typically identifies approximately 300 metabolic features which include amino acids, organic acids, sugars, sugar acids and polyamines.*

EMBEDDING IN IPK RESEARCH THEMES

The work being performed by members of the Metabolic Diversity group squarely falls under the aegis of Research Theme 4 “Growth and Metabolism”. The main interests of the group are aimed at understanding how the interplay of environmental and genetic factors effect the metabolic outcomes of crop plants and, by extension, their growth characteristics. While the majority of our work corresponds with this theme, we are also associated with Research Theme 5 “Mechanisms of Resistance and Stress Tolerance”.

OUTLOOK

The future priorities for the Metabolic Diversity group continue to focus on generating high quality metabolomic data regarding economically important crop plant species. Specifically, the next year will continue its focus on internal collaborations within the IPK dealing with barley and rye. The group will begin experiments regarding metabolites in fava beans as part of the increasing interest in protein crops at the IPK. Additionally, the group will continue working with medicinal plant species that are also important crops for Europe. We will be expanding the group’s cohort of graduate students via external funding as well as opportunities such as the IMPRS program (Max Planck Society).

More information: *www.ipk-gatersleben.de/en/research/molecular-genetics/metabolic-diversity*

RESEARCH GROUP
SEED DEVELOPMENT (SE)

Head: Dr. Jozefus Schippers

MISSION

The alternation of generations in plants is especially exemplified by the formation and germination of seeds. For humans, cereal grains have become essential for our dietary needs, for animal feeding and industrial processing. Current climate change and the associated increase in extreme weather events represent a major challenge for agricultural practice and productivity.
Our general goal is to understand molecular mechanisms controlling plant development with a focus on seed formation. Recent breakthroughs in cereal genomics have paved the way for functional genomics and the identification of biological mechanisms controlling relevant crop traits. We focus on seed development in barley but also study developmental processes and responses to abiotic stress in other plants species like wheat, rapeseed, sugar beet, rice and *Arabidopsis*. At the molecular level we are mainly interested in gene regulatory networks and plant hormone and reactive oxygen species (ROS) signalling cascades.

RESULTS

Elucidation of gene-regulatory-networks (GRNs) in barley during grain development will greatly contribute to our understanding of the molecular regulation of seed formation in a spatial and temporal resolution. In addition, it will enable us to assign functions and processes to genes that are currently undescribed. We developed DNA-affinity Purification Sequencing (DAP-SEQ) methodology for barley and wheat to elucidate GRNs and identify key transcriptional regulators of important grain traits (Figure 1). For this method we express a transcription factor of interest and provide it with a native genomic DNA library that is prepared from a plant tissue of interest at a given developmental stage. The extensive range of adaptability of DAP-SEQ to different transcription factors, plant species and genomic DNA libraries has the potential to advance the field of functional crop genomics in the coming years.

The Seed Development group has a long history on studying tissue-specific processes in cereals and has a strong expertise in laser capture microdissection (LCM) coupled to RNA-seq. Recently, a barley spike expression atlas has been published (Thiel *et al.* 2021, Sci Adv.). In addition, we collaborate with commercial partners to identify tissue-specific processes in crops. Tissue-specific expression libraries allow for selecting candidate genes with a potential role in the formation of specific tissues for functional genomics approaches. Current functional genomics studies focus on the role of the Two-Component Signalling (TCS) system during early endosperm specification and differentiation. To this end, transgenic barley lines have been established using classical RNAi but also the CRISPR/Cas9 technology. Knockdown of the TCS element histidine kinase 1 (HvHK1) impairs endosperm transfer cell formation resulting in a reduced grain size (Hertig *et al.* 2020, Plant J). Activation of the HvHK1-controlled signalling pathway results in a transcriptional reprogramming through the action of so-called RESPONSE-REGULATORs (RRs). Multiple RRs have been selected for a functional analysis through the establishment of transgenic models. Next to RRs, we

Selected Publications

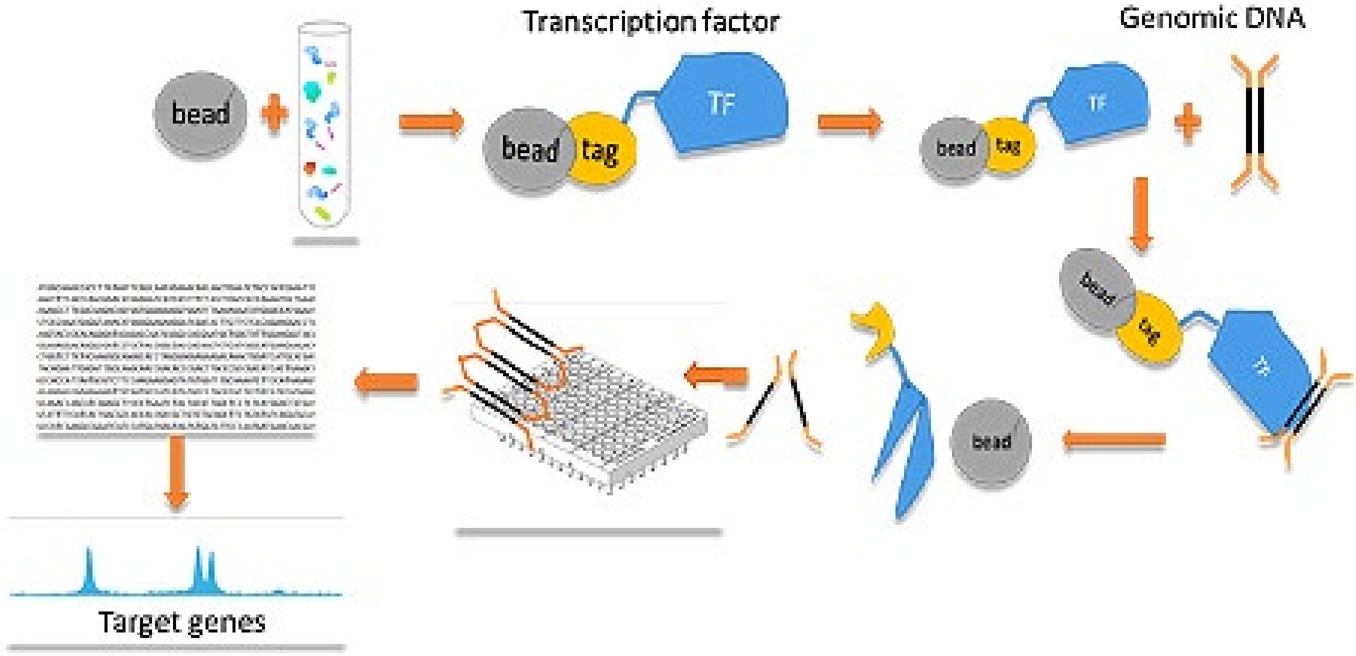
THIEL, J., R. KOPPOLU* et al.: Transcriptional landscapes of floral meristems in barley. Sci. Adv. 7 (2021) eabf0832. * joint first authorship*

HERTIG, C. et al.: Barley HISTIDINE KINASE 1 (HvHK1) coordinates transfer cell specification in the young endosperm. Plant J. 103 (2020) 1869-1884.

REIS, R.S. et al.: An antisense noncoding RNA enhances translation via localised structural rearrangements of its cognate mRNA. Plant Cell 33 (2021) 1381–1397.

SASIDHARAN, R. et al.: Redox and low-oxygen stress: signal integration and interplay. Plant Physiol. 186 (2021) 66–78.

MORA-RAMIREZ, I. et al.: The da1 mutation in wheat increases grain size under ambient and elevated CO2 but not grain yield due to trade-off between grain size and grain number. Plant-Environ. Interact. 2 (2021) 61-73.



study other grain transcription factors for which transgenic lines in barley have been obtained for a detailed characterisation in the coming time. In addition, we study the role of ROS gradients and homeostasis during plant development and evolution.

Figure 1: *Schematic overview of the DAP-SEQ methodology to decipher GRNs in cereals*

EMBEDDING IN IPK RESEARCH THEMES

The research within the Seed Development research group is covered by three IPK Research Themes 3 “Mechanisms of Plant Reproduction”, 4 “Growth and Metabolism” and 5 “Mechanisms of Resistance and Stress Tolerance”. We are highly connected with other research groups within the IPK but also collaborate with other research groups from other institutions, both national and international.

OUTLOOK

Currently the role of superoxide dismutase in plant growth and stress signalling is studied. Furthermore, we are part of the MAdLand consortium, to study the role of the enzyme in the alternation of generations and the conquest of land by plants, which is funded through a DFG priority programme. Also, we study embryo development in rapeseed as part of the BMBF-funded AVATARS project. Furthermore, the impact of ROS homeostasis on cell expansion and differentiation is studied in collaboration with KWS SAAT SE & Co. KGaA in sugar beet and *Arabidopsis*. Finally, we study the impact of protein-turnover on sink and source activity in plants by focusing on the transcriptional regulation of the proteasome.

The successful implementation of DAP-seq in the Seed Development group is expected to result in novel collaborations on the elucidation of GRNs in barley and other cereals. Furthermore, we aim at expanding our repertoire on methods for the detection and quantification of ROS *in planta*. One other aim of our group is to extend our research activities on abiotic stress tolerance in rice.

More information: *www.ipk-gatersleben.de/en/research/molecular-genetics/seed-development*

RESEARCH GROUP **ASSIMILATE ALLOCATION AND NMR** (AAN)

Head: PD Dr. Ljudmilla Borisjuk

Selected Publications

ROLLETSCHEK, H. et al.: Cellular plasticity in response to suppression of storage proteins in the Brassica napus embryo. Plant Cell 32 (2020) 2383-2401.

MEITZEL, T. et al.: Trehalose 6-phosphate promotes seed filling by activating auxin biosynthesis. New Phytol. 229 (2021) 1553-1565.

MUSZYNSKA, A. et al.: A mechanistic view on lodging resistance in rye and wheat: a multiscale comparative study. Plant Biotechnol. J. 19 (2021) 2646-2661.

ROLLETSCHEK, H. et al.: The process of seed maturation is influenced by mechanical constraints. New Phytol. 229 (2021) 19-23.

STURTEVANT, D. et al.: The genome of jojoba (Simmondsia chinensis): A taxonomically isolated species that directs wax ester accumulation in its seeds. Sci. Adv. 6 (2020) eaay3240.

MISSION

Our research aims to better understand the relationships between assimilate supply, metabolism and seed architecture, thereby uncovering mechanisms for improved traits in major crops. We apply topographical *in vivo* approaches for analysing assimilate uptake and transport towards and within the developing seed, and the conversion of assimilates into storage products. We are working on traditional crops and new plant models. Our approaches essentially rely on non-invasive imaging procedures such as magnetic resonance imaging (MRI), near-infrared microspectroscopy (FTIR) combined with mass spectrometry (MS) and molecular tools. Our method developments are at the forefront of MRI approaches on plants.

RESULTS

The teamwork of Assimilate Allocation and NMR has led to the following new findings:
(1) Trehalose 6-phosphate (T6P) promotes seed filling by activating auxin biosynthesis. We engineered transgenic pea plants to modulate T6P levels specifically in the growing embryo with the aim of investigating the role of this signalling sugar during seed filling. We found that T6P promotes the expression of the auxin biosynthesis gene *TRYPTOPHAN AMINOTRANSFERASE RELATED2* (*TAR2*), and the resulting effect on auxin levels is required to trigger storage processes and embryo differentiation. By modulating the T6P content in growing embryos of pea, we uncovered a link between this signalling sugar and the major plant hormone auxin. This discovery represents a significant step forward in understanding interactions between metabolites and hormones with T6P reporting the raising sucrose status in the maturing seed (Meitzel *et al.* 2021, New Phytol.).
(2) Cellular plasticity maintains the appropriate storage of carbon and nitrogen reserves for seed viability. We generated oilseed rape plants with RNAi-mediated suppression of the two dominant storage protein classes (napin and cruciferin) in seed. Protein storage in embryos of transgenic plants was balanced by an increased synthesis of the membrane protein oleosin. While the shift from vacuolar to membrane storage substantially altered the intracellular architecture of cells, the overall visible seed phenotype appeared to be unaffected. Detailed -omics and MRI analysis revealed a remarkable level of plasticity in the cellular architecture and metabolism of the embryo (Rolletschek *et al.* 2020, Plant Cell).
(3) A higher number of vascular bundles and a higher degree of their incline are the features of lodging-resistant versus lodging-prone lines in rye and wheat. MRI displayed the 3-dimensional assembly of vascular bundles in stem and FTIR spectroscopy further identified elevated levels of lignin and xylan as features associated with high lodging resistance. A simplistic mathematical model showed how mechanical forces distribute within the stem under stress. Our findings on mechanical stability may be important for breeders for the improvement of lodging resistance of tall posture cereal crops (Muszynska *et al.* 2021, Plant Biotechnol. J.).
(4) Elucidation of the molecular machinery for lipid synthesis and storage in the desert shrub Jojoba. In a collaborative study, MRI was used to provide a visualisation of lipid distribution in the nuts of Jojoba (*Simmondsia chinensis*) plants. This was combined with extensive transcriptome, proteome, and lipidome data to define the heterogeneous pathways for lipid storage.
(5) The process of seed maturation is influenced by mechanical constraints. We demonstrate that mechanical constraint can boost the seed's accumulation of lipid and protein by combining MRI with various analyses carried out at the molecular and biochemical level. Both *in planta* and *in vitro*, the developing *Brassica napus* embryo responds to physical restraint by an acceleration in its maturation (Rolletschek *et al.* 2021, New Phytol.).

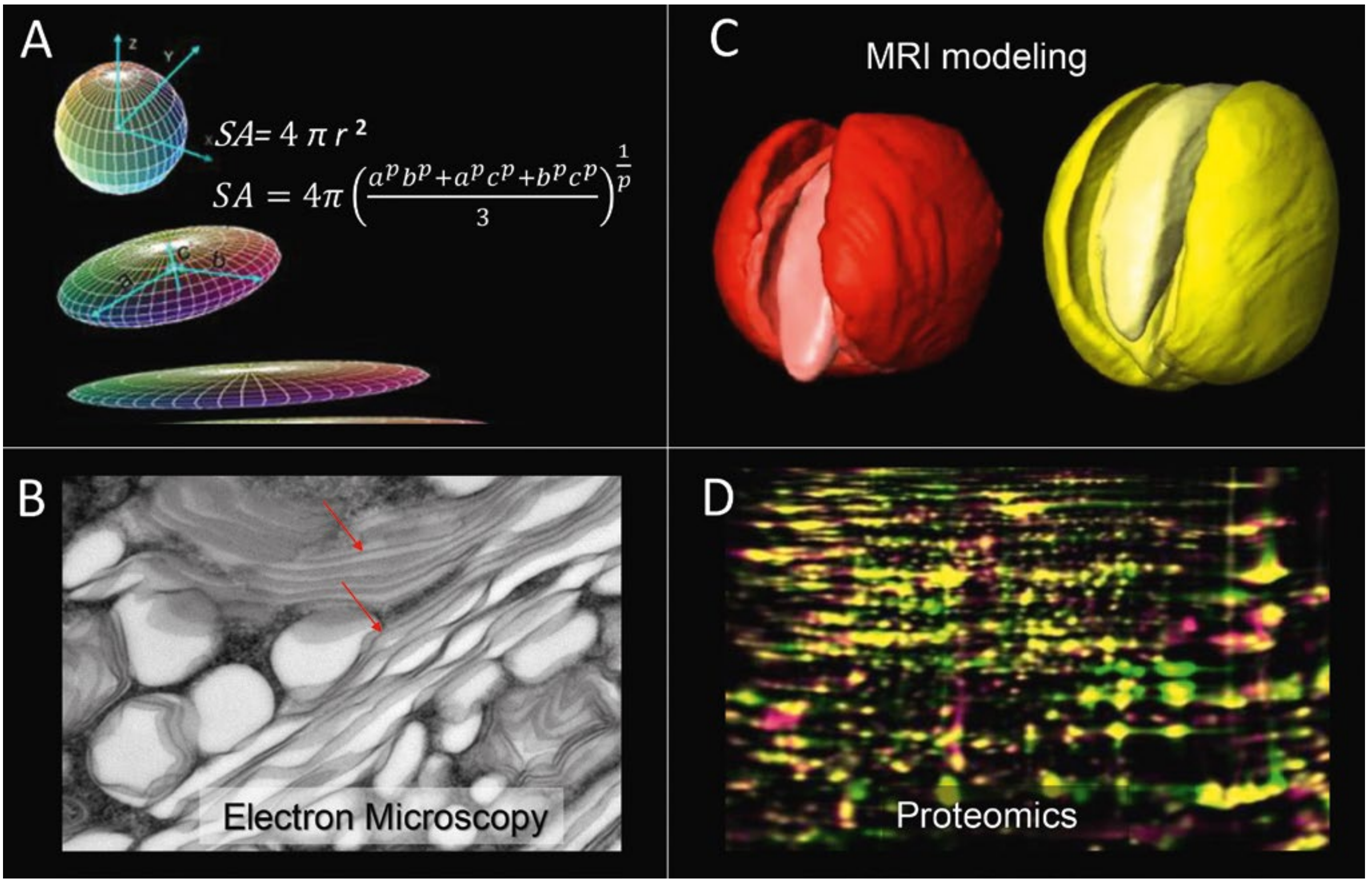


Figure 1: *Mechanistic insights into the intriguing link between lipid and protein storage in oilseed rapeseed. Suppressing key genes encoding napin and cruciferin led to the switch from vacuolar to membrane protein storage, so that embryonic cells elaborate membrane stacks enriched with oleosin protein (A, B). The phenotypic outcomes were comprehensively assessed using MRI-based 3D-modelling, proteomics and others (C, D). The apparent cellular plasticity in seeds protects against perturbations to its storage capabilities and, hence, contributes materially to homeostasis (for details Rolletschek et al., Plant Cell 2020).*

EMBEDDING IN IPK RESEARCH THEMES

Our work is integrated into the IPK Research Theme 4 “Growth and Metabolism”. In frame of the Molecular Genetics department research area Seed Biology, we are investigating mechanisms of assimilate allocation. We further contributed to IPK Research Themes 1 “Valorisation of Plant Genetic Resources” and 2 “Genome Diversity and Evolution” (studies on DEFECTIVE ENDOSPERM-D1, VPEs). New method developments enabled contributions to Research Theme 5 “Mechanisms of Resistance and Stress Tolerance” (logging resistance in rye/wheat; salinity/osmotic stress resistance in barley).

OUTLOOK

We plan to keep our scientific focus on the investigation of assimilate transport and assimilate usage for seed filling in major crops, such as barley, wheat, maize, rice, pea and oilseed rape. We are also starting to work with new plant models: *Lemna*, Amarantus, Coffea, Musa and Cactus. We are expanding our NMR platform by super-wide bore NMR (granted by “Europäischer Fonds für regionale Entwicklung”). This represents a major milestone for own future research and IPKs outstanding research infrastructure, and sets an additional scientific footprint of the IPK to the world map. The networking with the international scientific community toward dissemination of MRI technology will be intensified.

More information: *www.ipk-gatersleben.de/en/research/molecular-genetics/assimilate-allocation-and-nmr*

RESEARCH GROUP **NETWORK ANALYSIS AND MODELLING** (NAM)

Head: Dr. Jędrzej Jakub Szymański

MISSION

The research area of the Network Analysis and Modelling group can be defined as plant systems genomics. Our major objective is to uncover and investigate molecular mechanisms of phenotype emergence in crops by means of large-scale data integration on the genomic, transcriptomic, metabolomic and phenomic levels. Furthermore, we provide statistical expertise, machine learning solutions, and data visualisation tools allowing integration and interpretation of data generated in the Molecular Genetics department.

RESULTS

We investigate large-scale multi-omics datasets in search of molecular mechanisms linking variation of the genome sequence with complex phenotypes. Our approach has been exemplified in our recent studies in tomato, where integration of genomic, transcriptomic, metabolomic and phenotype data from fruits of 580 *Solanum lycopersicum* – *Solanum pennellii* backcrossed inbred lines resulted in the identification of two new enzymes of the steroidal glycoalkaloid (SGA) pathway, responsible for removal of phytotoxicity of the tomato fruits during the ripening process (Szymanski *et al.* 2020, *Nature Genetics*). Additionally, we have identified a community of genes and metabolites determining the resistance of tomato fruit to a common fungal pathogen *Botrytis cinerea* and validated the function of selected candidates. In another study, we performed an integrative analysis of transcriptomic and metabolic responses of *S. lycopersicum* to variation in the root microbiome. Identified relationships highlighted the existence of systemically induced root exudation (SIREM) in plants and the identification of the azelaic acid as its main signalling compound (Korenblum *et al.* 2020). Development of new methods for network-based evaluation of metabolic genome-wide association mapping (mGWAS) enabled the discovery of new genes involved in the lipid metabolism of *Arabidopsis thaliana*. Allelic variation of one of them (KCS4) has been shown to have an effect on fatty acid rearrangement under carbon starvation by our collaborators at the Ben Gurion University, in Israel. Finally, in collaboration with the Max Planck Institute of Molecular Plant Physiology in Potsdam we investigated principles of carbon flux through the pathways of photosynthesis and central metabolism in plants and algae representing different types of photosynthesis and carbon assimilation (Treves *et al.* 2020, Nature Plants). The results highlighted environmentally-driven adaptations of photosynthetic organisms on the level of metabolic fluxes.

Further collaborations.

We are collaborating closely with IGZ Großbeeren and IPB Halle in the frame of the Leibniz Collaborative Excellence project on tomato heat stress resistance. We collaborate with the Weizmann Institute of Science and Ben Gurion University on gene function discovery in specialised metabolism of tomato and lipid metabolism of *Arabidopsis*.

EMBEDDING IN IPK RESEARCH THEMES

The Network Analysis and Modelling group interacts with interested parties from all departments concerning transcriptomics and statistical data analysis without considering the particular research focus. The research focus of the group is directed to large-scale omics analyses and questions raised in the research groups Heterosis, Seed Development, and Assimilate Allocation and NMR, which makes the group a

Selected Publications

SZYMAŃSKI, J. et al.: Analysis of wild tomato introgression lines elucidates the genetic basis of transcriptome and metabolome variation underlying fruit traits and pathogen response. Nat. Genet. 52 (2020) 1111-1121.

KORENBLUM, E. et al.: Rhizosphere microbiome mediates systemic root metabolite exudation by root-to-root signaling. Proc. Natl. Acad. Sci. U.S.A. 117 (2020) 3874-3883.

TREVES, H. et al.: Multi-omics reveals mechanisms of total resistance to extreme illumination of a desert alga. Nat. Plants 6 (2020) 1031-1043.

SAHU, A. et al.: Advances in flux balance analysis by integrating machine learning and mechanism-based models. Comput. Struct. Biotechnol. J. 19 (2021) 4626-4640.

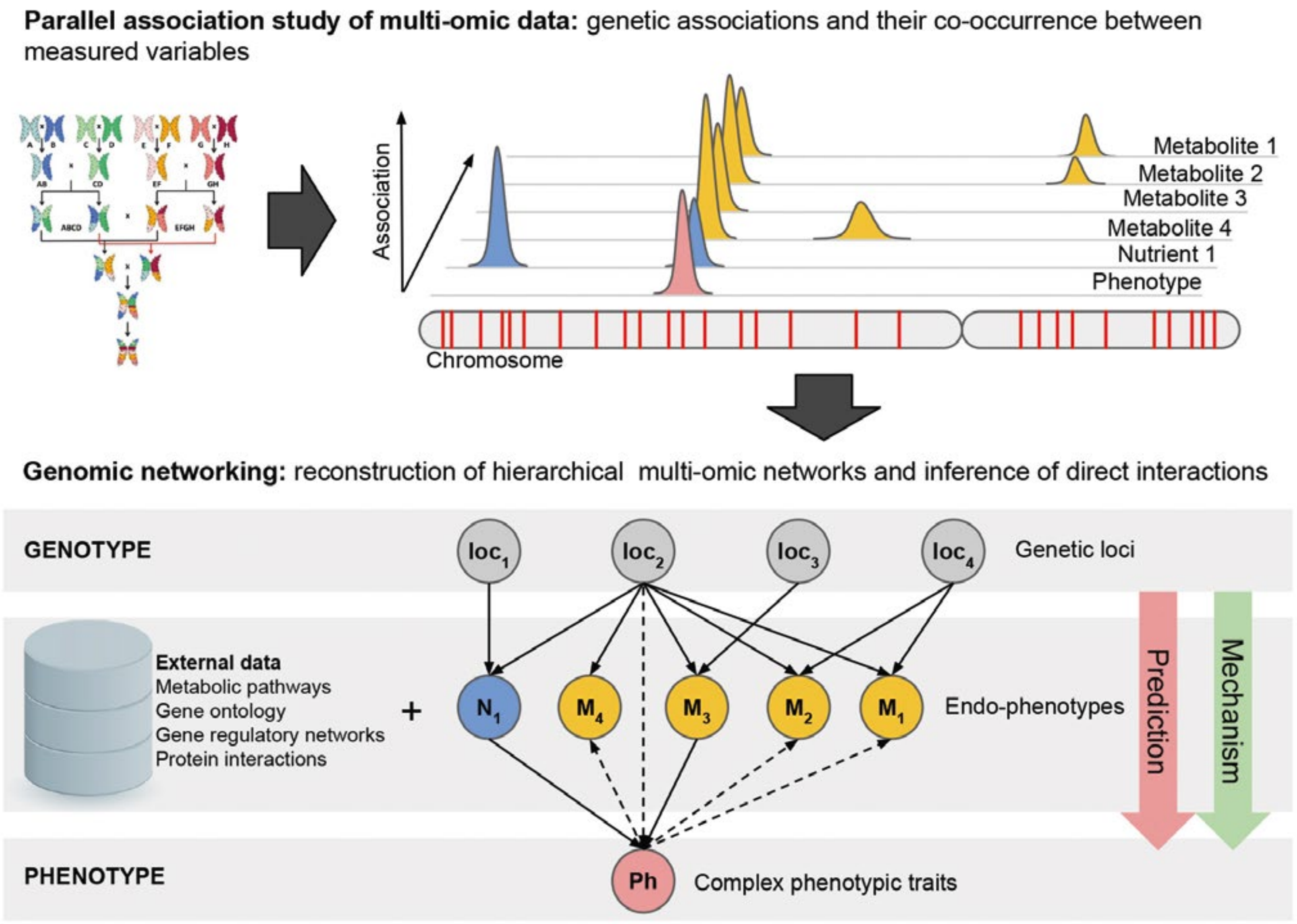


Figure 1: *Schematic representation of the multi-omic data integration using genomic networking applied recently in the study of a multi-parental nested association mapping population of barley in collaboration with the Applied Biochemistry group.*

member of the IPK Research Theme 4 “Growth and Metabolism”. Recent progress of the research group in deep learning-based sequence analysis tightened its links with the IPK Research Theme 2 “Genomdiversity and Evolution”.

OUTLOOK

In the near future, we will expand our activities in three main directions: systems genomics, deep learning approaches for genomic data, and gamification of molecular networks.

We currently focus on development and implementation of deep-learning algorithms to address the question of genetic variation of gene regulatory networks. We train the algorithms on DNA sequence combined with RNAseq, ChipSeq and DAPseq data to enable efficient capturing of polymorphisms responsible for genotype-specific regulation of gene expression. Another research direction in our lab is inspired by the parallels between biological systems and game design principles. We explore this theme by turning plant molecular networks into game engines, enabling both human actors as well as machine learning algorithms to learn how to play it and win for a given set of rules and game objectives. Our pilot “PlantEd Game” uses a generic plant genome-scale metabolic model and flux balance analysis in the background of simple real-time strategy gameplay. You can find the latest release of PlantEd on our Github together with the installation instructions and the gameplay tutorial: https://github.com/NAMlab/PlantEd

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More information: *www.ipk-gatersleben.de/en/research/molecular-genetics/network-analysis-and-modelling*

YOUNG INVESTIGATORS GROUP
INTEGRATED MECHANISTIC MODELS
(IMM) established 01.01.2021

Head: Dr. Mary-Ann Blätke

MISSION

The young investigator's group Integrated Mechanistic Models founded in the frame of the BMBF-funded AVATARS project at the beginning of 2021, thrives on driving innovations in crop breeding through computational biology. By developing and employing integrative approaches to multimodal data analysis, the group deciphers molecular mechanisms involved in plant growth and development and the regulation of metabolism. In this respect, the development of integrative data- and mechanism-based models provide the means for predicting a plant's performance in different environments or genetic settings while providing a level of explainability for trust-based decisions in breeding programmes for resilient, climatically adapted, and resistant crops.

RESULTS

Since the foundation of the young investigator's group in 2021, the research group Integrated Mechanistic Models has focused on deriving a metabolic network of *B. napus* seed metabolism in the form of a multi-organ whole seed model as part of AVATARS. As both A. *thaliana* and *B. napus* are members of the family Brassicaceae and therefore, closely related, we base the construction of the metabolic network for *B. napus* seed development on the curated AraCore model and reconstruction of lipid metabolism of the Brassicaceae family from AraLip, PlantCyc, KEGG and PlantSeed database. The metabolic network is compliant with current community standards and thus compatible with BiGG and ModelSeed database, which also allows for benchmarking and comparing the model and encouraging its reuse in the plant science community. For all reactions where information was available in any plant species, the likely flux carrying enzyme(s) or transport protein(s) were identified in the *B. napus* and *Arabidopsis thaliana* genome for comparison to earlier publications. In addition, the gene-annotated reactions allow for the integration of organ-specific time-resolved multimodal data sets obtained by the AVATARS project partners to shed light on the metabolic changes during seed development. In the future, associating flux balance derived metabolic phenotypes to seed traits will allow predicting seed traits, such as seed vigour and germination ability, with respect to genetic and environmental variations.

We published a Research Topic with Frontiers in Plant Sciences as a summary of the "Gatersleben Research Conference 2019 on Applied Bioinformatics for Crops" (Blätke *et al.* 2021, Blätke *et al.* 2021). A review titled "Advances in Flux Balance Analysis by Integrating Machine Learning and Mechanism-based Models" recently appeared in the Computational and Structural Biotechnology Journal (Sahu *et al.* 2021). Previous work on multimodal analysis of tomato fruit development accomplished as a member of the research group Network Analysis and Modelling is currently under preparation

Selected Publications

SAHU, A. et al.: Advances in flux balance analysis by integrating machine learning and mechanism-based models. Comput. Struct. Biotechnol. J. 19 (2021) 4626-4640.

BLÄTKE, M.-A. et al.: Editorial: Advances in applied bioinformatics in crops. Front. Plant Sci. 12 (2021) 640394.

BLÄTKE, M.-A. et al.: (Eds.): Front. Plant Sci., Frontiers Research Topic "Advances in Applied Bioinformatics in Crops". Lausanne: Frontiers Media SA (2021) pp.

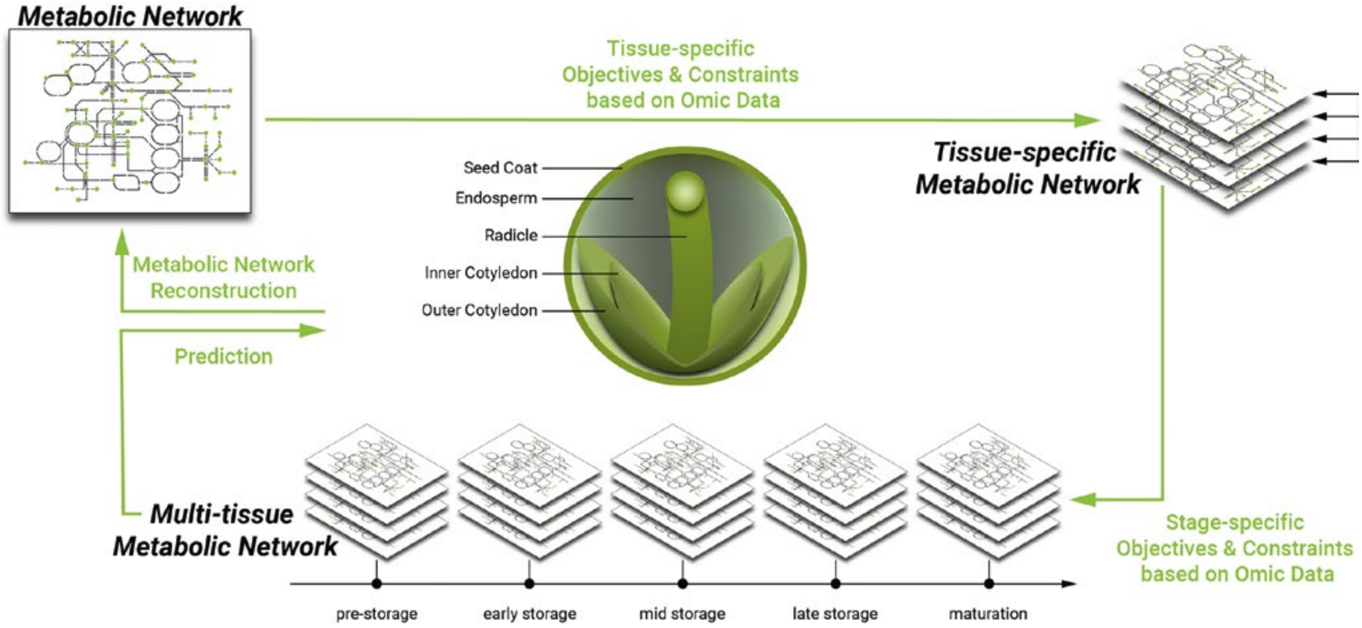


Figure 1: *Workflow to create an integrative metabolic whole seed model for B. napus seed development as part of the AVATARS project.*

for submission to Plant Cell. As part of the organising committee of the German Conference on Bioinformatics 2021 and 2022, we extend our professional network and increase the visibility of the research group in the bioinformatics community. A request for DFG funding to support GCB2022 was successfully granted.

EMBEDDING IN IPK RESEARCH THEMES

As part of the BMBF funded AVATARS project, the covered research is mainly related to Research Theme 4 "Growth and Metabolism". Within the collaborative project AVATARS, research questions are jointly approached with the research groups Heterosis, Seed Development, Assimilate Allocation and NMR and Image Analysis. Additionally, the IPK Research Theme 2 "Genome Diversity and Evolution" and 5 "Mechanisms of Resistance and Stress Tolerance" are touched in past and current research work.

OUTLOOK

The main priority of our group is to establish an internationally acknowledged and visible research profile. This will be driven by the vision of virtual breeding built on digital crop twins integrating scholarly knowledge, descriptive models (e.g. molecular networks, kinetic models) and data-driven models (ML/DL-based models) into executable knowledge graphs. Such platforms facilitate turning data into actionable knowledge to accelerate the breeding of resilient, climatically adapted, and resistant crops for a sustainable bioeconomy. In addition, communication and dissemination through publications in scientific journals and through science communication will promote visibility and scientific exchange.

More information:
www.ipk-gatersleben.de/en/research/molecular-genetics/integrated-mechanistic-models-young-investigators-group

PHYSIOLOGY AND CELL BIOLOGY

PHYSIOLOGY
AND
CELL BIOLOGY

MOLECULAR PLANT NUTRITION (MPE)

Prof. Dr. Nicolaus von Wirén

APPLIED BIOCHEMISTRY (ABC)

PD Dr. Hans-Peter Mock

YOUNG INVESTIGATOR GROUP SUSTAINABLE NUTRIENT MANAGEMENT (NNM)

Dr. Diana Heuermann

PLANT REPRODUCTIVE BIOLOGY (PRB)

Dr. Jochen Kumlehn

STRUCTURAL CELL BIOLOGY (SZB)

Dr. Michael Melzer

DEPARTMENT PHYSIOLOGY AND CELL BIOLOGY

Head: Prof. Dr. Nicolaus von Wirén

MISSION

Research in the department focuses on transport, metabolic and developmental processes in plants and yeast cells, which improve their stress tolerance, resource efficiency or their adaptation to agricultural or biotechnological production systems. These research goals are achieved by the establishment and steady improvement of analytical and technical platforms with related competences in physiology, biochemistry, cell biology and biotechnology. The department's fundamental and application-oriented research addresses core topics of the German National Sustainability Strategy and the Federal High-Tech Strategy, as well as several of the UN sustainability goals.

RESEARCH STATUS

Firmly committed to sustainable and resource-efficient plant production, departmental research strives for the improvement of physiological and agronomic traits in crops. Most of the research groups affiliated to the department have conducted large-scale screening approaches of accession lines or genotypes hosted in the IPK Gene Bank. In a collection of 220 spring barley accessions phenotyped in field trials over 3 years, the research group Molecular Plant Nutrition conducted a genome-wide association analysis and mapped QTLs for mineral element accumulation in grains. A major-effect QTL accounting for the largest proportion of grain boron (B) variation was located closely to HvNIP2;2/HvLSI6, encoding a putative B-transporting membrane protein. Transport studies conducted in heterologous expression systems and gene expression analysis by the departmental associated independent research group Metalloid Transport allowed characterising HvNIP2;2/HvLsi6 as a functional B channel, whose variation in transcript levels associates with root and shoot B concentrations as well as with root dry mass formation under B-deficient conditions (Jia *et al.* 2021, Physiol. Plant.). Follow-up studies on B transport and efficiency mechanisms will be continued in cooperation with the Technical University of Munich, where the departmental associated independent research group leader Patrick Bienert received a W3-professorship in Crop Physiology. Furthermore, mapping of grain concentrations of Zn and Mn allowed identifying a candidate gene coding for a tonoplast-localised metal transporter. In close cooperation, the research groups Plant Reproductive Biology and Molecular Plant Nutrition employed CRISPR-associated endonuclease-mediated gene editing to generate deletion mutants that show higher grain levels of Zn. A deeper characterisation of the physiological function of this transporter and its potential for biofortification is ongoing.

ω-transaminases are a class of enzymes that allow for the biotechnological production of enantiopure β- and γ-amino acids. In contrast to chemical synthesis, enzymes are stereo-specific. The bacterial ω-transaminase VboTA from *Variovorax boronicumulans* is a promising enzyme for the production of enantiopure β-amino acids. Recombinant expression of this enzyme in *E. coli* and enzymatic assays *in vitro* showed that it accepts a broad spectrum of β-amino acids. In contrast to many other ω-transaminases, VboTA is active at rather low temperatures and has a high enantio-selectivity. Biotechnological production of VboTA in *E. coli* yielded large amounts of the enzyme, which can be stored for several weeks. The mild reaction conditions and long shelf-life make this enzyme attractive for biotechnological production at industrial scale.

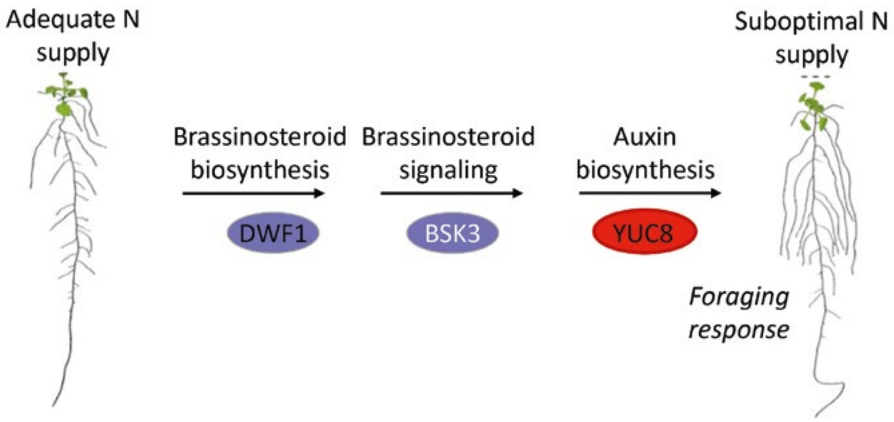


Figure 1: *Responses of the root system of Arabidopsis to nitrogen (N) supply in the growth medium. The length of the primary and the lateral roots increases under mild nitrogen deficiency. This foraging response is mediated by two different types of phytohormones, i.e. brassinosteroids and auxins. In three genes involved in brassinosteroid biosynthesis, signalling and auxin signalling, allelic variations modulate the extent of primary and lateral root elongation (DWF1, BSK3, YUC8).*

HIGHLIGHTS

Agricultural plant production needs to decrease fertilizer input in order to decrease overall carbon emission and to improve biodiversity and environmental quality of agro-ecosystems. A major goal in the department is to uncover mechanisms, which allow plants to better adapt to low nutrient supplies. One such response, known to be displayed by plants grown in low nitrogen conditions, is the elongation of primary and lateral roots to explore the surrounding soil. This "foraging strategy" allows the root system to exploit nutrients from a larger soil volume. Employing genome-wide association mapping, the Molecular Plant Nutrition group identified the hormonal regulation behind this root foraging response under low nitrogen conditions. Brassinosteroids are a class of growth-promoting hormones, and recently we found that mild N deficiency upregulates a large number of genes mediating the local biosynthesis of brassinosteroids in roots (Jia *et al.* 2020, Plant Physiol.). Once perceived by a receptor complex at the plasma membrane of root cells, the brassinosteroid signal is transduced to the transcription factor BZR1 (Jia *et al.*, 2019, Nat. Commun.), which drives the expression of auxin biosynthesis genes. The resulting local accumulation of auxin in primary and especially in lateral root tips enhances root elongation under mild nitrogen deficiency (Jia *et al.* 2021, Nat. Commun.). Interestingly, we found that allelic variations in three steps of this hormonal pathway are able to modulate the extent of the root elongation, which is in the biosynthesis of brassinosteroids, in their corresponding signalling pathway and the downstream biosynthesis of auxin. These findings pave the way for breeding of crops with more expanded root systems enabling more efficient nitrogen uptake.

In a cross-departmental activity of the Structural Cell Biology and Plant Reproductive Biology research groups with colleagues from the Seed Development group, we used RNA interference-mediated downregulation of the barley HISTIDINE KINASE 1 (HvHK1) along with the histological and ultrastructural characterisation of developing caryopses. It was demonstrated that reduced HvHK1 expression entails disturbed cell plate formation and cell fusions at the initiation of endosperm cellularisation, which revealed that HvHK1 triggers cytokinesis towards the formation of endosperm transfer cells. This work provides clues to previously unknown molecular mechanisms of endosperm cell specification, a process with fundamental impact on grain yield in cereals (Hertig *et al.* 2020, Plant J.).

In another study of the Structural Cell Biology and Plant Reproductive Biology groups along with the Plant Architecture, Seed Development and Domestication Genomics groups, the transcription factor SQUAMOSA PROMOTOR-BINDING PROTEIN-LIKE 14 (SPL14) of barley was functionally validated using Cas endonuclease technology and histological analyses. SPL14 loss-of-function mutants exhibited changes in plant height and number of internodes

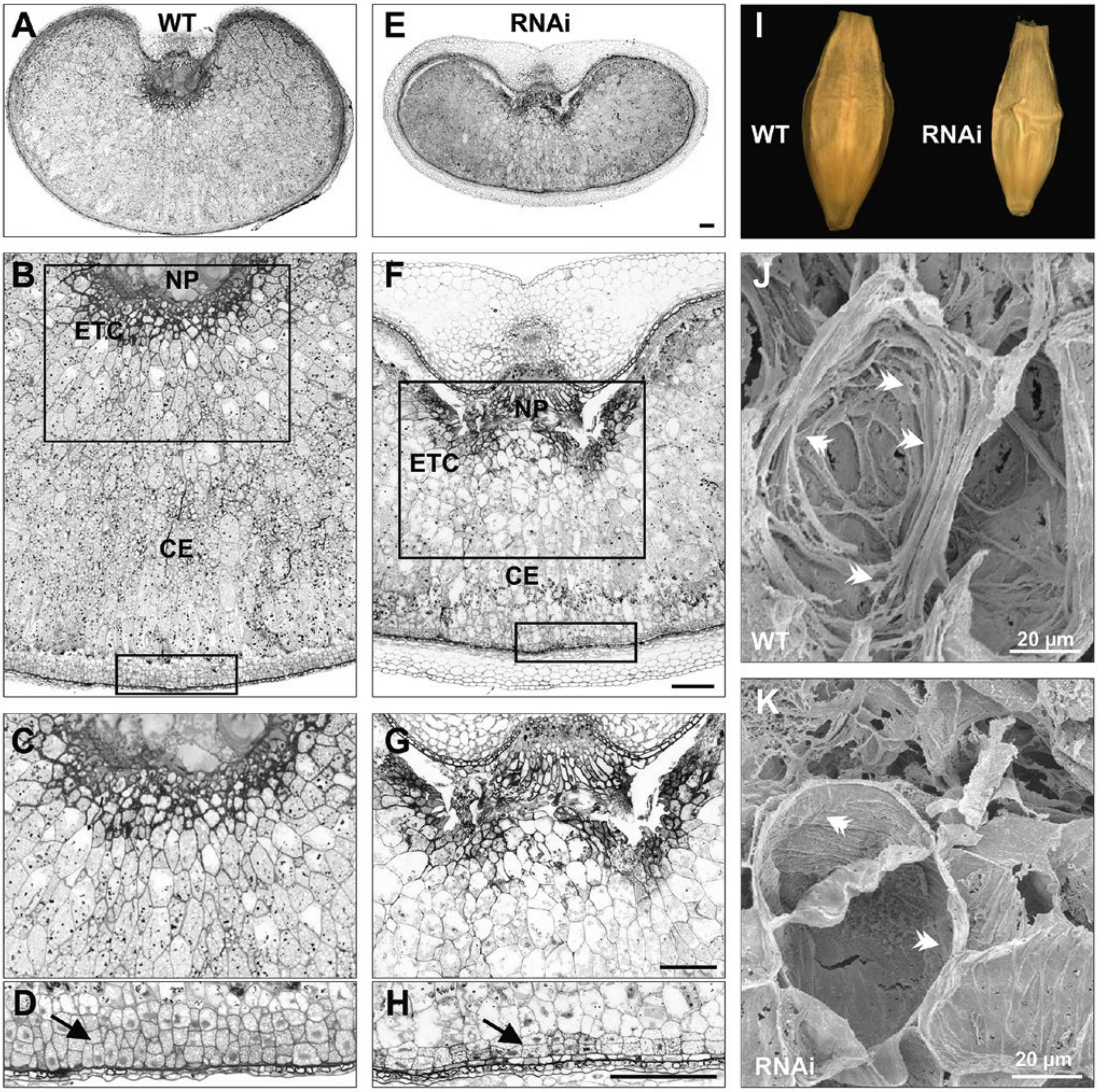


Figure 2: *HvHK1 repression in RNAi lines induces defects in endosperm transfer cell (ETC) differentiation and endosperm tissues. Light microscopy (A-H) and scanning electron microscopy images (J, K) of grains at 12 DAF of WT (A-D) and RNAi lines (E-F). (i)–(l) Radial arrangement of central endosperm cells is impaired in RNAi grains (B, F). Magnification of the ETC region depicts aberrant cell differentiation in the central part of RNAi lines (C, G). Two instead of three layers of aleurone cells are formed in the dorsal part of the endosperm of RNAi lines (indicated by arrows). Mature grains of RNAi lines are smaller than in the WT and depict a 'shrunken' phenotype (I). Scanning electron microscopy of the central ETC region confirms an extensive labyrinth of cell wall ingrowths (arrow heads) in the WT contrasting the poorly developed structures in grains of HvHK1 RNAi lines. CE, central endosperm; ETC, endosperm transfer cells; NP, nucellar projection. Space bars A-H = 100 µm. (M. Melzer; T. Rutten, J. Thiel)*

as well as in spike length and grain production. Our findings revealed the important role of SPL14 for the switch from vegetative to generative development of the shoot apical meristem (Thiel *et al.* 2021, Sci. Adv.).

OUTLOOK

Of major priority in departmental research is the advancement and application of novel methods of site-directed genome engineering which go beyond current targeted mutagenesis approaches by facilitating the generation of precisely intended modifications of the genomic DNA sequence. These approaches are going to be employed, for instance, to modify the function of genes that enhance abiotic and biotic stress tolerance, nutrient efficiency and plant architecture in cereals. In cooperation with groups of the other departments, promising variants of such genes have been identified by QTL mapping of relevant traits in barley and other cereals, or by re-sequencing of known genes in lines with contrasting phenotypes. In addition, knowledge about trait-modifying allelic variants of Arabidopsis genes will be used in translational approaches for precise genome editing in barley.

In succession of the yeast genetics group, a new research focus will be established to strengthen the profile of the department Physiology and Cell Biology in the area of root or root-related research topics. The new group leader shall be dedicated towards the physiology, architecture or development of plant roots and/or their importance for overall plant performance and stress tolerance. This group shall also engage in the development of new methods in root phenotyping using the infrastructure that has been set up in the Plant Cultivation Hall. The group leader position is upgraded by a joint professorship with the Faculty of Agricultural Sciences at University of Göttingen.

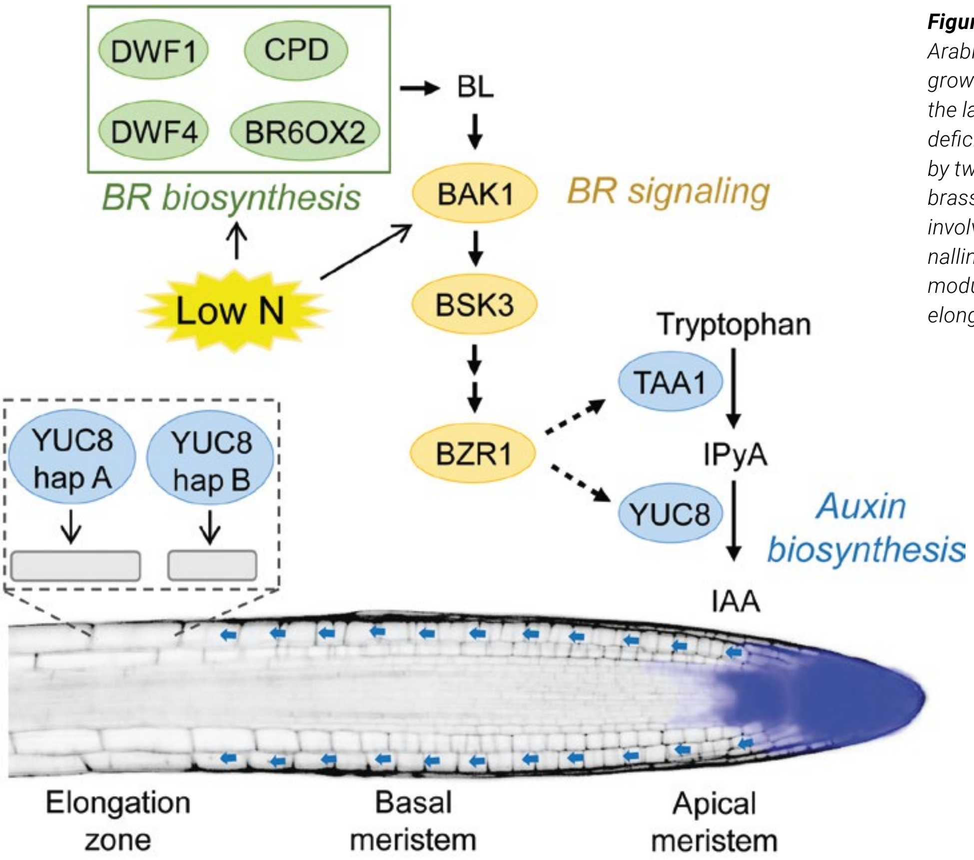


Figure 3: *Responses of the root system of Arabidopsis to nitrogen (N) supply in the growth medium. The length of the primary and the lateral roots increases under mild nitrogen deficiency. This foraging response is mediated by two different types of phytohormones, i.e. brassinosteroids and auxins. In three genes involved in brassinosteroid biosynthesis, signalling and auxin signalling, allelic variations modulate the extent of primary and lateral root elongation (DWF1, BSK3, YUC8).*

RESEARCH GROUP
MOLECULAR PLANT NUTRITION (MPE)

Head: Prof. Dr. Nicolaus von Wirén

MISSION

The Molecular Plant Nutrition group investigates the transport and metabolism of mineral nutrients, their impact on phytohormone regulation as well as their role in physiological and morphological responses to stress or to agricultural production conditions. Research includes nutrient sensing mechanisms, especially those involved with the adaptation of root developmental processes either to local nutrient supplies or to systemic plant signals. We further investigate mechanisms of nutrient enrichment in seeds as well as the redox- or nutrient-dependent regulation of stress responses.

RESULTS

To increase fertilizer use efficiency in plant production, nitrogen fertilizers in the form of ammonium are often supplied as a fertilizer band before sowing. Previously, we observed that the immediate contact of roots with ammonium provokes lateral root branching. Examining this growth phenotype in the model species *Arabidopsis* grown on agar plates with split roots allowed uncovering that increased lateral root formation is a consequence of enhanced radial movement of auxin. In fact, intense ammonium uptake leads to elevated auxin levels in the root vascular system as well as to apoplastic acidification and the conversion of auxin into its neutral form, which readily diffuses into outer root cells. There, auxin facilitates cell wall loosening and subsequent emergence of pre-formed lateral root buds (Meier *et al.* 2020, Nat. Plants).

In cereal crops, the number of tillers is an important yield component and highly responsive to nitrogen fertilization. We observed that in hydroponically grown barley, exclusive supply of nitrate increased tiller number in contrast to urea or ammonium. Transport studies with a synthetic cytokinin analog showed that its translocation to shoots was 2.5 times higher in presence of nitrate than in presence of urea or ammonium, suggesting that cytokinin loading into the xylem is affected by different nitrogen forms. In field trials conducted with winter wheat in four environments, nitrate fertilization significantly increased tiller number in a dose-dependent manner. We conclude that cytokinin-mediated signalling effects of fertilizer nitrogen forms can be employed as a management tool to regulate the tiller number in cereal crops according to seasonal variations (Bauer and von Wirén, 2020, Sci. Rep.).

There is an urgent need to improve phosphorus use efficiency in crop production. One key aspect to achieve this goal is to understand how plants adjust root phosphorus uptake with changes in whole-plant demand. Recent studies indicated that inositol pyrophosphates, small signalling molecules consisting of a phosphorylated myo-inositol ring and one or two pyrophosphate groups, regulate phosphorus homeostasis in plants. We determined that the levels of various inositol pyrophosphates tightly reflect the concentration of phosphorus in shoots, a response that we found to be conserved across different plant lineages. Disturbing the synthesis of specific inositol pyrophosphates in *Arabidopsis thaliana* by knocking out the gene encoding ITPK1 results in uncontrolled phosphorus accumulation in leaves and seeds.

Interestingly, assays with recombinant ITPK1 revealed that the enzyme sets the levels of regulatory inositol pyrophosphates by generating or removing 5-InsP7, according to phosphorus-dependent changes in ATP levels. Thus, ITPK1 activity integrates nutritional and energetic cues to ultimately switch on or off phosphorus deficiency responses in plants (Riemer *et al.*, 2021, Mol. Plant).

Selected Publications

MEIER, M. et al.: Auxin-mediated root branching is subject to the form of nitrogen supply. Nat. Plants 6 (2020) 1136-1145.

JIA, Z. et al.: The root foraging response under low nitrogen depends on DWARF1-mediated brassinosteroid biosynthesis. Plant Physiol. 183 (2020) 998-1010.

BAUER, B. & N. VON WIRÉN: Modulating tiller formation in cereal crops by the signalling function of fertilizer nitrogen forms. Sci. Rep. 10 (2020) 20504.

RIEMER, E. et al.: ITPK1 is an InsP6/ADP phosphotransferase that controls phosphate signaling in Arabidopsis. Mol. Plant 14 (2021) 1864-1880.

JIA, Z. et al.: Local auxin biosynthesis acts downstream of brassinosteroids to trigger root foraging for nitrogen. Nat. Commun. 12 (2021) 5437.

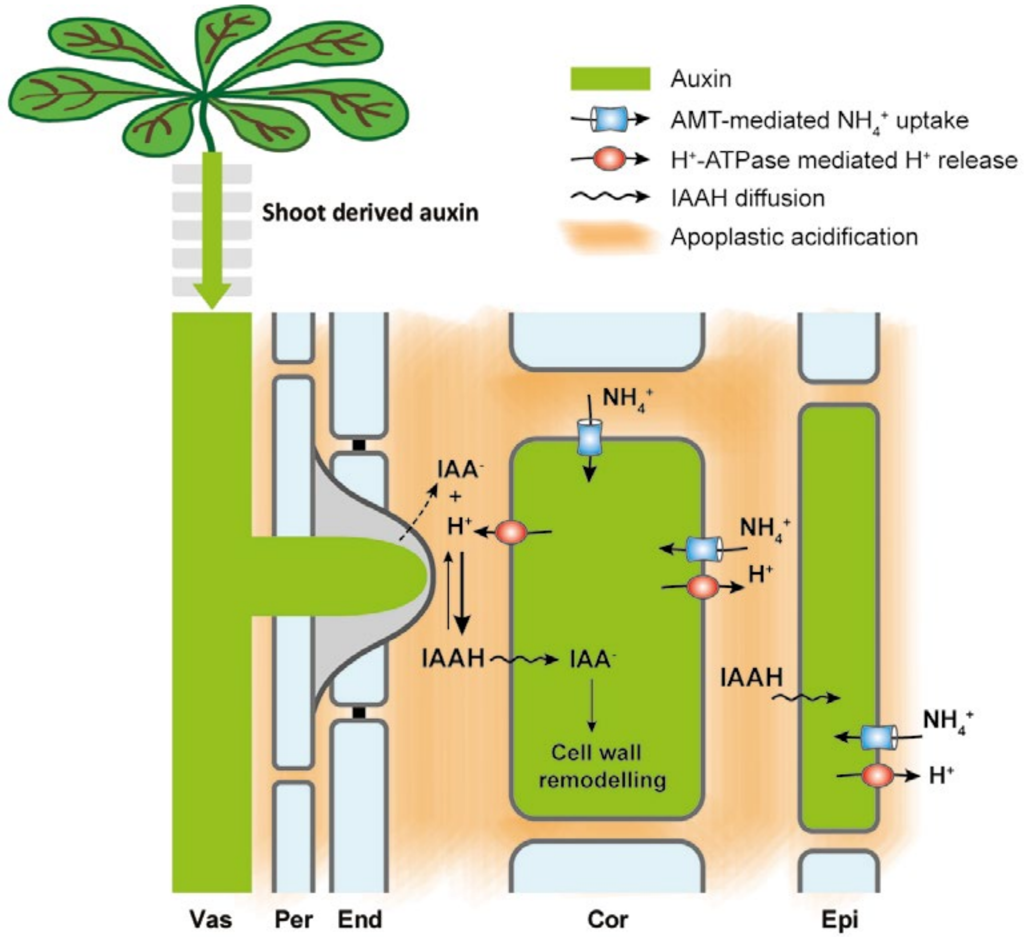


Figure 1: *Localised ammonium supply enhances the import and accumulation of shoot-derived auxin into the root vasculature, generating an auxin source for lateral auxin movement. Meanwhile, AMT-dependent ammonium uptake stimulates proton release via H$^+$-ATPases, leading to apoplastic acidification, subsequently promoting the protonation of IAA and radial diffusion of protonated IAA (IAAH) from the vasculature to outer root cells overlaying lateral root primordia. Auxin import into cortical and epidermal cells enhances expression of genes involved in cell wall loosening, decreasing the mechanical resistance required for lateral root emergence (Meier et al., 2020, Nat. Plants).*

EMBEDDING IN IPK RESEARCH THEMES

With discoveries on plant responses and adaptations to nutrient deficiencies, the group's research is central to IPK Research Theme 5 "Mechanisms of Resistance and Stress Tolerance". With association mapping approaches on root and seed traits in barley, the group closely cooperates across departments, thereby contributing also to Research Themes 1 "Valorisation of Plant Genetic Resources" and 4 "Growth and Metabolism".

Moreover, the research group 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).

OUTLOOK

Knowledge gained in *Arabidopsis* on the phytohormone signalling pathways that allow forming longer roots under mild nitrogen deficiency have potential to improve nutrient and water uptake efficiency when translated to crops. Notably, this approach builds on inherent regulatory pathways and natural adaptations of plants. Therefore, we are searching in the IPK Gene Bank for allelic variants of genes determining root elongation under mild nitrogen deficiency in barley. A great challenge here is to exploit favourable allelic gene variants found in lines of the IPK Gene Bank for the genetic improvement of elite lines. In this respect, liberalisation in the use of modern genome editing technologies (CRISPR-Cas technology) would be an important step forward.

More information: *www.ipk-gatersleben.de/en/research/physiology-and-cell-biology/molecular-plant-nutrition*

RESEARCH GROUP
APPLIED BIOCHEMISTRY (ABC)

Head: PD Dr. Hans-Peter Mock

MISSION

The main research interest of the 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 ingredients of our daily diet. Major goals are to gain insights into regulatory programmes and mechanisms of resource allocation into different branches of secondary metabolism and to unravel tissue-specific metabolite functions. Integrative approaches combining proteomics, metabolomics and transcriptome analysis are applied to study the integration of secondary metabolism into overall cellular defence mechanisms.

RESULTS

Analysis of the diversity of phenylpropanoid metabolism in barley and its genetic background has been continued (cooperation with K. Pillen, MLU Halle). The major aim was to uncover the genetic basis and physiological roles of specialised metabolites by using data sets obtained by applying an MS-based workflow on samples from field-grown mapping populations (Garibay-Hernandez *et al.* 2021). Multi-omics data were interrogated using machine learning and network-based approaches (in cooperation with research group Network Analysis and Modelling). As an example, N-containing specialised metabolites closely linked to powdery mildew susceptibility were found. Chalcone isomerase mutants have been characterised in field and lab conditions for their compromised basal resistance to host and non-host pathogens (cooperation with research groups Biotrophy & Immunity and Structural Cell Biology).

Responses to nitrogen deficiency and drought stress (applied singly or combined) of potato cultivars were studied by proteomic approaches (A. Jozefowicz in cooperation with T. Winkelmann, LU Hannover). As promising candidates for tolerance against stress, we have selected proteolytic enzymes (e.g. cysteine protease). Their activity is further tested using zymography. Another focus is set on the role of the aquaporins PIP1;1 and PIP1;3 in the tolerance to nitrogen deficiency. These proteins were identified in the root plasma membrane proteome. The role of these aquaporins is studied by functional complementation of *Arabidopsis* mutants (cooperation with research group Molecular Plant Nutrition and P. Bienert, TU Munich).

During the earlier KAIT project (cooperation with research group Cryo and Stress Biology) the role of the transcription factor *WRKY22* was studied with respect to the cryopreservation capacity of shoot meristems (Stock *et al.*, 2020). The putative regulatory network is further established in a PhD study by assessing a range of stress scenarios.

The storability of sugar beet taproots was studied in collaboration with industrial and academic partners (Beetstore project with E. Sehr at AIT Tulln, Austria). Metabolic pro-

Selected Publications

GARIBAY-HERNÁNDEZ, A. et al.: Untargeted metabotyping to study phenylpropanoid diversity in crop plants. Physiol. Plant. 173 (2021) 680-697.

PAHLKE, G. et al.: Antioxidant effects of elderberry anthocyanins in human colon carcinoma cells: a study on structure-activity relationships. Mol. Nutr. Food Res. 65 (2021) 2100229.

SCHUBERT, R. et al.: Effects of arbuscular mycorrhization on fruit quality in industrialized tomato production. Int. J. Mol. Sci. 21 (2020) 7029.

STOCK, J. et al.: The transcription factor WRKY22 is required during cryo-stress acclimation in Arabidopsis shoot tips. J. Exp. Bot. 71 (2020) 4993-5009.

XU, D. et al.: Cellulose defects in the Arabidopsis secondary cell wall promote early chloroplast development. Plant J. 101 (2020) 156-170.

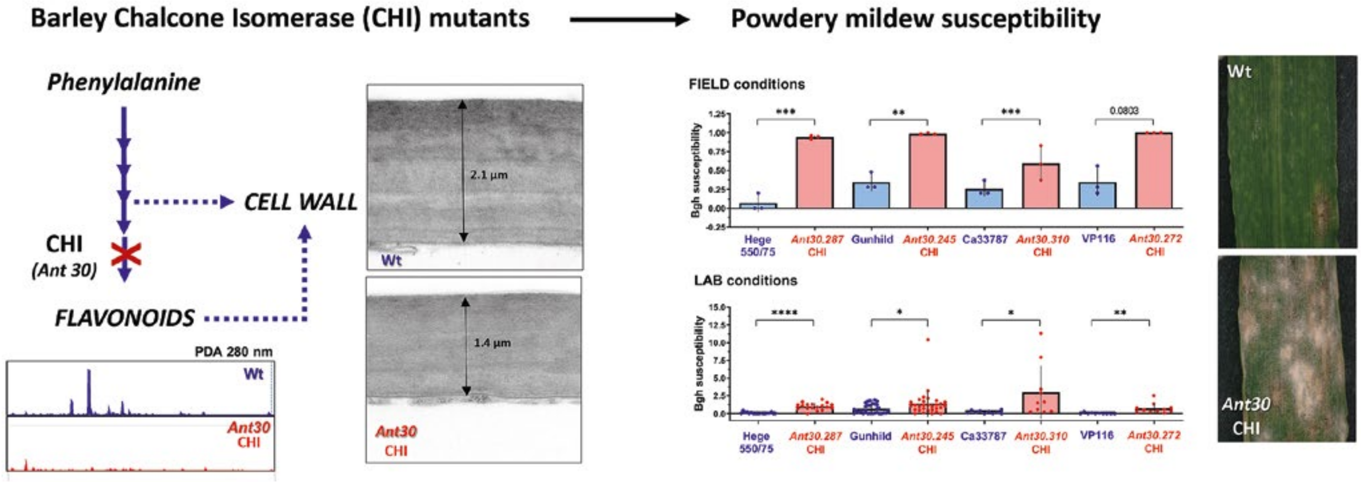


Figure 1: The Chalcone Isomerase mutation compromises barley resistance against powdery mildew. *The Chalcone Isomerase (CHI) catalyses a commited step for flavonoid synthesis, where its mutation results in plants devoid of flavonoids, impaired in the phenylpropanoid metabolism, and displaying an altered cell wall. The CHI mutants in barley have been mapped in four genotypic backgrounds to a single locus, Ant30. These consistently show a compromised resistance against powdery mildew in field and in laboratory conditions where the effects from environmental stressors (e.g. fluctuating temperature and UV radiation) are absent. Our current results support that the CHI mutation increases the susceptibility to powdery mildew due to an impaired penetration resistance at early stages of infection (before the first 24 h).*

files of several contrasting genotypes were correlated with transcriptional data. The processes underlying differential cold stress tolerance of selected sugar beet genotypes of the IPK Gene Bank were investigated (cooperation with research groups Metabolic Diversity and Molecular Plant Nutrition).

The metabolic profiles associated with the induction of androgenesis in wheat were studied as part of the processes enabling the production of DH lines. Based on a few metabolites, a predictive model was established. The model was challenged using a larger set of genotypes (INPUT project with SU BIOTEC GmbH).

Spatial distribution of metabolites in barley spikes is analysed by using MALDI-MS-based molecular imaging (cooperation with independent research group Plant Architecture). This study paves the way for the identification of novel pathways shaping early spike development in barley.

EMBEDDING IN IPK RESEARCH THEMES

Research in the Applied Biochemistry group is mainly situated within the Research Theme 5 “Mechanisms of Resistance and Stress Tolerance” by investigating the regulation of phenylpropanoid metabolism in the context of abiotic stress defence. Nutrient availability (e.g. C/N status) has a strong impact on the allocation of resources into different branches of secondary metabolites. To address these metabolic relations, the group has interactions with other groups of the department and the institute. The group continuously contributed to the phytochemical characterisation of IPK Gene Bank accessions of various species.

OUTLOOK

From the end of 2021, the research group will be led provisionally by Prof. Dr. N. von Wirén. The reason for this change is the retirement of the research group leader. Therefore priority has been placed on finishing the ongoing projects in due course. Transfer of methodology and instrumentation related to metabolite and protein analysis has been ensured by cooperation with groups having overlapping scientific research interests, in particular by cooperation with the research group Metabolic Diversity of Dr. J. D’Auria.

More information: *www.ipk-gatersleben.de/en/research/physiology-and-cell-biology/applied-biochemistry*

YOUNG INVESTIGATOR GROUP
SUSTAINABLE NUTRIENT MANAGEMENT
(NNM)

Head: Dr. Diana Heuermann

MISSION

The work of the young investigator group aims to improve nutrient use and nutrient cycling in agricultural plant production through the use of catch crops. To this end, we focus on the characterisation of morphological and physiological root traits of different catch crop species and their action on target crops. In detail, we address the following questions:
(i) What are the roles of the vertical root biomass distribution and root-released metabolites in nutrient uptake capacity of individual catch crop species and their mixtures?
(ii) To what extent can catch crops alter the root morphology and nutrient acquisition by the target crop?
(iii) Which catch crop traits increase the potential of individual catch crop species for reducing nutrient losses from agricultural soils?

RESULTS

Nitrogen (N) losses from agricultural soils are a major problem in plant production. By including catch crops in crop rotations during unfavourable periods for the growth of main crops, N can be scavenged and transmitted to the following crop, thereby reducing nitrate leaching. Moreover, catch crops can improve the acquisition of sparingly available nutrients by the following crop. However, different catch crop species come with different capacities for nutrient scavenging, as some species form large biomass while others improve the composition of the microbiome or build deeper roots. We studied thus the nutrient accumulation by four catch crops from diverse plant families over several years and sites and found that species with deep root systems, namely white mustard and lacy phacelia, were more effective in N capture and in depleting deep soil N pools than bristle oat or Egyptian clover. Phacelia with its large topsoil root biomass was superior in phosphorus and calcium accumulation due to larger concentrations of those elements in its biomass, while sulphur capture was best in mustard. The root system architecture played a fundamental role for exploring soil nutrient reserves. A mixture of the four mentioned species was dominated by mustard and phacelia. In sum, all species in the mixture accumulated robustly over different sites and years as much nutrients as the best-performing pure stand indicating that a mixture is more durable against environmental impacts.

Large and nutrient-enriched pores left over by decomposing catch crop roots may affect the root system distribution of the target crop. We analysed thus the root biomass of maize with a qPCR-based quantification method based on root DNA along the vertical soil profile after the four catch crops. Against our expectation, clover stimulated rooting depth of maize compared to a bare fallow-control. Mustard, phacelia and oat, which developed much deeper root systems than clover, led to decreased root elongation of maize. This effect appeared to be mediated to some extent by root exudates as revealed by an inhibition of maize root growth after the application of root exudates sampled from mustard, phacelia and oat in a hydroponic growth assay. Non-targeted LC-MS/MS-based metabolite analysis of root exudates sampled either in the field or hydroponically showed that especially mustard releases a bunch of indole-based compounds which are known to confer allelopathic action (cooperation with Prof. D. Scheel, IPB Halle). Elucidating the impact of catch crop root exudates on maize root growth will be part of further studies.

Nutrient carry-over to the target crop is determined by both, nutrient accumulation in the catch crop biomass and decomposition properties of the plant material. For N, we traced the transfer from pure stands and mixtures to the target crop maize using a 15N-labelling approach in the field (cooperation with the CATCHY consortium). Our

Selected Publications

HEUERMANN, D. et al.: Seed yield and nitrogen efficiency in oilseed rape after ammonium nitrate or urea fertilization. Front. Plant Sci. 11 (2021) 608785.

GENTSCH, N. et al.: Catch crop diversity increases rhizosphere carbon input and soil microbial biomass. Biol. Fertil. Soils 56 (2020) 943–957.

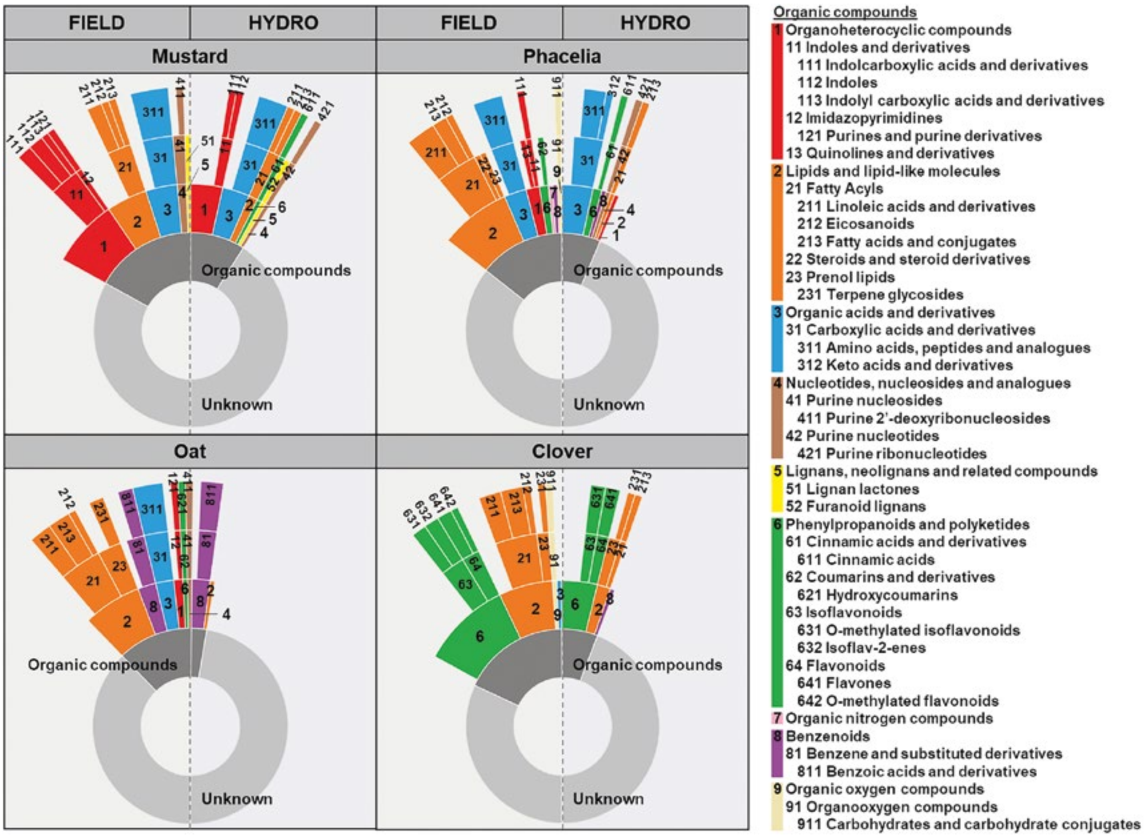


Figure 1: Putative chemical classification of the 100 most abundant features in root exudates of mustard, phacelia, oat and clover grown in the field (FIELD) or hydroponically (HYDRO). *Features were classified using the ClassyFire tool (http://classyfire.wishartlab.com; Djoumbou Feunang et al. (2016)). Figure legend shows superclass on rank 1 (e.g. 1 Organoheterocyclic compounds), class on rank 2 (e.g. 11 Indoles and derivatives) and subclass on rank 3 (e.g. 111 Indolcarboxylic acids and derivatives). Features without annotation were classified as "Unknown".*

results show that catch crop species and mixtures differ in temporal and quantitative N transfer to maize and that roots, especially those of legumes, contribute up to two times more N to maize nutrition than shoots. This emphasises the importance of the below-ground N pool for immediate nutrient carry-over in crop rotations.

EMBEDDING IN IPK RESEARCH THEMES

The Sustainable Nutrient Management group investigates the influence of the root architecture on nutrient acquisition of different catch crops in pure stands and mixtures, analyses the nutrient transfer to the subsequent crops maize and wheat, and identifies root-released metabolites from catch crops that influence the root growth of the subsequent crop. With those research questions we tackle especially topics of the IPK Research Theme 5 "Mechanisms of Resistance and Stress Tolerance".

OUTLOOK

The integral goal of the future research of the Sustainable Nutrient Management group is to understand functions of catch crop root traits and root exudates and their contribution to nutrient cycling and growth stimulation of target crops in agricultural crop rotations. We aim to identify catch crop cultivars and their root exudates with inhibitory action on the nitrification process and the underlying chemical compounds in order to stabilise ammonium pools in soils and to improve the N efficiency of the target crop. That the available N form can affect N efficiency has been recently shown for oilseed rape when we compared ammonium nitrate vs. urea fertilizer regarding their impact of nitrogen use efficiency (Heuermann *et al.* 2021).

By characterising soil metabolites present after the catch crop cultivation period together with the impact of catch crop root exudates on the microbial community in soils (cooperation with Prof. B. Reinhold-Hurek, University Bremen) we aim to address which soil metabolite patterns and microbial communities may be beneficial for the growth of target crops.

More information:
www.ipk-gatersleben.de/en/research/physiology-and-cell-biology/sustainable-nutrient-management-young-investigators-group

RESEARCH GROUP
PLANT REPRODUCTIVE BIOLOGY (PRB)

Head: Dr. Jochen Kumlehn

MISSION

The Plant Reproductive Biology research group has a strong focus on the establishment of enabling technologies such as plant genetic engineering and the generation of true-breeding plants originating from haploid cells. By providing biotechnological methods, the group aims to facilitate both, basic research as well as translational approaches to the improvement of crop plant performance. Special emphasis is laid upon biological mechanisms essentially involved in plant reproduction, domestication, plant-pathogen interaction and the formation of yield components in cereal crops.

RESULTS

The naked caryopsis character in barley is a domestication-associated trait defined by loss-of-function of the *NUDUM* (*NUD1*) gene that controls the formation of the cement-like layer between pericarp and both lemma and palea. Upon targeted knockout of the *NUD1* gene, barley plants exhibited the naked grain phenotype. Considering the high β-glucan content of barley grains, the newly given possibility to readily convert hulled into naked barley by genome editing allows for the utilisation of barley as particularly healthy human food (Gerasimova *et al.* 2020, BMC Plant Biology).

The barley yellow mosaic virus disease, caused by a group of bymoviruses, can lead to substantial yield losses in winter barley. Thanks to the *rym4* and *rym5* allelic variants of the *EUKARYOTIC TRANSLATION INITIATION FACTOR 4E* (*HvEIF4E*) susceptibility gene, more than two thirds of current European winter barleys are resistant to these viruses. However, several virus strains have overcome *rym4*- and *rym5*-based resistance. Aiming to generate new resistance-conferring *EIF4E* variants, this gene was subjected to targeted mutagenesis in a bymovirus-susceptible winter barley. Resultant knockout plants proved fully resistant to virus inoculation, showed normal growth habit and produced grains, yet exhibited a yield penalty (Hoffie *et al.* 2021, Frontiers in Genome Editing).

The biotrophic fungal pathogen *Ustilago maydis* causes galls on the aerial parts of maize. Aiming to engineer durable resistance in maize against *U. maydis*, we took a genome editing approach to generate loss-of-function mutations in *LIPOXYGENASE 3* (*LOX3*) which had been identified as a candidate susceptibility gene. *lox3* maize mutant plants exerted an enhanced pathogen-triggered ROS burst indicating enhanced defence activity. An assessment of disease symptoms and the quantification of fungal biomass on *lox3* mutant plants exposed to *U. maydis* revealed significantly decreased susceptibility (Pathi *et al.* 2021, Front. Plant Science).

The *BRANCHED HEAD* (*BH*) gene of the temperate cereal wheat plays a remarkable role in the shaping of spike architecture that itself is a major determinant of grain yield potential. Considering the three subgenomes of wheat, single, double and triple *bh* mutants were generated by genome editing. Additional combinations of loss-of-function homeoalleles were generated by assortative crossing of single and double mutant plants. Phenotypic evaluation revealed not only branching of spikes but also excessive formation of supernumarary spikelets in cases of double and triple homeoallele knockout plants, which was, however, associated with reduced floret fertility. In addition, an analysis of some single *bh* allele knockout plants revealed alterations in root development.

Selected Publications

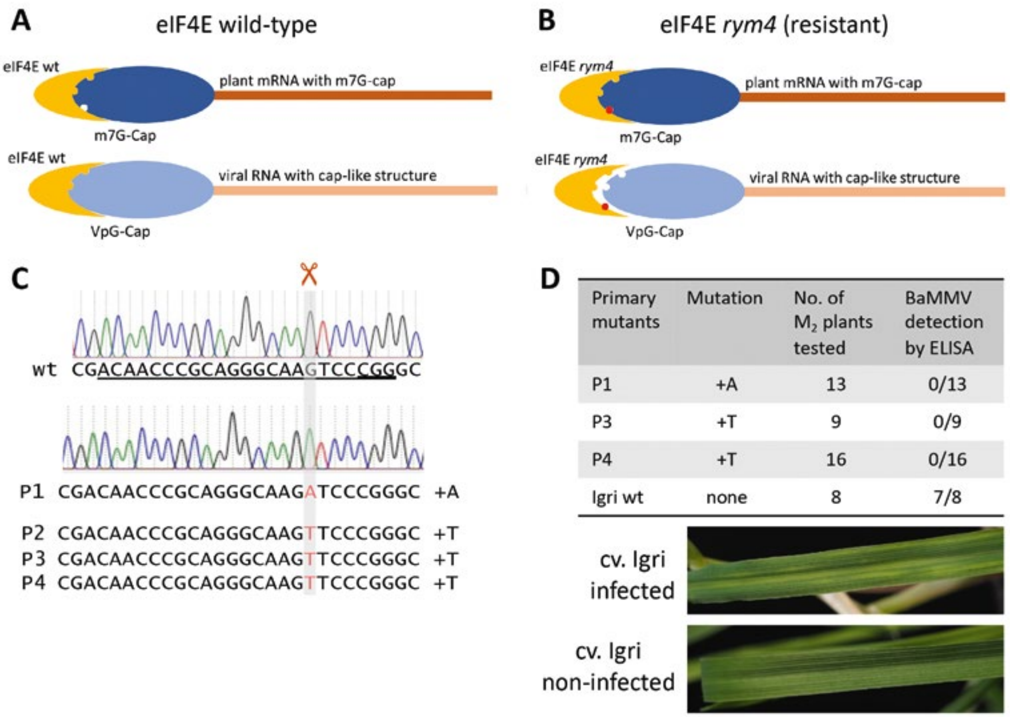
HOFFIE, R.E. et al.: Targeted knockout of Eukaryotic Translation Initiation Factor 4E confers bymovirus resistance in winter barley. Front. Genome Edit. 3 (2021) 784233.

THIEL, J., R. KOPPOLU* et al.: Transcriptional landscapes of floral meristems in barley. Sci. Adv. 7 (2021) eabf0832. * joint first authorship*

PATHI, K.M. et al.: Engineering smut resistance in maize by site-directed mutagenesis of LIPOXYGENASE 3. Front. Plant Sci. 11 (2020) 543895.

BUDHAGATAPALLI, N. et al.: Site-directed mutagenesis in bread and durum wheat via pollination by cas9/guide RNA-transgenic maize used as haploidy inducer. Plant Biotechnol. J. 18 (2020) 2376-2378.

GERASIMOVA, S. et al.: Conversion of hulled into naked barley by Cas endonuclease-mediated knockout of the NUD gene. BMC Plant Biol. 20 (2020) 255.



Primary mutants	Mutation	No. of M_2 plants tested	BaMMV detection by ELISA
P1	+A	13	0/13
P3	+T	9	0/9
P4	+T	16	0/16
Igri wt	none	8	7/8

Figure 1: *A: The Eukaryotic Translation Initiation Factor 4E (eIF4E) binds to the m7G-cap of eukaryotic mRNA to initiate the formation of the translation complex for protein biosynthesis. The wild-type protein of barley binds as well to the genome-linked viral protein (VpG) that mimics the m7G cap structure, enabling the virus to proliferate. B: The rym4 allele of the EIF4E gene carries several single nucleotide polymorphisms that lead to amino acid changes within the binding domain of the protein. eIF4E is still able to bind to the plants' mRNA, whereas the binding to the viral VpG cap is hampered, which prevents viral proliferation. By adaptation of the cap structure, some viral strains have overcome this resistance mechanism. C: By Cas9 endonuclease-triggered mutagenesis of the EIF4E gene, homozygous, 1-bp insertions were achieved in winter barley cv. 'Igri'. D: Results of genotypic and phenotypic screen of M2 progeny. After mechanical inoculation with Barley Mild Mosaic Virus (BaMMV), plants were screened for viral particles by DAS-ELISA and the target region was Sanger-sequenced. All M2 plants were homozygous for the mutation induced in the respective primary mutant and proved resistant to BaMMV-infection.*

Camelina (*Camelina sativa*) is an oilseed plant that is comparatively tolerant to various adverse conditions, such as drought and nutrient-poor soils. In addition, the unique fatty acid profile of its seeds renders camelina particularly suitable for the provision of food and health products. We have established a novel method of *Agrobacterium*-mediated transformation using immature zygotic embryo explants. In contrast to the previously available method, the novel principle proved successful in stable transgenesis in a current camelina cultivar.

EMBEDDING IN IPK RESEARCH THEMES

By providing cutting edge genetic engineering and haploid technologies, the Plant Reproductive Biology group takes in a major integrating function for cross-departmental research and is involved in all five strategic Research Themes. Furthermore the research group head Jochen Kumlehn coordinates the Research Theme 3 "Mechanisms of Plant Reproduction". In this context, the group has been involved in research on the manipulation of meiotic recombination and the initiation of adventitious embryogenesis.

OUTLOOK

Our major strategies to improve the precision in targeted genome modification approaches include the use of base-editing derivatives of Cas endonucleases as well as homology-directed repair of Cas endonuclease-processed DNA. To facilitate a broad implementation of genome editing technology in plant breeding, we aim at establishing intellectual property-independent methods. The research group will further pursue its efforts to establish advanced biotechnologies for scientifically important model plants and hitherto under-utilised crops.

More information: *www.ipk-gatersleben.de/en/research/physiology-and-cell-biology/plant-reproductive-biology*

RESEARCH GROUP
STRUCTURAL CELL BIOLOGY (SZB)

Head: Dr. Michael Melzer

MISSION

As the central facility for light and electron microscopy, the research group Structural Cell Biology provides a platform, which covers maintenance and guided use of equipment and the development of new protocols for preparation of plant tissue. In the framework of own research projects, internal and external cooperations, the group mainly focuses on plant morphology, cellular ultrastructure and the spatial distribution of plant enzymes and molecules as analysed by light, electron or fluorescence microscopy. The overall research goal of own projects in the field of crop improvement or biotechnological procedures are lodging resistance and drought stress.

RESULTS

In a joint DFG project with the research group Plant Reproductive Biology and the University of Silesia (Poland), we investigate the role of strigolactones (SLs) in barley in response to drought stress. Multiple SL-mutants defective in the biosynthesis (HvD27, HvCCD7, HvCCD8 and HvMAX1) or the signalling of SLs (HvD14, HvD53A and HvINT-C) have been generated using RNA-guided Cas9 endonucleases. These mutants are analysed with a focus on physiological, morphological and structural properties to gain insight into the role of this novel class of signalling molecules during drought stress. In this context, their possible crosstalk with other phytohormones, such as abscisic acid (ABA), is also of particular interest. Evaluation of the SL TILLING mutant hvd14.d has already shown that the drought-sensitive phenotype of the mutant might be caused by disturbed ABA metabolism and/or signalling, thus confirming cross-talk between SL signalling and ABA-dependent drought stress responses in barley (Fig. 1).

As part of our long-standing and successful cooperation with the research group Molecular Plant Nutrition and the University Rosario (Argentina), we have shown that cyanobacterial flavodoxin expressed in plant chloroplasts complements ferredoxin deficiency and improves tolerance to multiple sources of biotic, abiotic and xenobiotic stress. Recent characterisation of these plants revealed a high-light acclimation-like phenotype characterised by 15% thicker leaves compared to the wild type, while chloroplast ultrastructure remained unchanged. It was further demonstrated, that flavodiiron proteins (Flvs), another cyanobacterial protein class not present in angiosperms, mitigate the photoinhibition of photosystem I under high or fluctuating light. The Flv1/Flv3 transgenics displayed an increased production of ATP, an acceleration of carbohydrate metabolism and a more pronounced partitioning of sucrose into starch. The results suggest that Flvs are able to establish an efficient electron sink downstream of photosystem I, thereby ensuring efficient photosynthetic electron transport at moderate to high light intensities. Altogether, our findings suggest that Fld and Flv plants are better prepared to cope with adverse growth conditions.

Although the vasculature of the cereal rachis plays a crucial role in the supply of the developing grains, little is known about the factors controlling its organisation. In cooperation with the research groups Plant Architecture and Assimilate Allocation and NMR we discovered that in barley the basic vascular lay-out is a highly static feature and similar in both 2-rowed and 6-rowed varieties. However, the total volume of the vascular structures is highly flexible and directly correlated with the number of mature spikelets attached to a spike but not to the number of fertile florets.

Several collaborations with the research group Chromosome Structure and Function focus on the ultrastructural characterisation of cell nuclei. Based on high-pressure freezing for sample preparation, we were able to show that chromatin structure differs between micronuclei and primary nuclei, supporting data about the precise elimination of supernumerary B chromosomes of *Aegilops speltoides* in roots early in embryo development.

Selected Publications

HERTIG, C. et al.: Barley HISTIDINE KINASE 1 (HvHK1) coordinates transfer cell specification in the young endosperm. Plant J. 103 (2020) 1869-1884.

MARZEC, M. et al.: Barley strigolactone signaling mutant hvd14.d reveals the role of strigolactones in ABA-dependent response to drought. Plant Cell Environ. 43 (2020) 2239-2253.

MUSZYNSKA, A. et al.: A mechanistic view on lodging resistance in rye and wheat: a multiscale comparative study. Plant Biotechnol. J. 19 (2021) 2646-2661.

POURSAREBANI, N. et al.: COMPOSITUM 1 contributes to the architectural simplification of barley inflorescence via meristem identity signals. Nat. Commun. 11 (2020) 5138.

RUBAN, A. et al.: Supernumerary B chromosomes of Aegilops speltoides undergo precise elimination in roots early in embryo development. Nat. Commun. 11 (2020) 2764.

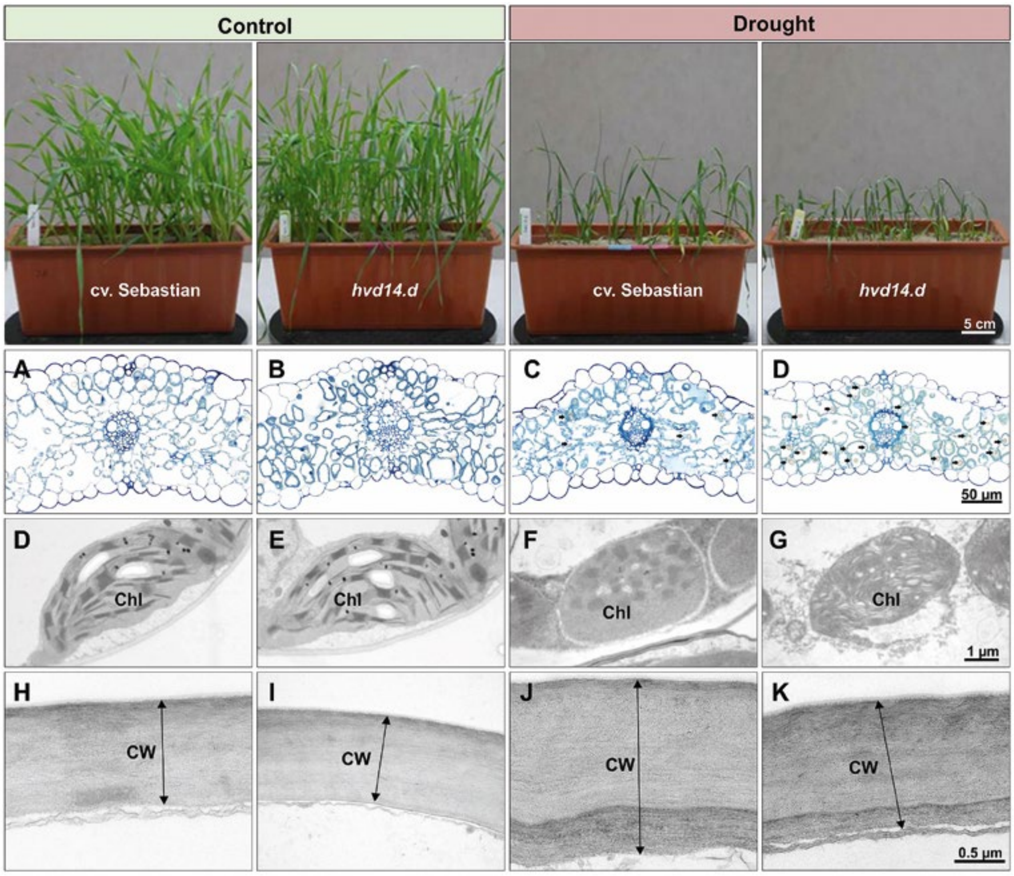


***Figure 1:** Morphological and ultrastructural characterisation of leafs of barley of cultivar Sebastian and strigolactone signalling mutant hvd14.d after exposure to drought. Light microscopy images of transversal leaf sections after histological stain (A-D). Transmission electron microscopy images of chloroplasts (D-G) and the outer epidermal cell wall (H-K). Lipid droplets (arrows in C, D). Chl, chloroplast; CW, cell wall. (I. Fontana, M. Melzer)*

EMBEDDING IN IPK RESEARCH THEMES

The project on the role of strigolactones in barley in response to drought (DFG) and our studies on lodging resistance contribute to Research Themes 4 "Growth and Metabolism" and 5 "Mechanisms of Resistance and Stress Tolerance".
As the central facility for light and electron microscopy, the research group is also involved in a large number of internal and external collaborations that cover a wide range of research topics. The work of the group is thus linked to all Research Themes of the IPK.

OUTLOOK

In collaboration with the research groups Resources Genetics and Reproduction and Metabolic Diversity analysis of the lodging resistant rye hybrid "Stabilstroh" will be continued by investigating cell wall components and morphological traits relevant for lodging at different developmental stages. The latter profits from a screening approach, in which we examined 50 accessions of wheat and of barley for lodging susceptibility in order to identify the most contrasting genotypes. In a long-term cooperation, we were able to describe an abnormal vasculature differentiation as an irreversible symptom of boron deficiency in rape seed. To uncover genes responsible for the vascular de-differentiation we will continue the work with the Crop Physiology group (Prof. Patrick Bienert) of the Technical University of Munich.

More information: *www.ipk-gatersleben.de/en/research/physiology-and-cell-biology/structural-cell-biology*

INDEPENDENT RESEARCH GROUPS

PLANT ARCHITECTURE (PBP)

Prof. Dr. Thorsten Schnurbusch

MEIOSIS (ME)

Dr. Stefan Heckmann

APPLIED CHROMOSOME BIOLOGY (ACB)

Prof. Dr. Hua Jiang

METABOLIC SYSTEMS INTERACTIONS (MSI)

Dr. Nadine Töpfer

INDEPENDENT RESEARCH GROUP (HEISENBERG-GROUP): **PLANT ARCHITECTURE** (PBP)

Head: Prof. Dr. Thorsten Schnurbusch

MISSION

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 utilising natural spike variants from barley and wheat as well as induced spike mutants from barley to clarify the genetic make-up of genes underlying developmental phenotypes for reduced and increased grain number per spike.

RESULTS

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 programme with an emphasis on using available genetic resources to identify, isolate and functionally characterise QTL, to reveal gene regulatory networks determining spikelet survival during the critical spike growth period, and to elucidate spatiotemporal 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.

Seeking crops with balanced parts for the ideal whole

Crop domestication and breeding considerably increased productivity over centuries but unconsciously lowered 'selfish plant behaviour' or individual plant fitness. Paradoxically, enhancing individual plant fitness is mistakenly equated with crop improvement. Because agriculture relies on community performance, embracing an agroecological genetics and genomics viewpoint might maximise communal yield by matching crop genotypes to target environments. Pursuing this in crop plants will require field phenotyping and selection under relevant conditions in a community context. Thus, connecting genetic principles with ecological and evolutionary concepts by treating agricultural production as an ecosystem or adopting an ecological engineering approach may open the way to a more holistic view of agroecological genetics and genomics of crop plant populations for enhancing yield. In principle, this viewpoint refers to unravelling the underlying genetics/genomics of exterior and interior architectural traits of crop plants in their ('unnatural') agricultural environment for maximising communal yield (as either monoculture or a mixture). During the EFRE-funded ALIVE project and one Alexander-von-Humboldt postdoctoral fellowship, we thus will apply these principles

Selected Publications

THIRULOGACHANDAR, V. & T. SCHNURBUSCH: 'Spikelet stop' determines the maximum yield potential stage in barley. J. Exp. Bot. 72 (2021) 7743-7753.

THIEL, J., R. KOPPOLU* et al.: Transcriptional landscapes of floral meristems in barley. Sci. Adv. 7 (2021) eabf0832. * joint first authorship*

POURSAREBANI, N. et al.: COMPOSITUM 1 contributes to the architectural simplification of barley inflorescence via meristem identity signals. Nat. Commun. 11 (2020) 5138.

ABBAI, R. et al.: Seeking crops with balanced parts for the ideal whole. Trends Plant Sci. 25 (2020) 1189-1193.

SAKUMA, S. & T. SCHNURBUSCH: Of floral fortune: tinkering with the grain yield potential of cereal crops. New Phytol. 225 (2020) 1873–1882.

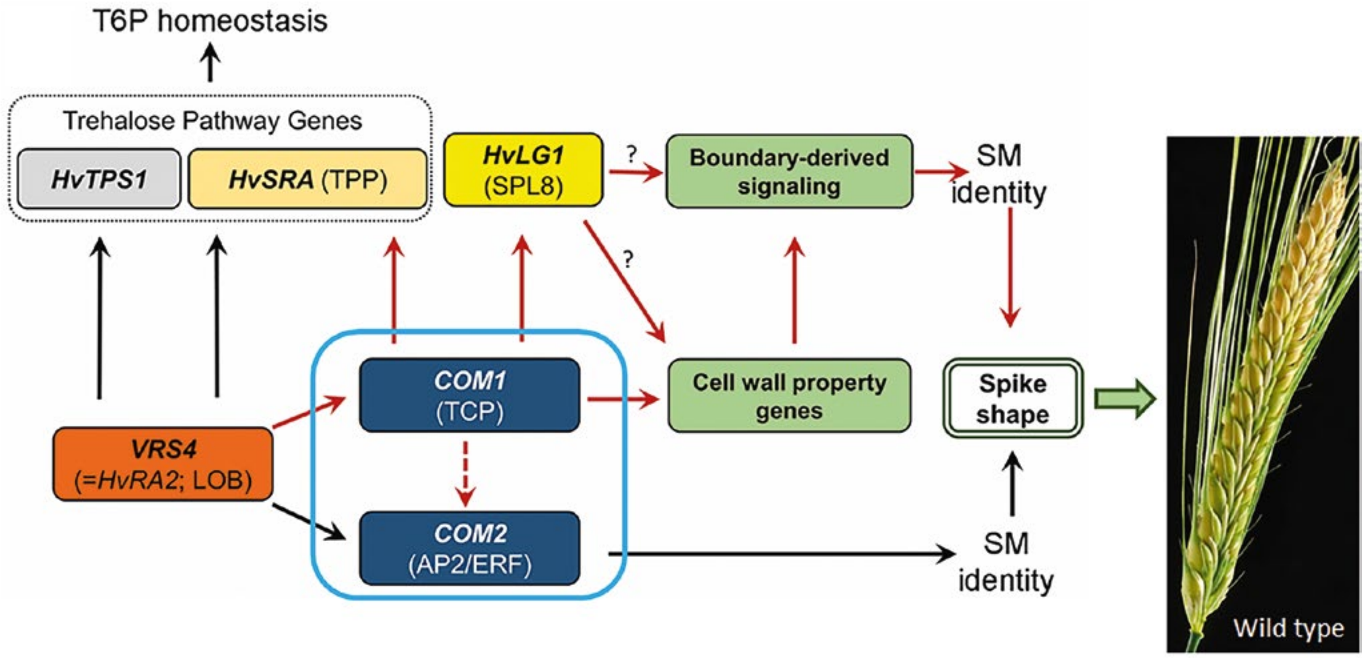


Figure 1: *Model of COM1 transcriptional regulation in barley.*

for the discovery of loci/genes/alleles related to improved community performance, allometric growth and enhanced grain numbers using bi-parental mapping populations and chromosome introgression lines of wheat and barley.

COMPOSITUM 1 contributes to the architectural simplification of barley inflorescence via meristem identity signals

Grasses have varying inflorescence shapes; however, little is known about the genetic mechanisms specifying such shapes among tribes. Here, we identify the grass-specific TCP transcription factor COMPOSITUM 1 (COM1) expressing in inflorescence meristematic boundaries of different grasses. COM1 specifies branch-inhibition in barley (Triticeae) versus branch-formation in non-Triticeae grasses. Analyses of cell size, cell walls and transcripts reveal barley COM1 regulates cell growth, thereby affecting cell wall properties and signalling specifically in meristematic boundaries to establish identity of adjacent meristems. COM1 acts upstream of the boundary gene Liguleless 1 and confers meristem identity partially independent of the COM2 pathway. Furthermore, COM1 is subject to purifying natural selection, thereby contributing to specification of the spike inflorescence shape. This meristem identity pathway has conceptual implications for both inflorescence evolution and molecular breeding in Triticeae.

EMBEDDING IN IPK RESEARCH THEMES

Research within the independent HEISENBERG-Research Group Plant Architecture relates predominantly to the IPK Research Theme 4 “Growth and Metabolism”.

OUTLOOK

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. Besides, we will continue our path taken towards developing agroecological genetics approaches with the view of deeper insights into allometric growth responses and biomass allocation in a crop canopy context.

More information: *www.ipk-gatersleben.de/en/research/independent-research-groups/plant-architecture*

INDEPENDENT RESEARCH GROUP
MEIOSIS (ME)

Head: Dr. Stefan Heckmann

MISSION

The research focus of the independent research group Meiosis until 09/21 majorly funded by the German Federal Ministry of Education and Research (BMBF) and by 10/21 primarily funded by the European Research Council (ERC) is plant meiosis. Meiosis generates genetic variation through homologous recombination (HR) that is harnessed during plant breeding. However, particularly in cereal crops including barley meiotic recombination events are limited and skewed towards chromosome ends whereby a large portion of the genetic information keeps untapped in breeding programmes. Hence, novel strategies and tools are needed to manipulate plant meiotic recombination landscapes (frequency/distribution of meiotic recombination events).

RESULTS

Research activities aim to a) better understand the mechanisms underlying the control of HR in both barley and *Arabidopsis*, b) develop novel tools and strategies to study and alter meiotic recombination outcome, and c) translate acquired knowledge into barley. Embarking on molecular genetics, biochemistry and cytogenetics, key results of our team include:

(a) Isolation and analysis of barley mutants defective for meiotic DNA double strand break (DSB) and for class I crossover (CO) formation. In plants defective for DSB-induction complex member *MTOPVIB* DSB formation and HR are absent. Plants defective for the ZMM member *HEI10* form no interference-sensitive class I CO with residual CO being interference-insensitive. Notably, plants heterozygous for *hei10* have reduced chiasma numbers compared with WT due to lower HEI10 dosage. Also, approaches to induce site-specific DSBs during meiosis were explored to trigger targeted meiotic HR indicating that meiotic site-specific DSBs can be induced by using genome editing tools or the endogenous DSB-induction complex. Moreover, analysis of plants defective for the axis-associated protein ASY1 and the axis-remodelling protein PCH2 showed that meiotic chromosome axis formation and remodelling are critical for meiotic fidelity and the recombination landscape in *Brassica rapa*. In collaborative studies we could show for instance that light-sheet fluorescence microscopy (LSFM) can be employed for the spatiotemporal dissection of reproductive processes, that chromosome engineering can be employed to manipulate local meiotic recombination outcome or we functionally dissected the role of MutS homologues 4 and 5 during wheat meiosis.

(b) A novel crystal digital PCR-based single barley pollen nucleus genotyping approach likely applicable for diverse plants to genotype single nuclei was established. It enables measuring recombination rates in defined chromosomal intervals in high throughput. In addition, virus-based tools were established for reproductive gene studies in barley, i.e. germline BSMV-VIGS (barley stripe mosaic virus-virus-induced gene-silencing) to study transiently meiotic gene function and BSMV-VIGE (virus-based guide RNA delivery for plant Genome Editing) to induce heritable edits. Moreover, proximity-dependent Biotin Identification (BioID) in meiocytes to identify new meiotic players and LSFM-imaging of reproductive processes including meiosis were established.

(c) We have studied in barley mutants defective for *RECQ4* and *FIGL1*, so-called anti-CO factors known to limit CO formation in other species. In both *recq4* and *figl1* meiotic fidelity is nearly untouched and while in *recq4* increased chiasma numbers are found in *figl1* a slight decrease in chiasma numbers is found. Moreover, as alternative

Selected Publications

AHN, Y.J. et al.: High throughput measuring of meiotic recombination rates in barley pollen nuclei using Crystal Digital PCR TM. Plant J. 107 (2021) 649-661.

CUACOS, M. et al.: Meiotic chromosome axis remodelling is critical for meiotic recombination in Brassica rapa. J. Exp. Bot. 72 (2021) 3012-3027.

SCHMIDT, C. et al.: Changing local recombination patterns in plants by CRISPR/Cas mediated chromosome engineering. Nat. Commun. 11 (2020) 4418.

DESJARDINS, S.D. et al.: MutS homologue 4 and MutS homologue 5 maintain the obligate crossover in wheat despite stepwise gene loss following polyploidization. Plant Physiol. 183 (2020) 1545-1558.

VALUCHOVA, S. et al.: Imaging plant germline differentiation within Arabidopsis flowers by light sheet microscopy. eLife 9 (2020) e52546.

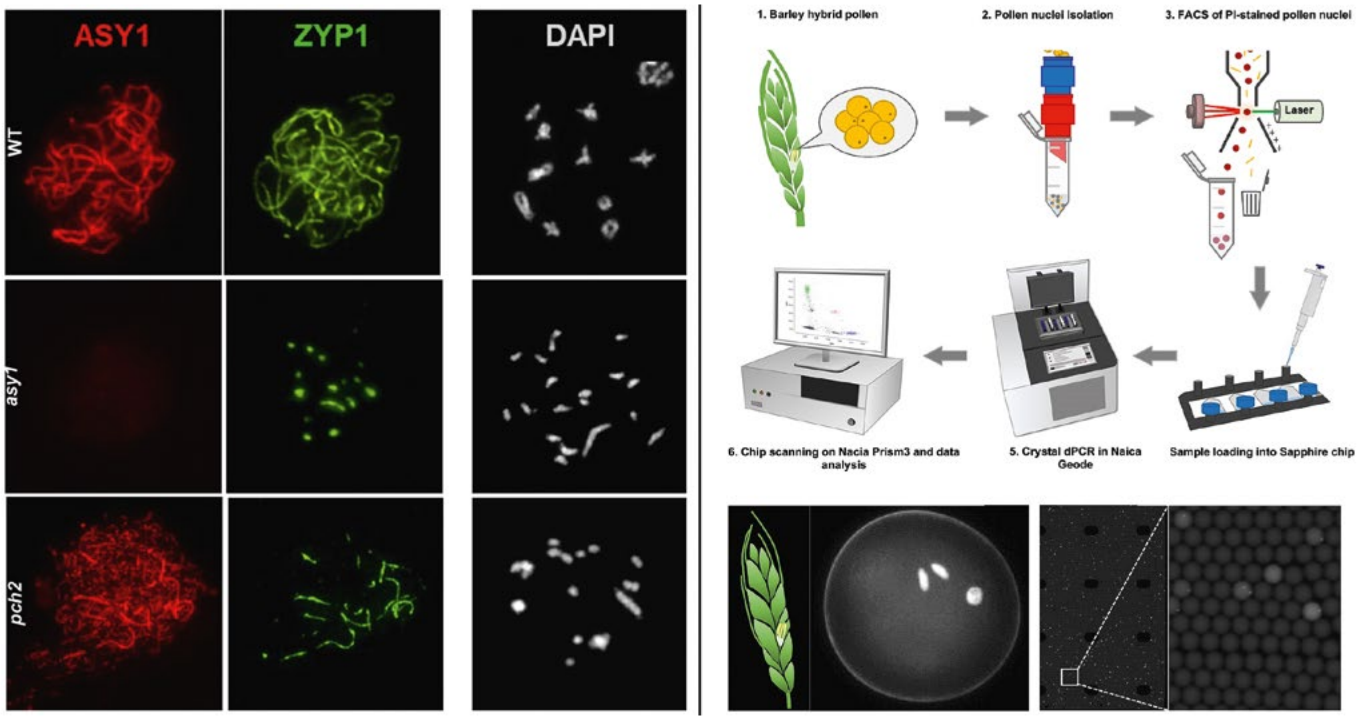


***Figure 1:** Selected research activities of the independent research group Meiosis: Male meiotic chromosome behaviour of isolated mutants in B. rapa showing defective synapsis and CO formation (Left: Cuacos et al. 2021) as well as single pollen nucleus genotyping using Crystal digital PCR to measure meiotic recombination rates in barley (Right: Ahn et al. 2021).*

approaches to possibly alter the recombination landscape in barley, we have isolated lines that carry additional copies of *HEI10* with varying expression levels of *HEI10* and we have tested a number of chemical compounds for their impact on the barley recombination landscape.

EMBEDDING INTO IPK RESEARCH THEMES

Our research on meiosis assuring genetic variation is closely-linked to the research of the department Breeding Research, in particular to the area of chromosome biology. We contribute with our research efforts on meiotic chromosome behaviour and recombination control underpinning plant fertility to the IPK Research Theme 3 “Mechanisms of Reproduction”.

OUTLOOK

The main research topics of our team will be: Dissect the influence of identified candidate genes or genes known to affect meiotic recombination on the barley recombination landscape. Apply (a-)biotic factors and virus-based tools to modify the barley recombination landscape. Further develop and employ novel single pollen nuclei genotyping approaches in barley and LSFM for spatio-temporal analysis of plant (reproductive) processes. Explore novel approaches for targeted induction of meiotic DSBs to trigger HR. Functionally dissect newly identified meiotic players by BioID. Address the question on frequency and tract lengths of gene conversion (GC) events in plants.

***More information:** www.ipk-gatersleben.de/en/research/independent-research-groups/meiose*

INDEPENDENT RESEARCH GROUP
APPLIED CHROMOSOME BIOLOGY (ACB)

Head: Prof. Dr. Hua Jiang

MISSION

The research focus of the independent research group Applied Chromosome Biology is focused on genetic and epigenetic regulation of reproductive development. Reproduction and fertility are the main targets of crop breeding. Hence, understanding the molecular mechanisms of reproductive development is crucial for manipulating fertility. In addition, reproduction is susceptible to increased temperature and associated with reduced global yields of crops. Thus, novel knowledge and approaches to enhance reproductive thermotolerance is required for ensuring fertility and crop yield under climate changes.

RESULTS

Research activities aim to a) Identify the role of epigenetic regulation in reproduction and thermotolerance, b) Understand how cytoplasmic compartments maintain ploidy stability during meiosis under normal and heat stressed conditions, and c) identify novel regulators required for enhanced reproductive thermotolerance. Embarking on genetics, epigenetics, biochemistry, and cytogenetics, key results of our team include:

a) Identifying the role of H3K9 demethylation in reproduction. Our current work reveals the role of H3K9 demethylation in male meiosis and indicates the cohesin cofactors are recruited by H3K9 demethylases to the targets, activating downstream genes essential for male meiosis. These findings uncover a novel role of H3K9me2 removal in meiosis and improve our understanding of the H3K9 demethylation-mediated transcriptional activation pathway. Moreover, through interacting with a transcription factor, H3K9 demethylases also activate multiple genes essential for pollen wall formation. We are developing a model to show that transcription factors recruit H3K9 demethylases to the targets and regulate pollen development.

b) Exploring how cytoplasmic compartments separate spindles during male meiosis. We have isolated several mutants that affect the distribution of vesicles and spindle separation in male meiosis through a mutant screen. We have identified one of the candidates that encode a vacuole-localised protein. Disruption of the candidate could partially recover the organisation of cytoplasmic compartments in meiosis. Moreover, we are identifying another candidate required for spindle separation under normal and heat stress conditions.

c) Identifying epigenetic alterations in polyploids and doubled haploids. We showed that in *Arabidopsis*, 4x Col-0 and 4x Ler presented different flowering times, with a delayed flowering time in 4x Col-0 but not in 4x Ler. The level of a repressive epigenetic mark, trimethylation of histone H3 at lysine 27 (H3K27me3), was significantly decreased in 4x Col-0 but not in 4x Ler, potentially leading to different transcription levels of FLC and flowering time in 4x Col-0 and 4x Ler. Our results showed a role of H3K27me3 alterations in response to genome duplication in *Arabidopsis* autopolyploids and that flowering time variation potentially functions in autopolyploid speciation. In addition to polyploids, we identified variations in DNA methylation in doubled haploid (DH) *Arabidopsis* Col-0, although the ploidy of DH Col-0 is recovered by chromosome doubling. We identified both random and common differential DNA methylation regions (DMRs) in DH Col-0, suggesting that doubled haploid induction could be used as an alternative approach to induce epigenetic alleles for crop improvement.

Selected Publications

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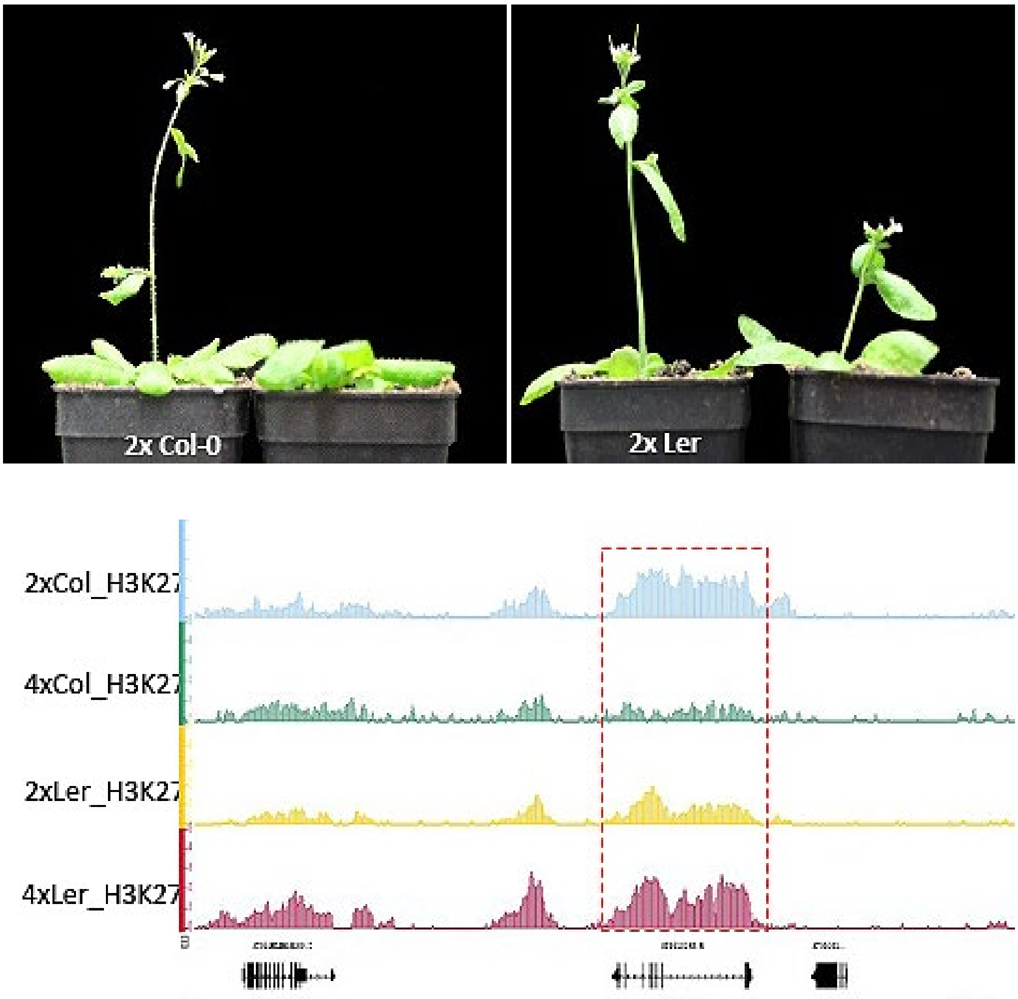

Figure 1: *Selected research activities of the independent research group Applied Chromosome Biology: Flowering-time variation in 2x and 4x Col-0 and Ler (up); screen shot of the level of H3K27me3 at the FLC locus in 2x and 4x Col-0 and Ler (lower) (Cheng et al. 2021).*

EMBEDDING IN IPK RESEARCH THEMES

Our research on reproduction and fertility is closely-linked to the research of the department Breeding Research, in particular to the area of chromosome biology. We contribute with our research efforts on genetic and epigenetic regulation of fertility to the IPK Research Theme 3 “Mechanisms of Reproduction”.

OUTLOOK

The main research topics of our team will be: Explore how H3K9 demethylation regulates male meiosis and pollen development. Investigate how H3K9me2 and CHG DNA methylation protect reproduction under heat stressed conditions. Explore how cytoplasmic signals control spindle separation during male meiosis II under normal and heat stressed conditions. Identify novel factors required for reproductive thermotolerance in *Arabidopsis* and barley.

More information: *www.ipk-gatersleben.de/en/research/independent-research-groups/applied-chromosome-biology*

INDEPENDENT RESEARCH GROUP
METABOLIC SYSTEMS INTERACTIONS
(MSI)

Head: Dr. Nadine Töpfer

MISSION

The mission of the research group Metabolic Systems Interactions is to gain a better understanding of plant metabolism in its functional context. The group uses large-scale metabolic network models to simulate and analyse metabolic processes and to reveal constraints and capacities that affect plant's performance. Our work focuses on network reconstruction and model integration, the study of abiotic plant-environment interactions, the development of (data-integrative) methods to study cell-, tissue- and organ interactions, the curation and computational integration of specialised metabolism, and software development. The group collaborates closely with internal and external experimental partners.

RESULTS

Over the past two years the group has grown in personnel as well as research projects. Three major topics are currently covered by the group: (i) the study of abiotic interactions between the plant leaf and its environment, (ii) the development of cell type-, tissue- and organ-specific metabolic models, and (iii) the development and refinement of whole-plant to ecosystem models.

The first main topic covers three research projects: (i) the study of water-saving flux modes in a leaf metabolic model, (ii) osmotic and metabolic constraints in guard cell metabolism, and (iii) the plasticity of C3 and C4 photosynthesis. In our studies on water-saving flux modes we coupled a time-resolved model of leaf metabolism to a biophysical gas-exchange model (Figure 1). Using this model, we were able to identify an alternative carbon fixation pathway involving mitochondrial isocitrate dehydrogenase which could lead to up to 10% water-saving (Töpfer et al. 2020). A related project uses a spatio-temporally resolved model of guard cell and mesophyll metabolism to disentangle the role of guard cell metabolites as a source of osmotica and energy. Our model predictions clearly support recent experimental observations that glucose, and not malate, is the major starch-derived metabolite that fuels stomatal opening. Furthermore, the model suggests that in vivo ion limitation might be a driver for starch utilisation during guard cell opening. Overall, the study highlights the potential of computational models to resolve seemingly conflicting experimental observations. Together these two studies contribute towards engineering more water-saving crop plants for future climate scenarios. A third project, that recently started, investigates metabolic plasticity in C3 and C4 photosynthesis with respect to light and nitrogen availability. To achieve this goal, we are currently developing a modelling framework that allows for a better account of the enzymatic nitrogen cost.

The second major research topic involves the reconstruction and curation of cell type-, tissue- and organ-specific models. This involves adding and removing metabolic reactions and pathways to account for the metabolic differences of different metabolic subsystems. Since no adequate tools were available to perform these actions in a reproducible and high-quality manner, we developed the CobraMod tool. CobraMod can use metabolic pathway information from various databases to extend and curate large-scale metabolic models (Camborda et al. 2020, Bioinformatics) and is currently used to reconstruct tissue-specific models for maize and tomato. These models serve as a basis for studying metabolic constraints and capacities in seed/fruit metabolism (collaboration with research groups Assimilate Allocation and NMR, Network Analysis and Modelling, Biotrophy and Immunity).

The third major topic involves developing new modelling approaches that allow simulating whole-plant metabolism and ultimately plant-plant and plant-microorganism interactions. The PlantEd computer game is a "playful" approach to this topic and

Selected Publications

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TÖPFER, N. et al.: Alternative Crassulacean acid metabolism modes provide environment-specific water-saving benefits in a leaf metabolic model. Plant Cell 32 (2020) 3689-3705.

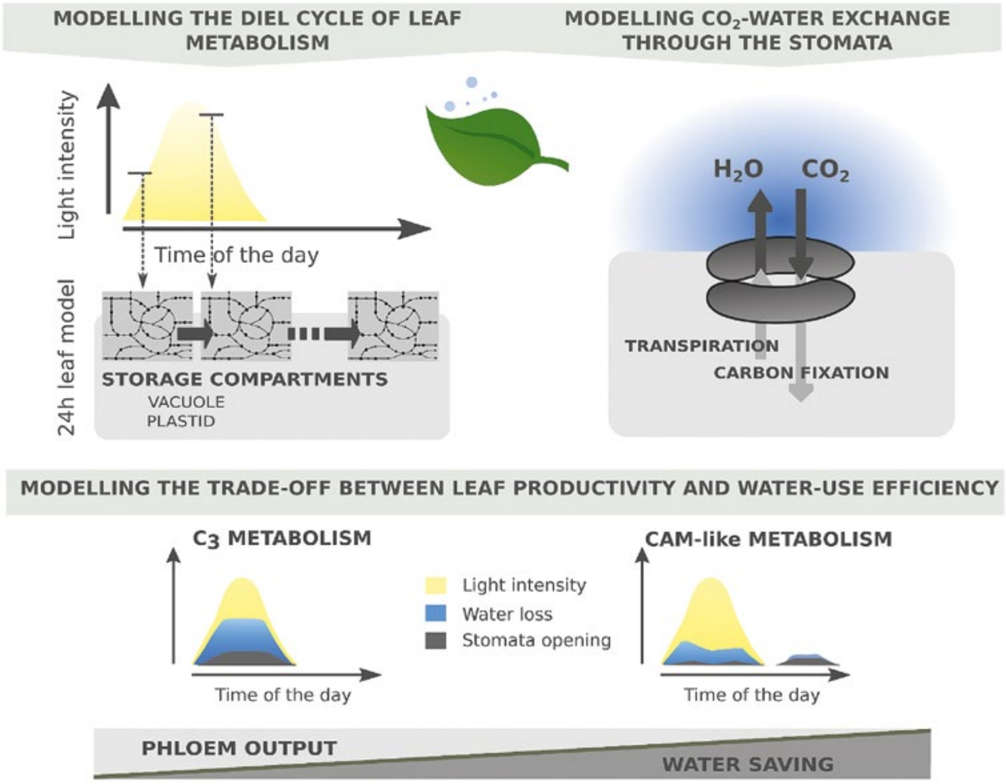

Figure 1: *Graphical representation of a time-resolved, environment-coupled model of leaf metabolism and its application to study water-saving flux modes. A 24-hour leaf metabolism model (upper left) and a biophysical gas-exchange model (upper right) are coupled to study the trade-off between productivity and water saving and how this affects metabolic flux modes, i.e., C3 and CAM photosynthesis (bottom).*

involves a simple whole-plant metabolic model and requires the player to develop optimal resource allocation strategies for different environmental scenarios (collaboration with Network Analysis and Modelling).

EMBEDDING IN IPK RESEARCH THEMES

The research of the group is well embedded in Research Theme 4 “Growth and Metabolism”. The group uses computational methods to identify existing and predict novel mechanisms that shape plant metabolism, growth and ultimately affect plant’s performance. Additionally, data-integrative and evolutionary algorithms are employed and connect the group with Research Theme 2 “Genome Diversity and Evolution”. Research Theme 5 “Mechanisms of Resistance and Stress Tolerance” is mainly studied on the level of abiotic interactions of the plant leaf with its environment.

OUTLOOK

In the future, the group will focus on developing whole-plant to ecosystem models. To achieve this goal, existing metabolic models and modelling approaches will be further developed and refined. A medium to long-term goal is to develop efficient modelling approaches combining mechanistic metabolic models with artificial intelligence to model anticipatory behaviour and to study ecosystem dynamics and evolutionary trajectories. As such, the above-mentioned PlantEd game marks a milestone in the development of such modelling frameworks. Moreover, the group will continue to investigate abiotic plant-environment interactions with a particular focus on C3 and C4 photosynthesis and study source-sink interactions.

More information: *www.ipk-gatersleben.de/en/research/independent-research-groups/metabolic-systems-interactions*

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Kicherer, L.: Gezielte Mutagenese in Gersten-Protoplasten (*Hordeum vulgare* L.): Temperatureinfluss und simultane Adressierung von zwei Zielgenen. (Bachelor Thesis) Hochschule Anhalt, Fachbereich Landwirtschaft, Ökotophologie und Landschaftsentwicklung, Bernburg (2021) 69 pp.

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THIRD PARTY PROJECTS

Third-party funded projects acquired and ongoing in the 2020 / 2021 reporting period.

Acronym: Project Name / Funding Code	**Principle Investigator (Pi)** Project Participants at IPK	**Funding Agency**	**Duration** (Start)	**Overall budget**
IPD-DSI: Unterstützung der internationalen Prozesse sowie der Diskussionen zum Thema DSI unter Einbeziehung von Positionen der Forschung – Teilprojekt IPK / 3519532A11	**Freitag, J.;** Scholz, U.	BFN	5/20/2021 1/31/2022	24.400
BigData: Nutzung von Big Data in Weizen zur Präzisionszüchtung / 2818408B18	**Reif, J.;** Scholz, U.	BLE	2/1/2020 1/31/2023	445.488
GENDIV: Integrative Nutzbarmachung der genetischen Diversität bei Winterweizen zur Erhöhung des Kornertrages – Teilprojekt IPK / 2814603713	**Börner, A.;** Weise, S.	BLE	1/1/2018 3/31/2020	48.099
GrasFest: Nutzung genetischer Diversität und Entwicklung innovativer Verfahren zur züchterischen Verbesserung der Samenausfallfestigkeit bei Gräsern – Teilprojekt IPK / 2818203115	**Dehmer, K.;** Willner, E. Melzer, M.	BLE	4/11/2017 4/10/2020	173.610
HYFLOR: Erforschung der Genetik der Blühbiologie bei Weizen zur effektiven Erzeugung von Hybridweizen / 2818401A18	**Reif, J.;** Schnurbusch, T.	BLE	10/1/2019 9/30/2022	633.303
InnoLuteus: Verbundvorhaben: Innovative Züchtungsstrategien zur Verbesserung der Anbauwürdigkeit der Gelben Lupine (Lupinus luteus) in Deutschland – Teilprojekt IPK: Merkmalserfassung von IPK Genbankakzessionen / 22036618	**Lohwasser, U.**	BLE	4/1/2019 3/31/2022	184.614
LINSEL: Selektion geeigneter Sortentypen von Linsen (Lens culinaris) für nachhaltige Anbausysteme / 2815EPS078	**Lohwasser, U.**	BLE	2/15/2019 2/28/2022	36.250
FUGE: Monitoring der Fusariumarten und Entwicklung genomischer Werkzeuge zur effektiveren Züchtung von Saathafer / 28AIN02C20	**Mascher, M.**	BLE	12/15/2020 5/31/2020	168.945
P-Stärke: Züchterische Verbesserung der Phosphor-Aneignungseffizienz von Stärkekartoffeln und eine ressourcenschonende Rohstoffproduktion – Teilprojekt IPK / 22002117	**Dehmer, K.**	BLE	3/1/2019 2/28/2022	206.153
Effikar: Selektion und Züchtung nährstoffeffizienter Phytophthora-resistenter Kartoffelzuchtstämme für einen nachhaltigen ökologischen Landbau / 2818NA003	**Dehmer, K.**	BLE	11/1/2019 10/31/2022	230.327
LuzNutz: Erhöhung der Anbauwürdigkeit von Luzerne (Medicago sativa L.) als Futterpflanze - Neue Impulse für die Königin der Futterpflanzen / 2818EPS035	**Dehmer, K.**	BLE	2/1/2021 1/31/2024	297.057
Verbundvorhaben: Vermeidung des Eintrages von gefährlichen Unkrautarlen in Arznei-und Gewürzpflanzenbestände über das Saatgut. / 22011718	**Otto, L.-G.**	BLE	12/1/2018 11/30/2021	116.124
Sterilkam2: Entwicklung der Elternkomponenten für die Erzeugung einer sterilen Kamillesorte / 22008718	**Otto, L.-G.**	BLE	2/1/2019 1/31/2022	509.134
DETECT: Machbarkeitsstudie zu Nachweis- und Identizierungsverfahren für genomeditierte Panzen und panzliche Produkte – Teilprojekt IPK / 2820HS001	**Kumlehn, J.;** Mascher, M.	BLE	1/1/2021 12/31/2022	478.092
DIVHA: Neue allelische Diversität für das ertragsbestimmende Merkmal Halmlänge des Weizens durch gezielte, genspezifische Mutagenese / 2814603113	**Kumlehn, J.**	BLE	6/1/2015 5/31/2020	662.237
Rootshape: Sink-Konkurrenz zwischen Bestockung und Wurzelentwicklung bei Weizen / 2814603413	**v. Wirén, N.**	BLE	6/1/2015 11/30/2020	575.352
FASTFLOW: Verbundprojekt: Generationsbeschleunigung bei Winterweizen durch vernalisationsunabhängige Induktion der Ährenbildung – Teilprojekt IPK / 2818402A18	**Kumlehn, J.**	BLE	4/1/2020 3/31/2023	512.641
VALPROKAR: Validierung Identifizierter Markerproteine als Grundlage für die züchterische Entwicklung stickstoffeffizienter und trockentoieranter Stärkekartoffeln; Teilvorhaben 2: Charakterisierung von Kanidatengenen der N-Effizienz und massenspe / 22007018	**Mock, H.-P.**	BLE	10/1/2018 1/31/2022	244.518

BulbOmics: Nutzbarmachung von Virusresistenzen aus Hordeum bulbosum für eine nachhaltige Gerstenzüchtung mit Hilfe von GenOmics – Teilprojekt IPK / 2818201615	**Stein, N.**	BLE	10/15/2016 3/31/2020	327.481
DRYeGRASS: Genetische Analyse der Trockenstresstoleranz bei Deutschen Weidelgras (Lolium perenne L.) mittels phänologischer, physiologischer und molekularer Differenzierungsmethoden – Teilprojekt IPK / 2818208715	**Willner, E.**	BLE	9/1/2016 3/31/2020	56.529
KIBREED: Verbundprojekt Züchtung von Standortangepassten Sorten mittels Algorithmen der Künstlichen Intelligenz – Teilprojekt IPK / 28DK131A20	**Reif, J.**	BLE	6/1/2021 5/31/2024	369.334
Sus-Agri-CC: InnovativeBiodünger zur Ertragssteigerung von Getreide und Gartenbaukulturen unter dem globalen Klimawandel / 2821ERA18C	**Hajirezaei, M.**	BLE	6/1/2021 5/31/2024	170.146
AVATARS: Pflanzenzüchtungsforschung-Verbundvorhaben: Modernste Virtualitäts- und erweiterte Realitätsverfahren für den Zyklus von Samen zu Samen – Teilprojekt IPK / 031B0770A	**Altmann, T.;** Lange, M. Schippers, J.; Freitag, J. Borisjuk, L.; Gladilin, E. Blätke, M.	BMBF	6/1/2019 11/30/2021	2.355.684
DPPN: Deutsches Pflanzenphänotypsierungs Netzwerk – Teilprojekt IPK / 031A053B	**Altmann, T.;** Schweizer, P. Lange, M.; Borisjuk, L.; Gladilin, E.; Junker, A.; Mock, H.-P.; V. Wirén, N.	BMBF	10/1/2012 3/31/2021	13.365.133
Genebank 2.0: Genomik-basierte Nutzbarmachung genetischer Ressourcen im Weizen für die Pflanzenzüchtung – Teilprojekt IPK / 031B0880A	**Reif, J.** Stein, N.; Mascher, M.; Röder, M.; Djamei, A.; Scholz, U.; V. Wirén, N.	BMBF	11/1/2019 10/31/2022	1.950.784
HaploTools: Erzeugung von Haploidie-Induktionen mit Hilfe des Genome Enginieering - neue Werkzeuge für die schnellere Züchtung von mono- und eudikotyledonen Kulturpflanzen – Teilprojekt IPK / 031B0192A	**Houben, A.;** Kumlehn, J.	BMBF	9/1/2016 4/30/2020	1.116.005
HERBY: Meiotische Rekombination in der Gerste (Hordeum vulgare) nutzbar machen / 031B0188	**Heckmann, S.;** Kumlehn, J.	BMBF	10/1/2016 9/30/2021	1.218.219
OSIRIS: Untersuchung des Ertragspotentials neuer Weizen-Ährenformen durch genomweite Assoziationsstudien (GWAS) und gezielte Mutagene mit RNA-vermittelten Endonukleasen / 031B0201A	**Kumlehn, J.;** Schnurbusch, T.	BMBF	10/1/2016 1/31/2020	798.686
SHAPE: Strukturelle Genomvariation, Haplotypendiversität und das Gerste-Pan-Genom-Erforschung der strukturellen Genomdiversität für die Gerstezüchtung – Teilprojekt IPK / 031B0190A	**Stein, N.;** Mascher, M.; Reif, J.; Scholz, U.	BMBF	11/1/2016 1/31/2020	2.224.171
SHAPE: Strukturelle Genomvariation, Haplotypendiversität und das Gerste Pan-Genom – Erforschung der strukturellen Genomdiversität für die Gerstezüchtung / 031B0884A	**Stein, N.;** Mascher, M.; Reif, J.; Scholz, U.	BMBF	2/1/2020 1/31/2023	1.400.887
BRIWECS: Pflanzenzüchterische Innovation bei Weizen für resiliente Anbausysteme – Teilprojekt IPK / 031A354G	**Graner, A.**	BMBF	10/1/2014 7/31/2020	571.179
Physics4Seeds: Effekte einer Plasmabehandlung auf Keimfähigkeit von Rotklee und Rispengras / 03WIR2805D	**Dehmer, K.**	BMBF	7/1/2020 10/31/2022	199.975
TomKin: Produktion haploider Tomaten mit Hilfe der Manipulation des Kinetochors / 01DK20022	**Lermontova, I.**	BMBF	5/1/2020 4/30/2022	20.000
de.NBI-Etablierungsphase - Leistungszentrum - GCBN-German Crop BioGreenformatics Network / 031A536A	**Scholz, U.**	BMBF	3/1/2015 12/31/2021	946.970
CAMPRO: Etablierung einer qualitativ hochwertigen Ölpflanze für magere Böden – Teilprojekt IPK / 031B0343C	**Kumlehn, J.**	BMBF	10/1/2017 9/30/2020	386.483
PRECISE: Plattform für einen präzisen Austausch von Genvarianten unter Nutzung synthetischer Endonukleasen / 031B0547	**Hensel, G.**	BMBF	6/1/2018 10/31/2020	311.732
DELITE: Zielsequenz-spezifische Genom-Modifikation von Getreide-Elitematerial durch DNA-integrationsfreie Applikation RNA-vermittelter Endonukleasen im Kontext Haploidie-induzierender Kreuzungen / 031B0550	**Kumlehn, J.**	BMBF	7/1/2018 9/30/2020	432.085
BARLEY BIODIVERSITY: Steigerung der Biodiversität und Produktivität der Gerste mit Hilfe der Assoziationskartierung von zwei Wildgersten-Introgressionsbibliotheken und der sensorgestützten Hochdurchsatz-Phänotypisierung im Feld / 031A352B	**Mock, H.-P.**	BMBF	10/1/2014 1/31/2021	323.768

POISE: Phytopathogenese: Eine gute Möglichkeit, den Ernteertrag und die Qualität unter wechselnden Umweltbedingungen zu verbessern / 01DR17010	**Hajirezaei, M.**	BMBF	6/1/2017 11/30/2020	26.900
INPUT: Entwicklung eines Schnell-Test-Systems zur Steuerung des Produktionsfaktoren-Inputs während der Erzeugung doppelt haploider Weizenlinien – Teilprojekt IPK / 031B0804B	**Mock, H.-P.**	BMBF	5/1/2019 4/30/2022	257.665
CATCHY 2: Zwischenfrüchte als agronomische Maßnahme für nachhaltige Bodenfruchtbarkeit und Ertragssicherheit – Teilprojekt IPK / 031B0507B	**v. Wirén, N.**	BMBF	4/1/2018 3/31/2021	551.371
Mycotom: Einsatz arbuskulärer Mykorrhizapilze als Bodenhilfsstoff zur Produktion qualitativ hochwertiger Tomaten im Gewächshaus – Teilprojekt IPK / 031B0292C	**Mock, H.-P.**	BMBF	2/1/2017 10/31/2020	192.204
FDCAzymes: Lignocellulose-basierte Enzyme zur Konversion von 5-Hxdroxymethylfurfural zu 2,5 Furandicarbonsäure – Teilprojekt IPK / 031B0355B	**Matthes, F.**	BMBF	6/1/2017 8/31/2020	310.799
NEMARES: Die Bedeutung von Wurzelläsionsnematoden im Pflanzenbau in Deutschland und Entwicklung von Strategien zur Züchtung resistenter Sorten – Teilprojekt IPK / 031B0186C	**Stein, N.**	BMBF	10/1/2016 3/31/2020	217.987
PrimedPlant: Priming als eine Strategie zur Verbesserung der Resistenz von Kulturpflanzen und ein mögliches Züchtungsziel / 031B0196D	**Reif, J.**	BMBF	10/1/2016 1/31/2020	82.499
IdeMoDeResBar: Identifikation, Modifikation und Nutzung von Resistenzen gegen bedeutende Pathogene der Gerste – Teilprojekt IPK / 031B0199C	**Kumlehn, J.**	BMBF	11/1/2016 1/31/2020	331.932
PrimedPlant 2: Priming als eine Strategie zur Verbesserung der Resistenz von Kulturpflanzen und ein mögliches Züchtungsziel / 031B0886D	**Douchkov, D.**	BMBF	2/1/2020 1/31/2023	219.419
IdeMoDeResBar-II: Identifikation, Modifikation und Nutzung von Resistenzen gegen bedeutende Pathogene der Gerste – Teilprojekt IPK / 031B0887C	**Kumlehn, J.**	BMBF	2/1/2020 1/31/2023	440.033
CATCHY 3: Zwischenfrüchte als agronomische Maßnahme für nachhaltige Bodenfruchtbarkeit und Ertragssicherheit – Teilprojekt IPK / 031B1060B	**v. Wirén, N.**	BMBF	4/1/2021 3/31/2024	435.777
Crops4Future: Crops for the Future – aber was soll das sein? / 01WJ2107	**Freitag, J.**	BMBF	3/1/2021 12/31/2021	52.801
FABUNITY: The Fabulous Fabrication Community - Teilvorhabenz IPK / 16MCJ1085D	**Freitag, J.**	BMBF	1/1/2021 12/31/2023	40.400
WiLDSi-VorweRts: Wissensbasierte Lösungsansätze für Digitale Sequenzinformation - Wissenschaftliche Lösungsansätze für digitale Sequenzinformation: Vorbereitung weitere Ratschläge – Teilprojekt IPK / 16LW0063	**Freitag, J.**	BMBF	8/1/2021 1/31/2023	132.562
Züchtung innovativer Gartenbohnensorten durch Assoziationskanierung; Identifizierung neuer Marker für Bakteriose-Resistenzen, Hülsen-Qualitätsparameter und Durchwurzelungstiefe bei der Gartenbohne und Nutzbarmachung der genetischen Diversität / ZF4061309MD8	**Otto, L.-G.;** Lohwasser, U.; Mascher, M.	BMWI	4/1/2019 3/31/2022	189.880
DH-radish: Erzeugung von Rettich / Radieschen DH-Inducerlinien / 03THWST001	**Lermontova, I.**	BMWI	11/1/2020 10/31/2022	119.993
HORTENSIEN: Entwicklung hochgradig phyllodulcinhaltiger Teehortensien (Hydrangea ssp.) zur großindustriellen Nutzung in der Lebensmittel- und Getränkeindustrie; Biochemische und physiologische Untersuchungen zur Erhöhung des Phyllodulcingehaltes / ZF4061310MD9	**Hajirezaei, M.**	BMWI	10/1/2019 9/30/2022	187.362
Selektion und Herstellung geeigneter rekombinanter mikrobieller Bindeproteine/-peptide zur spezifischen Uran- bzw. Arsen Entfernung / ZF4061307RH7	**Giersberg, M.**	BMWI	11/1/2017 7/31/2020	165.464
Stammkonstruktion zur Herstellung rekombinanter ω-Transaminasen / ZF4061308AJ7	**Giersberg, M.**	BMWI	5/1/2018 4/30/2021	190.000
Spitfire/Cornet: Screening of Pisum sativum (pea) accessions for pea necrotic yellow dwarf virus resistance / CORNET	**Lohwasser, U.**	BMWI	11/1/2021 10/31/2023	241.258
Public Private Partnership Serbien 2019 / 57448498	**Mock, H.-P.**	DAAD	1/1/2019 12/31/2020	2.625

Forschungsksotenzuschuss zur Unterstützung eines Forschungsvorhabens / 331 434 042	**Reif, J.**	DAAD	9/15/2021 9/14/2023	4.800
DAAD Saravanakumar Somasundaram / 91767722	**Houben, A.**	DAAD	10/1/2020 9/30/2022	2.000
Forschungsaufenthalt Dr. Stanislav Isayenkov, Ukraine / 91679203	**Borisjuk, L.**	DAAD	12/1/2017 9/30/2021	10.795
Aufklärung des Wirkmechanismus von BROAD LEAF1 bei der Kontrolle des Blattwachstums in Gerste / STE1102/4-2/630759	**Stein, N.**	DFG	10/1/2016 1/31/2021	26.259
ALBOSTRIANS: Funktionelle Analyse des Gerste Genoms albostrians und dessen Bedeutung für die Ausbildung von Variegation und die Bildung von Chloroplaste / STE 1102/13-1 - 0632393	**Stein, N.**	DFG	12/1/2016 6/30/2020	320.511
BARN: Ertragsassoziiertes Gen-Netzwerk in Gerste / STE 1102/13-1 - 0632393	**Stein, N.**	DFG	9/1/2018 8/31/2021	493.496
Primeln: Aufklärung der Funktion und Evolution des Heterostylie-Supergens bei Primeln / HI 2076/1-1/651779	**Himmelbach, A.**	DFG	1/1/2020 12/31/2022	24.400
Genetische Grundlagen der Grannen- und Stigmabehaarung in Gerste- oder, warum braucht Kulturgerste raue Grannen? / STE 1102/17-1; 660741	**Stein, N.**	DFG	11/1/2019 10/31/2022	221.650
Untersuchungen und physikalische Kartierung von Genen im hexaploiden Weizen, verantwortlich für die Embryoentwicklung in Weizen-Roggen-Hybriden durch Interaktion mit dem Roggengenom / BO1423/17-2/638830	**Börner, A.**	DFG	6/1/2017 8/31/2020	207.702
Umwandlung eines Heisenberg-Stipendiums in eine Heisenberg-Professur / SCHN 768/15-1/646674	**Schnurbusch, T.**	DFG	2/1/2018 8/31/2021	376.399
MITOCHROM: Dreidimensionale Chromatinorganisation während des pflanzlichen Zellzyklus / MA6611/4-1 - 646327	**Mascher, M.**	DFG	7/1/2018 9/30/2021	223.411
Safrangenom: Identische Genome, doch verschiedene Eigenschaften - Der Safrankrokus als Modell für die Epigenetik von Qualitätsmerkmalen und Umweltanpassungen / BL 462/19-1 664282	**Blattner, F.**	DFG	7/1/2020 6/30/2023	10.650
Verbreitungsdynamik und Klimageschichte des eurasiatischen Steppengürtels: Gene dokumentieren Geschichte / BL462/18-1/634251	**Blattner, F.**	DFG	1/1/2017 6/30/2021	230.362
NGS Analyse für eine aufgelöste Phylogenie der Gattung Crocus L. (Iridaceae) / HA7550/2-1/636737	**Harpke, D.**	DFG	5/1/2017 12/31/2020	69.778
SAFRAN2: Die Herkunft von Safran - Die Rolle von Polyploidie für die Safran Matabolite / BL462/15-2; 649440	**Blattner, F.**	DFG	1/1/2019 12/31/2021	344.899
6. Int. Konferenz Wasserlinsen, Juni 2021 (Pandemie bedingt verschoben Mai/Juni 2022) / SCHU 951/19-1; 665513	**Schubert, I.**	DFG	1/1/2021 12/31/2021	12.200
Aufklärung der funktionellen Rolle von A. thaliana KNL2 zur epigenetischen Regulation der Kinetochore-Ausbildung der Pflanzen / LE 2299/3-1/653865	**Lermontova, I.**	DFG	4/1/2019 3/31/2022	203.350
MEIOREC: Meiotische Rekombination in Pflanzen - Der Übergang von DNA Doppelstrangbrüchen zu genetischen Crossovern und dessen Beeinflussung / HE7950/1-1/646020	**Heckmann, S.**	DFG	9/1/2018 8/31/2021	372.050
Analyse der Gewebe-spezifischen Eliminierung von B Chromosomen während der Embryogenese von Aegilops speltoides / HO1779/26-1/625601	**Houben, A.**	DFG	9/1/2016 2/29/2020	192.042
Entwicklung einer CRISPR-FISH Methode zur Sichtbarmachung genomischer Seqenzen in lebenden Pflanzen und ihrer Anwendung bei der Analyse der Zentromerstruktur und dem Prozess der Chromosomen Kondensation in lebenden Zellen / HO1779/28-1/638253	**Houben, A.**	DFG	4/17/2017 7/31/2020	200.313
Dreidimensionale Chromatinorganisation während des pflanzlichen Zellzyklus / SCHU762/11-1/646328	**Schubert, V.**	DFG	10/1/2018 9/30/2021	210.398
Chromosomen drive von Roggen B Chromosomen - Analyse der molekularen Grundlagen / HO 1779/30-1/645965	**Houben, A.**	DFG	3/1/2018 5/31/2021	224.246
Analyse von Cluster-Holocentromeren - eine neuartige Zentromer Variante der Lililaes Chionographis / HO 1779/32-1 663542	**Houben, A.**	DFG	9/1/2020 8/31/2023	208.050
DroRep : Ultrastruktur-Untersuchungen zur DNA-Replikation in Drosophila Polytän-Chromosomen mit Hilfe von Super-auflösender Mikroskopie / SCHU762/12-1664804	**Schubert, V.**	DFG	4/1/2020 3/31/2023	14.950

Zur Bedeutung von Mechanosensing für die Samenreifung / RO2411/6-1/645339	**Rolletschek, H.**	DFG	2/1/2018 4/30/2021	201.256
Maiskornentwicklung - Untersuchungen zur Maiskornentwicklung und Relevanz von Sauerstoffmangel im Endosperm / RO 2411/7-1/651806	**Rolletschek, H.**	DFG	2/1/2019 1/31/2022	196.500
SWEETs: Aufklärung der Zuckerallokation in den Samen von Gerste und Reis / BO1917/5-2; 659605	**Borisjuk, L.**	DFG	7/1/2019 9/30/2021	276.084
MAdLand: Molekulare Adaptation an das Land - Evolutionere Anpassung der Pflanzen an Veränderung. Erscheinung und Funktion von CuZnSOD-Proteinen während der Evolution früher Landpflanzen / SCHI 1130/9-1/ 666714	**Schippers, J.**	DFG	9/1/2020 8/31/2023	221.369
Interaktion komplexierender und reduzierender Wurzelexsudate in der pflanzlichen Eisenaneignung / WI 1728/21-1/629281	**v. Wirén, N.**	DFG	3/1/2017 7/31/2020	205.867
Nutrient and water transporters actively shape spatiotemporal rhizosphere organization processes / BI 1668/4-1/650537	**Bienert, G.**	DFG	10/1/2018 12/31/2021	115.974
REGION: Identifizierung von transkriptionellen Regulatoren des Pflanzenionoms / HE 8362/1-1/653050	**Giehl, R.**	DFG	1/1/2019 12/31/2021	352.425
ARF: Funktionelle Charakterisierung Eisen-abhängiger Mechanismen. die die Bildung von Adventivwurzeln in Petunienstecklingen fördern / HA 2996/11-1/656997	**Hajirezaei, M.**	DFG	7/1/2019 11/15/2022	393.150
INSIGHT: Untersuchungen der Rolle von Strigolactonen in Gerste als Antwort auf Trockenheit / ME 3356/7-1 662066	**Melzer, M.**	DFG	1/1/2020 12/31/2022	225.100
CYBDOM: Proteins HYP1 beim Phosphormangel-abhängigen Primärwurzelwachstum / WI 1728/24-1 662995	**v. Wirén, N.**	DFG	3/1/2020 2/28/2023	228.050
WURZELLÄNGE: Verlängerte Wurzeln zur effizienten Erschließung von Stickstoffquellen durch Veränderung der Brassinosteroid- und Auxinbioynthese und Signaltransduktion / WI 1728/25-1	**v. Wirén, N.**	DFG	12/1/2020 11/30/2023	344.400
Aufklärung des Mechanismus der nicht reduzierten Gametenbildung bei Arabidopsis thaliana / JI347/5-1/672315	**Jiang, H.**	DFG	7/1/2021 6/30/2024	222.528
CRISPR-FISH: Entwicklung eines CRISPR-Imaging-Toolsets zur Abbildung von DNA und RNA in strukturell konserviertem Chromatin, das für Superauflösungsmikroskopie und Elektronenmikroskopie geeignet ist, und seine Anwendung / HO 1779/33-1/675680	**Houben, A.**	DFG	6/1/2021 5/31/2024	210.550
Das Protein-Protein-Interaktionsnetzwerk von KNL2 in Pflanzen / LE 2299/5-1; 676966	**Lermontova, I.**	DFG	6/15/2021 6/30/2024	216.650
NFDI4BioDiversity - A Consortium for the National Research Data Infrastructure – Teilprojekt IPK / NFDI 5/1, 670406	**Scholz, U.**	DFG	1/1/2021 12/31/2029	561.900
GCB2022: Deutsche Konferenz für Bioinformatik 2021, Halle/Saale / BL1848/1-1; 677819	**Blätke, M.**	DFG	6/1/2021 9/30/2022	30.500
BRACE: Reaktion und Adaption der Gerste auf sich wandelnde Umweltbedingungen / NE 2007/2-1/675235	**Neumann, K.**	DFG	6/1/2021 5/31/2024	49.800
CATCH-BNI: Erhöhte Stickstoffnutzungseffizienz in der / WI 1728/26-1/675237	**v. Wirén, N.**	DFG	4/1/2021 3/31/2024	276.050
Euroduckweed: Etablierung eines Europäischen Zentrums für Wasserlinsenforschung in Kiew / 01 DK21015	**Schubert, I.**	BMBF	12/1/2021 11/30/2022	35.009
DROMAMED: Nutzung von mediterranen genetischen Ressourcen von Mais zur Verbesserung der Stresstoleranz – Teilprojekt IPK / 01DH21011	**Altmann, T.**	BMBF	6/1/2021 5/31/2024	249.936
KABA-2021: Innovative Technologien für die verbesserte Züchtung und Vermehrung von Kaffee- und Bananenpflanzen in Kuba / 01DN21019	**Rolletschek, H.**	BMBF	7/1/2021 6/30/2024	62.954
AGENT: Activated GEnebank NeTwork / GA862613	**Stein, N.;** Weise, S.; Mascher, M.; Reif, J.; Scholz, U.	EU	4/1/2020 3/31/2025	3.486.176
CAPITALISE: Combining approaches for photosynthetic improvement to allow increased sustainability in European agriculture / GA 862201	**Junker, A.;** Altmann, T.; Lange, M.; Neumann, K.	EU	4/1/2020 11/30/2024	693.398
CHROMADAPT: The role of chromatin in the long-term adaptation of plants to abiotic stress / GA725295	**Kumlehn, J.;** Junker, A.; Scholz, U.	EU	5/1/2017 4/30/2022	70.925
EPPN2020: European Plant Phenotyping Network 2020 / GA 731013	**Altmann, T.;** Börner, A.	EU	5/1/2017 4/30/2021	422.625

G2P-SOL: Linking genetic resources, genomes and phenotypes of Solanaceous crops / 677379 — G2P-SOL	**Stein, N.**	EU	3/1/2016 12/31/2021	533.010
INCREASE: Intelligent Collections of Food Legumes Genetic Resources for European Agrofood Systems / GA 862862	**Oppermann, M.;** Graner, A.; Lange, M.	EU	5/1/2020 4/30/2025	900.038
TRANSFER: Edaphic adaptation in barley wild relatives and its transfer to the domesticate / GA949873	**Mascher, M.;** v. Wirén, N.; Börner, A.	EU - ERC	2/1/2021 1/31/2026	1.499.928
LUSH SPIKE: Genetic and Molecular Determinants of Spikelet Survival in Cereal Crops / GA681686	**Schnurbusch, T.**	EU	7/1/2016 6/30/2021	1.972.659
EUCLEG: Breeding forage and grain legumes to increase EU's and China's protein self-sufficiency / GA727312	**Weise, S.**	EU	9/1/2017 12/31/2021	184.949
Farmers Pride: Networking, partnerships and tools to enhance *in situ* conservation of European Plant Genetic Resources / GA774271	**Weise, S.**	EU	11/1/2017 10/31/2020	27.990
GenRes Bridge: Joining forces for genetic resources and biodiversity management / GA 817580	**Weise, S.**	EU	1/1/2019 12/31/2021	82.756
MEICOM: Meiotic Control of Recombination in Crops / MSCA-ITN-2017-ETN, GA765212	**Heckmann, S.**	EU	1/1/2018 12/31/2021	240.216
CROPDIVA: Climate Resilient Orphan croPs for increased DIVersity in Agriculture / GA 101000847	**Börner, A.**	EU	9/1/2021 8/31/2025	53.000
MEIOBARMIX: Meiosis in barley: Mixing it up / GA949618	**Heckmann, S.**	EU - ERC	2/1/2021 1/31/2026	1.497.875
STARGATE: Sensors and daTA tRaininG towards highperformance Agri-food sysTEms / GA 952330	**Neumann, K.**	EU	1/1/2021 11/30/2024	143.619
ALIVE: Untersuchungen zur Introgression von QTL-Allelen mit hoher Ährchen-bzw. Blütchenfertilität in Gerste zur Verbesserung der Ertragsbildung in Getreide / ZS/2018/09/94616	**Schnurbusch, T.**	Investitions-bank SA	7/1/2019 6/30/2022	514.375
Erweiterung der NMR-Plattform des IPK um ein Super Wide Bore NMR-Gerät / ZS/2019/09/101444	**Borisjuk, L.**	Investitions-bank SA	12/1/2019 4/30/2022	2.746.000
HyperSpEED: Hypericum multi Spezies Exploration der Extrakt-Diversität als Beitrag zur Verbesserung der Lebensqualität im Alter / ZS/2019/07/99749	**Rizzo, P.**	Investitions-bank SA	6/5/2020 9/30/2022	386.092
INDUCEPROT: Induced Accumulation of Recombinant Proteins in Barley Endosperm / ZS/2018/06/93171	**Hensel, G.**	Investitions-bank SA	3/1/2019 6/30/2022	180.306
Gaterslebener Chancengleichheits-Programm (GCP) / ZS/2017/03/84910	**Deike, S.**	Investitions-bank SA	7/1/2017 11/30/2022	408.000
TEMPURA: Molecular Mechanisms for Barley Acclimation to Warm Temperature / I 155	**v. Wirén, N.**	MWWD	5/20/2021 4/30/2022	195.500
Carlsberg: HiC assembly of the hop genome / Carlsberg hop genome	**Stein, N.**	SONSTIGE	6/1/2019 5/31/2020	21.000
Maintenance and development of the EURISCO Internet Search Catalogue / LOA/14HQ/078	**Weise, S.**	SONSTIGE	4/15/2014 12/31/2023	928.786
Implementation of the ECPGR European Evaluation network (EVA) on wheat/barley and vegetable crops (carrot, lettuce and pepper), GenR 2019-2 / LOA/14HQ/078	**Weise, S.**	SONSTIGE	6/1/2020 9/30/2022	140.000
Australien: Improved Genetic Gain through GRDC / 9176507	**Mascher, M.**	SONSTIGE	9/1/2018 6/30/2020	120.992
ImprovLoliumCol / L19HQ179	**Willner, E.**	SONSTIGE	9/1/2019 8/31/2021	725
Hy-Gain: Capturing Heterosis for Smallholders / OPP ID1209850	**Houben, A.**	SONSTIGE	3/19/2020 2/28/2023	510.561
Novel Wheat III: Evalution of wheat plants with altered carbon assimilation, allocation and partitioning / 4/08/b0077-8	**Rolletschek, H.**	FIRMA	11/1/2013 10/31/2022	3.437.000
Laser Capture microdissection-based RNA-seq of phloem and transfer tissues in wheat / TTR_41_00074	**Thiel, J.**	FIRMA	10/1/2017 12/31/2020	294.280
Stage and tissue-specific RNA isolation of the developing spike in wheat / TTR_41_00075	**Thiel, J.**	FIRMA	10/1/2017 6/30/2021	197.700
FTIR: Efficacy of carbon partitioning technologies for improvement of assimilate translocation and/or partitioning in transgenic oilseed rape plants using FT-IR / 4/19/b00087	**Borisjuk, L.**	FIRMA	4/1/2019 7/31/2022	611.903

Improved brewing quality / TTR/41/00073	**Kumlehn, J.**	FIRMA	2/1/2017 2/29/2020	81.000
Impact of silicon (Si) nutrition on barley plants under drought stress or potassium (K) deficiency - Insight into transcriptional, hormonal oand metabolic regulation / CNTRCT	**v. Wirén, N.**	FIRMA	11/1/2016 12/31/2020	220.979
Wheat Germplasm: Development of a heat Germplasm Panel to aim at identification and understanding of allele frequencies relevant for yield formation in the course of wheat breeding history / 4/17/b00383	**Mascher, M.;** Röder, M.	FIRMA	11/15/2017 6/30/2021	507.000
Carlsberg: PacBio IsoSeq sequencing of 20+2 barley pan-genome genotypes / Carlsberg barley pan-genome	**Stein, N.**	FIRMA	12/1/2019 5/31/2021	40.000
Transcriptome profiling of phloem tissues in Soybean / TTR_41_0144_zu_TTR_41_C2-2021_	**Thiel, J.**	FIRMA	6/29/2021 8/31/2022	61.000
WATERUP: Uncovering the function of ABA in Si-mediated allviation of drought stress in barley / TTR_41_00145_zu_TTR_41_C3-2021	**v. Wirén, N.**	FIRMA	1/1/2021 12/31/2021	65.001
Beitrag zur Förderung der landwirtschaftlichen Produktivität in Äthiopien / 81233466 / 2017.9079.9-002.00	**Lohwasser, U.**	SONSTIGE	1/12/2018 10/30/2020	39.483
Kartofffelkryo: Transkriptionelle Änderungen während der Kartoffelkryokonservierung / GDK Kartoffelkryokonservierung	**Nagel, M.**	SONSTIGE	4/1/2019 12/31/2021	5.000
USDA, NIFA Tools & Germplasm for Hybrid Wheat, Uni Nebraska / 256222081- 2017-67007-25931	**Reif, J.**	SONSTIGE	12/15/2016 12/14/2020	24.433
USDA, PLANT BREEDING PARTNERSHIP: Continuing to develop and validate the tools for Hybrid Wheat, Uni Nebraska / 2020-67013-30872	**Reif, J.**	SONSTIGE	6/1/2020 4/30/2023	25.598
Aufenthalt Dr. Sabrina Mehdiyeva, Aserbaidschan / Dr. Sabrina Mehdiyeva	**Houben, A.**	SONSTIGE	7/1/2019 8/16/2021	6.000
Wirtswechsel ermöglichende Faktoren im Pilz/Gras Pathosystem / I 3033-B22	**Douchkov, D.**	SONSTIGE	1/1/2019 3/31/2022	220.152
ELIXIR-2019: Collaboration agreement with the node/ Commissioned Services Contract 06/ DE-IPK-2019-Plants / DE-IPK-2019-Plants	**Scholz, U.**	SONSTIGE	1/1/2020 6/30/2021	20.391
ELIXIR-2017: Collaboration agreement with the node/ Commissioned Services Contract 06/ DE-IPK-2017-Integration / DE-IPK-2017-integration	**Scholz, U.**	SONSTIGE	1/1/2020 6/30/2021	44.640
IWBDC-2020: Int. Whole-genome sequening of the Wild Barley Diversity Collection / Crowd Funding	**Mascher, M.**	SONSTIGE	12/1/2020 12/31/2021	211.090
IWBDC-2020: Int. Whole-genome sequening of the Wild Barley Diversity Collection / Crowd Funding	**Mascher, M.**	FIRMA	12/1/2020 12/31/2021	19.902
Cucurbitlocal: Exploitation of Cucurbita local germplasm for sustainable agriculture / TTR_41_00139_zu_TTR_41B1-2021	**Lohwasser, U.**	SONSTIGE	4/26/2021 1/15/2023	6.000
Erhaltung der Diversität des Apenninenschwingels / 627001258	**Willner, E.**	SONSTIGE	10/15/2020 12/31/2022	9.377
SINO - Chinesisch-Deutsches Mobilitätsprogramm: The mechanism of chromatin de-condensation in the companion vegetative nucleus during male germline maturation in Arabidopsis / M-0398	**Jiang, H.**	SONSTIGE	1/1/2021 12/31/2023	88.956
ELIXIR Hub-2021: Collaboration agreement with the node/ Commissioned Services Contract DE-IPK-2021-Communityled / DE-IPK-2021-Communityled	**Beier, S.**	SONSTIGE	7/8/2021 7/7/2023	13.125
A 100 year Seed Longevity Experiment in the Svalbard Global Seed Vault / TTR_45_00032_zu_TTR_45_A1-2021	**Nagel, M.**	SONSTIGE	3/12/2021 3/11/2031	26.464
GRDC-OAT: Oat genomics resources for breeders and pre-breeders / Murduch University	**Mascher, M.** **Stein, N.**	SONSTIGE	11/1/2020 12/31/2022	85.000
Georg Forster-Forschungsstipendium für Dr. Agostina Belen Sassone (AvH) / Ref. 3.2 - 1205837 - ARG-GF-P	**Blattner, F.**	STIFTUNG	11/1/2019 10/31/2021	21.600
EpiOrg: Preventing food fraud - DNA methylation patterns to identify organic food (VW-Stiftung) / J03080389	**Altmann, T.**	STIFTUNG	1/1/2019 8/31/2020	3.899
Produktion von oligomeren Vogelgrippevakzinekandidaten in planta und ihre praktische Testung / 2018_T10	**Conrad, U.**	STIFTUNG	1/1/2019 12/31/2020	333.788

Humboldt-Forschungsstipendium für Postdoktoranden an Dr. Matias Schierenbeck / 3.2-1209728-ARG-GF-P	**Börner, A.**	STIFTUNG	3/1/2021 2/28/2023	19.200
Forschungskostenzuschuss für Dr. Amira Mourad / Ref. 3.4 - 1218304 - EGY -GF-P	**Börner, A.**	STIFTUNG	7/1/2021 6/30/2023	19.200
Humboldt-Forschungsstipendium für Postdoktoranden an Herrn Guy Golan / 3.4-ISR-1205002-HFST-P	**Schnurbusch, T.**	STIFTUNG	9/1/2019 8/31/2022	25.600
Humboldt-Forschungsstipendium für Postdoktoranden an Herrn Dr. Raz Avni / 3.4-1216215-ISR-HFST-P	**Mascher, M.**	STIFTUNG	3/1/2021 2/28/2023	23.300
Anlage, Pflege und Präsentation eines Lehrgartens für Futterpflanzen / TTR/42/00062	**Willner, E.**	FIRMA	3/1/2020 12/31/2021	3.600
Beet-ROS: Regulating sugar beet size through the modulation of cell proliferation and expansion by reactive oxygen species / 460-19(905)TI-DE	**Schippers, J.**	FIRMA	2/1/2020 1/31/2023	310.000
BeetStore: Transkriptomik und Metabolomik zur Charakterisierung der Lagerfähigkeit von Zuckerrüben / AIT 855706	**Mock, H.-P.**	FIRMA	4/1/2017 3/31/2020	85.376
WiLDSI: Wissenschaftsbasierte Lösungsansätze für Digitale Sequenzinformation (DSI) in Vorbereitung für COP 15 (Beijing 2020) / 6220030	**Freitag, J.**	Leibniz	9/1/2019 11/30/2020	30.000
Generation of rapeseed haploid inducer lines / 613-19(905)JC-DE	**Lermontova, I.;** Houben, A.	FIRMA	11/1/2019 10/31/2022	525.000
Anlage eines Parzellenversuchs zu Wildpflanzenmischungen	**Willner, E.**	FIRMA	1/13/2015 3/24/2021	800
Leibniz-WissenschaftsCampus Phosphorforschung Rostock: Efficiency of forage legumes and their capacity to utilize P from recycling products – Teilprojekt IPK / W19/2018	**Dehmer, K.**	Leibniz	11/1/2019 10/31/2022	144.150
KETCHUP: Klimate Enhanced Tomato breeding Capturing Heat-resilience Using integrative Phenotyping / SAW-2020-IGZ-1.1.1.1-KETCHUP	**Szymanski, J.**	Leibniz	4/1/2020 3/31/2023	402.496
VolCorn: Volatilome of a Cereal Crop-Microbiota System under Drought and Flooding / SAW-2019-ZALF-3-VolCorn	**Hajirezaei, M.**	Leibniz	4/1/2019 3/31/2022	199.002

LECTURES

GATERSLEBEN LECTURES 2020

25. Februar 2020
“How to tango with four: Meiotic adaptation to whole genome duplication“
Prof. Dr. Kirsten Bomblies
ETH Zürich, Switzerland

20. Oktober 2020
“Unlocking the polyploid potential of wheat through genomics“
Prof. Dr. Cristobal Uauy
John Innes Centre, UK

10. November 2020
„Analysis of NLR immunity signalling across seed plant species.“
Prof. Dr. Jane E. Parker
Max Planck Institute for Plant Breeding Research, Germany

8. Dezember 2020
“Unexpected diversity of grass abscission zones“
Prof. Dr. Elisabeth A. Kellogg, & Robert E. King
Donald Danforth Plant Science Center, USA

GATERSLEBEN LECTURES 2021

16. February 2021
“The last step is the hardest – lignin and suberin formation in the cell wall”
Prof. Dr. Niko Geldner
Université de Lausanne, Switzerland

09. March 2021
“The Taming of the Spud – how genomics can enable the green revolution of potato”
Prof. Dr. Sanwen Huang
Chinese Academy of Sciences, China

13. April 2021
“Mechanisms of quantitative trait variation in plants”
Prof. Dr. Zachary Lippman
Cold Spring Harbor Laboratory, USA

18. May 2021
“Comparative population genomics of closely related plant pathogens from natural grasslands and agro-ecosystems”
Prof. Dr. Eva H. Stukenbrock
Christian-Albrechts University Kiel & Max Planck Institute for Evolutionary Biology, Germany

08. June 2021
“Supergenes and their role in plant adaptation, speciation, and breeding”
Prof. Dr. Loren Rieseberg,
University of British Columbia, Canada

20. July 2021
“The early evolution of land plants”
Prof. Dr. Stefan A. Rensing
University of Marburg, Germany

14. September 2021
“Complex traits: a genomic approach to gene discovery”
Prof. Dr. Scott Allen Jackson
University of Georgia, USA

19. October 2021
“Gene expression complementation during heterosis manifestation in maize hybrids”
Prof. Dr. Frank Hochholdinger
University of Bonn, Germany

16. November 2021
“A 3D Code in the Human Genome”
Prof. Dr. Erez S. Lieberman-Aiden
Baylor College of Medicine & Rice University, USA

07. December 2021
“Next Generation CRISPR Technologies and their Applications in Crop Improvement”
Prof. Dr. Caixia Gao
Chinese Academy of Sciences, China

GENETIC SEMINARS 2020

22. January 2020
“The influence of asymmetrical meiosis on the evolution of polyploid dogroses”
Dr. Christiane Ritz & Dr. Veit Herklotz
Senckenberg Museum für Naturkunde, Germany

26. February 2020
“Exploring barley drought response using TILLING mutants”
Dr. Agata Daszkowska-Golec
University of Silesia in Katowice, Poland

11. March 2020
“Acquisition of brittle rachis: preparation period for domestication in the tribe Triticeae”
Dr. Takao Komatsuda
National Agriculture and Food Research Organization, Japan
Genetic Seminars 2021

24. March 2021
“Impact of nutrient availability on plant development”
Dr. Vanessa Wahl
Max Planck Institute of Molecular Plant Physiology, Germany

01. December 2021
“Revisiting chromosome evolution in Phaseolus and allied species using cytogenetic and genomic tools”
Prof. Dr. Andrea Pedrosa-Harand
Universidade Federal de Pernambuco, Brazil

VAVILOV-SEMINARS 2020

15. January 2020
"Conservation of Plant Genetic Resources at Georgian *Ex situ* Gene Bank"
Prof. Mariam Betsiashvili
Agricultural University of Georgia, Georgia

22. January 2020
"Automated phenotyping of individual seeds: multi-size and multi-species"
Dr. Robert Koller
Forschungszentrum Jülich, Germany

19. February 2020
"Seeds for future: Predictive scope of a non-destructive viability test and beyond"
Prof. Klaus Mummenhoff und Dr. Samik Bhattacharya
Universität Osnabrück, Germany

VAVILOV-SEMINARS 2021

20. Januar 2021
"Adapting Lentil to New Environments"
Prof. Kirstin Bett
University of Saskatchewan, Canada

24 November 2021
"Plant cryobiotechnology: Nature inspired solutions to design innovative species conservation options"
Dr. Daniel Ballesteros
University of Valencia, Spain

WATERMAN SEMINARS 2020

04. February 2020
"A Petri net framework for spatial and multiscale modelling of plant biochemistry"
Prof. Dr. Ing. Monika Heiner
Brandenburg University of Technology Cottbus-Senftenberg, Germany

21. July 2020
"From Bits to Bytes: Software development for genetic resources, genetics and plant breeding"
Paul Shaw and Sebastian Raubach
The James Hutton Institute, Scotland

WATERMAN SEMINARS 2021

23. February 2021
"Implementation of the Data Stewardship Program at the TU Delft – Approach and Experiences"
Dr. Yan Wang
Delft University of Technology, The Netherlands

13. April 2021
"HBimpute – Increasing calling accuracy, coverage, and read depth in sequence data by the use of haplotype blocks"
Dr. Torsten Pook
University of Göttingen, Germany

26. April 2021
"Can we apply the FAIR Data Principles to scholarly knowledge?"
Dr. Markus Stocker
Leibniz Information Centre for Science and Technology in Hannover, Germany

25. May 2021
"Semantic modelling of plant phenotyping experiment analysis for dataset discovery"
Dr. Hanna Ćwiek-Kupczyńska
Polish Academy of Sciences, Poland

02. June 2021
"Photosynthesis: its dynamics and possible role in secondary metabolism"
Dr. Anna Matuszyńska
Heinrich-Heine-University Düsseldorf, Germany

22. June 2021
"iPlants@PT – a repository of *in silico* models of Portuguese plant life"
Dr. Oscar Dias
University of Minho, Portugal

29. June 2021
"Comparative genomics and the stress response toolkit of the earliest land plants"
Jun.-Prof. Dr. Jan de Vries
Georg-August-University Göttingen, Germany

11. August 2021
"Pixel-wise intensity correlation analysis for deconvolution and metabolite identification in MALDI imaging"
Dr. Yonghui Dong
Weizmann Institute of Science, Israel

15. September 2021
"Computational Stress Response Analysis in Plants Using 'PhysioSpace'"
Ali Hadizadeh Esfahani
RWTH Aachen University, Germany

12. October 2021
"Improvement of genomic resources for Northern Wild Rice (*Zizania palustris* L.)"
Dr. Matthew Haas
University of Minnesota, USA

13. October 2021
"Research Institute for Farm Animal Biology (FBN): Established and future plans to improve Research Data Management"
Sarah Fischer
Research Institute for Farm Animal Biology, Germany

CELL BIOLOGY SEMINARS

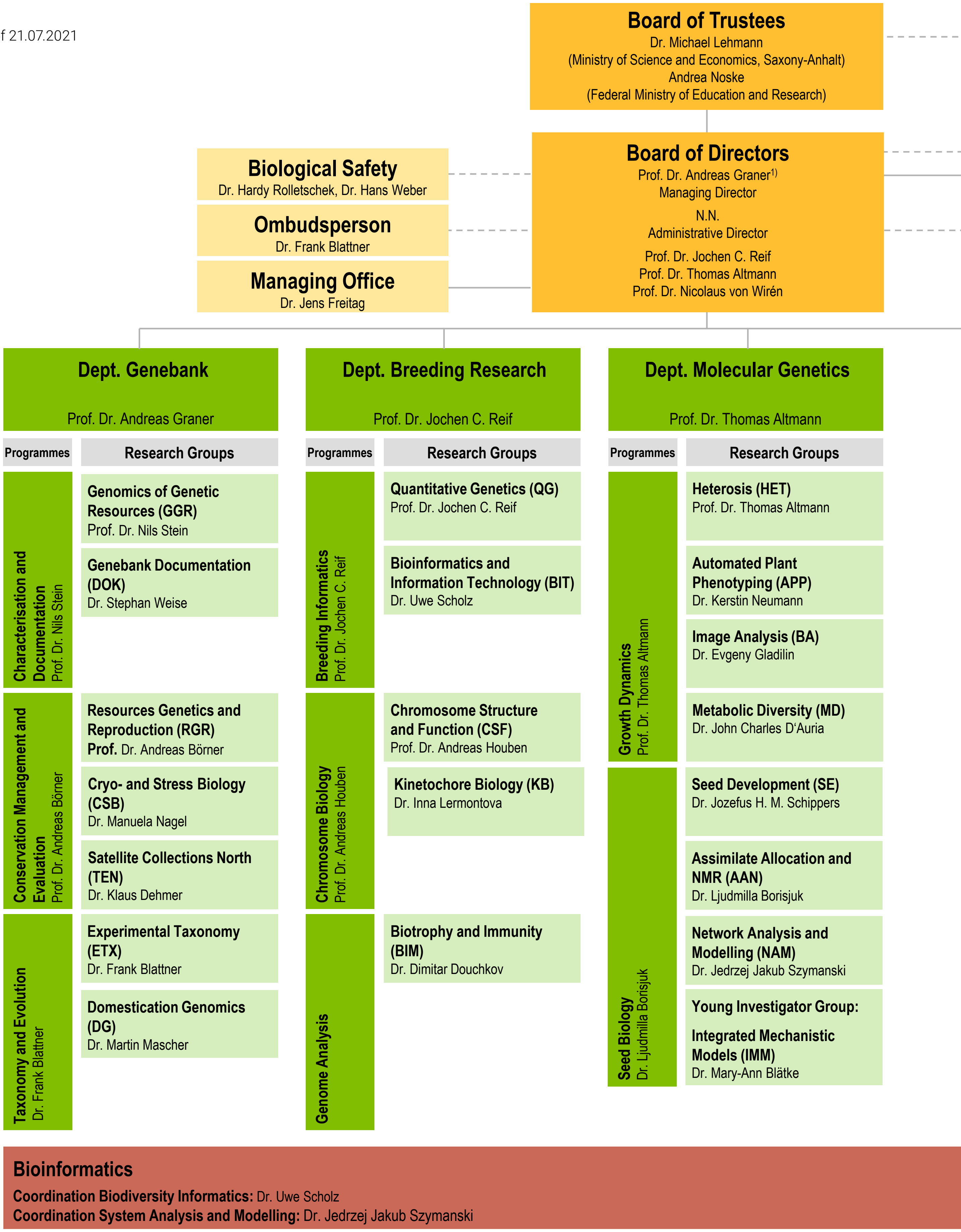
17. November 2021
"Applying genome editing to remove allergens from plant crops"
Prof. Dr. Jens Boch
Leibniz University Hannover, Germany

23. November 2021
"Pan-cistrome analysis links diffrences in transcription factor binding to trait variation in maize"
Dr. Thomas Hartwig
Heinrich-Heine-University Düsseldorf & Max Planck Institute for Plant Breeding Research, Germany

29. November 2021
"Root Phenotypes for crop improvement"
Dr. Hannah Schneider
Wageningen Universty, The Netherlands

ORGANIGRAM

As of 21.07.2021



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- **Experimental Taxonomy (ETX)**
  Dr. Frank Blattner
- **Domestication Genomics (DG)**
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- **Network Analysis and Modelling (NAM)**
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- **Young Investigator Group:**
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	Applied Biochemistry (ABC) Dr. Hans-Peter Mock
	Young Investigator Group: **Sustainable Nutrient Management (NNM)** Dr. Diana Heuermann
Cell Biology and Biotechnology Dr. Jochen Kumlehn	**Plant Reproductive Biology (PRB)** Dr. Jochen Kumlehn
	Structural Cell Biology (SZB) Dr. Michael Melzer

Independent Research Groups

Research Groups

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(Heisenberg group, DFG)
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Meiosis (ME)
Dr. Stefan Heckmann

Applied Chromosome Biology (ACB)
Prof. Dr. Hua Jiang

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