LEIBNIZ-INSTITUT FÜR
PFLANZENGENETIK UND
KULTURPFLANZENFORSCHUNG

IPK
LEIBNIZ-INSTITUT

RESEARCH REPORT

2024/2025



Leibniz Association

Imprint

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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 Pomerania.



Foreword

by Professor Nicolaus von Wirén

Recent global crises in climate change, political conflicts, and pandemics have uncovered the immense vulnerability of global supply chains. This vulnerability also affects food security, either directly through lost productivity or indirectly by impeding worldwide transportation of food crops or fertilisers. Together with increasing losses of arable land and biodiversity, including in Europe, these crises call for a **transformation of the agricultural sector**.

Against this background, IPK's vision is to advance the integration of genetic resources, biological knowledge, and digital tools to develop high-performing crops under increasingly challenging environmental conditions. By establishing the most advanced **Biodigital Resource Centre** for crop biodiversity, our research drives innovation in breeding methods and technologies and contributes to improving resilience-, yield-, and sustainability-related traits in crops.

At our institute, the years 2024 and 2025 were marked by a redesign of our research strategy. This was motivated by the completion of the most important milestones in our former research strategy and by the upcoming institute's evaluation by the Leibniz Association, when a reviewing panel of 12 renowned national and international scientists and delegates from the state and federal ministries inspected IPK during a two-day onsite visit. We have addressed this challenge over the past two years by going with all group leaders to two retreats and developing a **new research strategy** using a bottom-up approach. We identified five major research themes that profit from the recent transformation of IPK's genebank into a **Biodigital Resource Center** and leverage the latest research achievements, like the pangenome inventory of barley, the development of AI-assisted prediction tools and the identification of gene functions. We have also advanced our **phenotyping technologies**, foremost IPK's PhenoSphere, which has laid new ground for the research concept, together with large-scale omics data on different plant traits. As shown on the next pages, these high-end infrastructure facilities support the research themes and help systematically explore the genetic diversity in our genebank.

In preparation for the evaluation, we took the opportunity to establish further institution-wide **strategies** for research data management, scientific publication, third-party funding, sustainable campus management, and transferring research into society. These strategies provide guidelines for a comprehensive and balanced progression of the institute's activities.

An outstanding highlight in 2025 was IPK's inclusion in a German Excellence Cluster. As one partner in the CEPLAS **"Cluster of Excellence in Plant Sciences"**, led by the University of Düsseldorf, IPK is deepening its research scope, particularly in basic plant sciences, with partners from the University of Cologne, the Max-Planck Institute for Breeding Research in Cologne, and the Research Centre in Jülich. This also brings educational and training opportunities for our early-career researchers, as well as funding opportunities, including a new W2 professorship at IPK. Participation in this excellence cluster expands IPK's research network considerably beyond the University of Göttingen and the University of Halle, which remain the department heads' main affiliations.

IPK's scientific productivity remained high in both 2024 and 2025. The institute published 168 and 191 scientific articles in these years, and received nearly 15 and 16 million euros in third-party funding.

All this progress relies firmly on our highly dedicated staff, our partners, and supporters from other institutions and industry, as well as on the reliable commitment of our funding bodies. Without all their unwavering support, IPK could not meet its ambitious research goals. This merits great gratitude!

We now invite you to explore our research report and hope our concept and achievements will serve as a source of inspiring insights into the fascinating world of plant sciences.

We thank you for your interest and hope you will enjoy reading
Nicolaus von Wirén

Structural and Organisational Developments at the Institute in 2024/2025

During the 2024/2025 reporting period, the IPK systematically developed its scientific and administrative structures. The changes included the establishment and closure of research groups and Young Investigator Groups (Perspektivgruppen), changes in leadership roles, the reorganisation of responsibilities, and the further development of institutional frameworks for vocational training, equal opportunities and scientific career development. The following account records the changes, together with their respective effective dates and durations.

Genebank Department

With effect from 1 January 2024, the Young Investigator Group (Perspektivgruppe) 'In Silico Genebank Proteomics' (IGP), led by Dr. Amanda Souza Camara, was established. The group is funded until 31 December 2026 through a grant from the State of Saxony-Anhalt and resources provided by the Genebank Department. On 1 September 2024, the Northern Satellite Collections were divided into two units with equal leadership status. The unit 'Diversity and Collection Management' (TEN), based in Groß Lüsewitz and Malchow/Poel, remained under the leadership of Dr. Klaus J. Dehmer. The IPK and the JKI established a new unit, 'Quantitative Genetics and Potato Breeding Methodology' (PQG), jointly operated and funded in Groß Lüsewitz under the leadership of Dr. Delphine Van Inghelandt. On 1 November 2024, the new research group 'Genetics of Environmental Adaptation' (GEA), led by Dr. Laura Dixon, also commenced its work as part of the research area 'Taxonomy and Evolution'. After Dr. Frank Blattner's retirement the research group 'Experimental Taxonomy' (ETX) was closed on 31 May 2025. Since 1 June 2025, Dr. Martin Mascher is heading the 'Taxonomy and Evolution' research area. At the same time, taxonomy and the management of







the comparative collections were consolidated, until further notice, in the structural unit 'Taxonomy and Comparative Collections' (TVS), led by Dr. Dörte Harpke, and integrated into the Domestication Genetics research group. Anticipating Prof. Dr. Andreas Börner's retirement on 31 December 2025, Dr. Anna Elisabeth Backhaus assumed leadership of the research group 'Resources Genetics and Reproduction' (RGR), while Prof. Dr. Nils Stein assumed leadership of the 'Collection Management and Evaluation' research area.

With effect from 1 September 2025, Dr. Stephan Weise assumes leadership of the department's 'Characterisation and Documentation' research area.

Breeding Research Department

The Young Investigator Group (Perspektivgruppe) 'Agroecological Breeding' (AB), led by Dr. Samira El Hanafi, was established on 1 April 2024. Its initially defined term ends on 31 March 2027.

Molecular Genetics Department

Following PD Dr. Ljudmilla Borisjuk's retirement on 31 August 2025, leadership responsibilities were reassigned. Since 1 September 2025, PD Dr. Hardy Rolletschek is leading the research group 'Assimilate Allocation and NMR' (AAN). On the same date, Dr. Jozefus Schippers assumed leadership of the 'Seed Biology' research area. The Young Investigator Group (Perspektivgruppe) 'Integrated Mechanistic Models' (IMM), led by Dr. Mary-Ann Ebeling, was closed on 30 September 2025.

Independent Research Groups

Among the independent research groups, the closure of existing units was accompanied by the establishment of new, externally funded groups. The research group 'Applied Chromosome Biology' (ACB), led by Prof. Dr. Hua Jiang, was closed on 29 February 2024. The research group 'Grain Legume Genomics' (GLG), led by Dr. Murukarthick Jayakodi, was closed on 31 August 2024. The independent research group 'Functional Plant Structures' (FPS), led by Dr. Yongyu Huang, was established on 1 June 2024. Funded under the Emmy Noether Programme of the German Research Foundation, the group initially has a term ending on 31 May 2027. Subject to a positive evaluation of an interim report at the end of the third year, the group is intended to continue until 31 May 2030. Technical support and coaching is provided by the Physiology and Cell Biology Department. The independent research group 'Plant Reproductive Genetics' (PRG), led by Dr. Steven Dreissig, was established on 1 January 2025. It has a fixed term ending on 31 December 2027 and receives funding under the Emmy Noether Programme for a project on meiotic recombination, pollen size and allelic selection in rye under nutrient limitation. The group is associated with the Breeding Research Department. On 1 June 2025, the independent research group 'Biotechnology and Genome Editing' (BGE), led by Dr. Robert Eric Hoffie, was established. Its term ends on 30 April 2029. The group receives funding for the PROGRESS project under the Federal Ministry of Education and Research programme 'Modern Breeding Research for the Climate- and Site-Adapted Crops of Tomorrow'. The Physiology and Cell Biology Department provides coaching and administrative support.

Accordingly, there were four independent research groups in 2025, compared with three in 2024. In addition, two Young Investigator Groups (Perspektivgruppen), each led by a female scientist for a three-year term, were established. This format is intended to strengthen the scientific visibility and independence of talented female scientists.

Administration and Central Services

The research group 'Technology Transfer and Law' (TTR), until most recently headed on an acting basis by Dr. Ingmar Schmidt, was closed retrospectively with effect from 31





January 2024. At the same time, Dr. Britt Leps, carrying these responsibilities, moved as a new member to the group 'Finance, Knowledge Transfer and Third Party Funding' with effect from 1 February 2024. This move brought finance-related, transfer-oriented, and third-party-funding responsibilities together within a single organisational unit.

Vocational training and dual study programmes

As of 31 December 2025, the IPK employed twelve vocational trainees in six occupational fields, compared with twelve trainees in five fields in 2024. IPK hosted eight dual-study students in two subject areas, compared to twelve in the previous year. Overall, the number of vocational trainees and dual-study students decreased from 24 to 20. The number of plant technologist trainees rose from one to two, while the number of trainee chefs fell from three to one. Numbers in the other vocational training occupations listed remained stable. In the dual study programmes, the number of students in biotechnology fell from ten to seven and the number in computer science from two to one. To safeguard training quality, the IPK provides intensive individual support, customised training content, partly in cooperation with external partners and other Leibniz institutes. In 2025, three prospective biology laboratory technicians completed a four-week work placement abroad at the University of Valencia, funded by ERASMUS+. Following the expansion of the dual study programme in biotechnology from B.Sc. to M.Sc. level in 2023, the first two students successfully completed their M.Sc. in 2024.

Equal opportunities and family

Increasing the proportion of female scientific leaderships in scientific leadership positions remaines a central objective to achieve equal opportunities. Through proactive recruitment measures the use of scientific networks and invited specialist lectures at the IPK, the proportion of female research group leaders reached 32%, exceeding the target of 29%. By 2030, the IPK aims for women to account aims at increasing this number to 40%. Of the two department head positions to be filled by then, at least one is to be held by a female scientist. Also at the level of department heads, IPK strives for the recruitment of female top scientific leaders. Improving organisational conditions that enable staff to reconcile work with family or private life provide an important measure for achieving this objective. In the 2025 recertification process, the 'berufundfamilie' audit, which the IPK earned in 2010, has been successfully extended by diversity aspects ("berufundvielfalt"). This systematically broadened IPK's family- and life-stage-conscious human resources policy to include a diversity-oriented perspective. The respective areas of focus are ethnic origin and nationality religion and belief; sex and gender identity; age; and physical and mental abilities.

Scientific career development

The Institute further embedded support for postdoctoral researchers in its organisational structures. The Postdoc Board supports the development of an independent professional identity and has a self-administered budget for professional development measures—including travel, retreats, trainings, teaching and laboratory management—and for a Summer School held every two years. Its members participate in conferences, workshops, and teaching activities; at least once a year, they meet with the Board of Directors to discuss the status and further development of these activities. The professional development phase relies on coaching and mentoring based on personal engagement. Its purpose is to sharpen individual research profiles, skills, and career planning for careers within and outside academia. In this context, IPK follows the Leibniz

External funding sorted by funding body

Funding body	2024	2025
BMFTR	3,375,391	4,417,618
BMELH	1,707,002	1,551,277
BMWK	112,000	–
BMWI	17,233	–
EU	3,832,013	2,329,602
DFG	2,279,217	3,076,408
Federal states	2,268,373	3,587,281
Leibniz Association	497,626	429,045
Research cooperation	298,514	344,287
Foundations	105,309	14,778
Contract research	143,886	9,965
Other	39,933	151,841
Total	**14,676,497**	**15,912,176**

IPK budget

Funding (million euro)	Share of total expenditure	
	2024	2025
Core funding	36,67	39,39
Third-party funding	14,68	15,91
Carryovers	1,21	1,51

Association's career development guidelines, provides transparency regarding career paths and, among other measures, defines various group leadership formats. For postdoctoral researchers in the advanced consolidation phase, three to six years after completing their doctorate, support also includes mentoring and coaching on applications, for example under the Emmy Noether Programme, and on funding opportunities offered by the Federal Ministry of Research, Technology and Space or the European Research Council. Heads of departments or experienced group leaders with relevant expertise support application and interview preparation.

Independent research groups are administratively assigned to one of the four scientific departments but retain their independent research status to develop their own research agenda and scientific profile. Their leaders report directly to the Board of Directors. As a rule, these groups exist for no more than six years and are expected to gain international visibility and qualification for leadership positions in academia or industry. Depending on performance, strategic fit and budget, permanent employment and integration into a core-funded unit may be possible. Since 2018, three particularly successful early-career researchers holding ERC grants have been appointed as research group leaders at this career stage. The Young Investigator Group format, introduced in 2021, targets postdoctoral researchers seeking to increase their research independence and develop their leadership skills. Selection is based on the research proposal and previous achievements. These groups are externally funded, structurally integrated into a research area, and receive coaching as well as shared financial and, where appropriate, human resources from the research area's core budget. Permanent employment requires strategic fit and outstanding scientific achievements, or a successful application for an open position funded by the IPK. The Scientific Advisory Board evaluates independent research groups and Young Investigator Groups annually.

In parallel with these career paths, the IPK aims to expand its cooperation with universities in Saxony-Anhalt, as well as nationally and internationally. A particular focus is on strengthening cooperation with the Martin Luther University Halle-Wittenberg through additional joint appointments, junior professorships, honorary professorships and adjunct professorships. Beyond Saxony-Anhalt, the IPK currently has a joint appointment with the University of Göttingen. Efforts to expand this cooperation with the University of Göttingen are ongoing. The same applies to cooperation with Heinrich Heine University Düsseldorf within CEPLAS, the DFG-funded Excellence Initiative.





IPK's Research Strategy 2025–2030

As a leading research institute in crop genetics, IPK advances knowledge through original and innovative research to develop new genetic strategies for crop improvement, enhance plant performance and resilience to abiotic and biotic stresses, and adapt crops to climate change. With this mission, we address major global challenges in food security, shrinking natural resources, and climate change, striving to support the transformation of the agricultural sector.

IPK organises its research across **four scientific departments**, each with a complementary specialist profile. In 2025, the Institute hosted 32 scientific research groups, including four independent groups. Departmental research topics cover different subjects, technologies, and areas of competence, with genetics being the overarching discipline. The **Genebank Department** maintains the large collection of plant genetic resources (PGR) and uses genotyping and sequencing to create baseline information for more informed selection of PGR for research and pre-breeding. Reference and pangenomes are made available for IPK lead crop species (Triticeae and related grasses, grain legumes) to underpin intra- and interdepartmental research on the genetics of domestication, adaptation, and development. The **Breeding Research Department** generates knowledge and employs innovative approaches to harness crop genetic diversity for future breeding progress. Research spans the entire breeding cycle: creating genetic variation, fixing variety parents, selecting superior genotypes, and conducting maintenance breeding. In the **Molecular Genetics Department**, plant genetics and omics analyses are integrated to uncover the molecular processes that determine plant performance in changing environments. It operates innovative research infrastructures, such as the IPK-PhenoSphere and the MRI platform, and uses other novel methodologies to identify determinants of vegetative growth dynamics, metabolism, and seed development and filling, and to elucidate their regulation at the cellular, organ, and whole-plant levels. The **Department of Physiology & Cell Biology** explores the molecular basis of morphological, anatomical, and physiological plant traits that affect abiotic stress resilience and nutrient efficiency, with a particular focus on roots. It also develops precise genome-editing technologies and operates major platforms for microscopy, crop transformation, genome editing, metabolomics, and ionomics. Independent Research Groups are established transiently for several years, have their own funding, and are assembled in those departments that are most closely related to their research topic. Major criteria for establishing **Independent Research Groups** include exploring and establishing new research fields at IPK and helping promising researchers advance their careers by gaining international visibility through new, original topics. In addition, the **Department of Central Services and Administration** manages the personnel and financial resources required to fulfil IPK's mission and maintains the campus and technical infrastructure.

IPK researchers have defined **five complementary research themes** that build on leveraging genetic diversity in the genebank and the associated genetic and phenotypic information. With the recent installation of unique phenotyping technologies, particularly the IPK-PhenoSphere and nuclear magnetic resonance imaging (MRI), IPK has greatly increased the actual and potential gain of phenotypic data from genebank germplasm. Against this background, each of the five research themes focuses on generating impactful scientific advances or technical innovations and enhancing IPK's international visibility.

While each research theme defines methodological or scientific milestones to be reached in due time and serves as a nucleus for developing new concepts and grant proposals, their crosstalk increases synergistic potential and feeds into IPK's overarching research strategy. Accordingly, the research themes rely on the disciplinary and methodological competences of the four departments, which support them with human and financial resources.

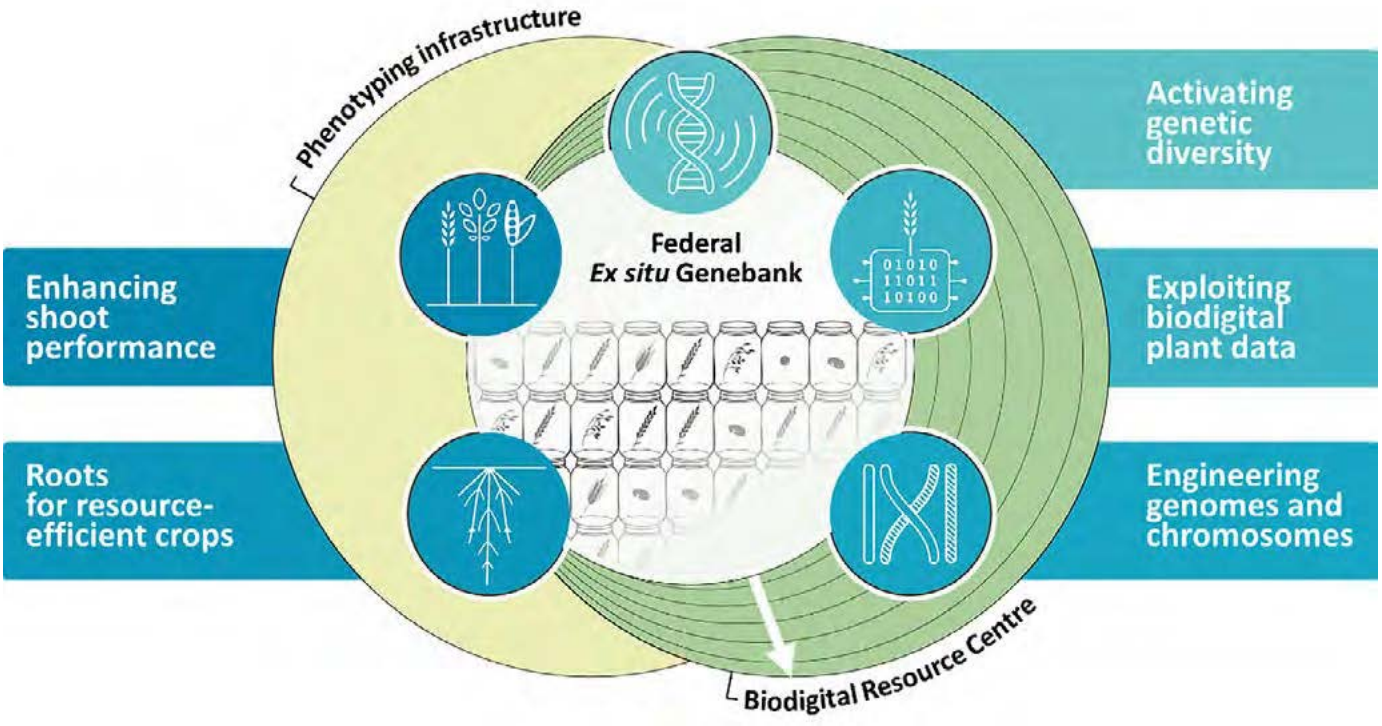


Figure 2: Schematic representation of IPK's research strategy for 2025 to 2030. *Five research themes revolve around the Federal Ex situ Genebank hosting the plant genetic resources, profiting from its transformation into a Biodigital Resource Centre and from the installation of a broad plant phenotyping infrastructure.*

1. **'Activating genetic diversity'** will advance the transformation of IPK's genebank into a Biodigital Resource Centre by genotyping and phenotyping of sub-collections to develop translational approaches allowing to harness genetic diversity in plant breeding.

2. **'Exploiting biodigital plant data'** will pave the way for uncovering biological relationships across diverse digital data resources by breaking through the limitations of diverse data formats to address key data gaps, extend insights to underexplored species, and develop predictive models of plant performance.

3. **'Engineering genomes and chromosomes'** will elucidate and engineer chromosome-biological processes and related gene functions for accelerated breeding and trait modification in crops.

4. **'Roots for resource-efficient crops'** will discover and characterise genes and processes modulating root traits that are relevant for resource efficiency and confer enhanced resilience to crop plants growing in challenging soil conditions.

5. **'Enhancing plant shoot performance'** will acquire knowledge and develop solutions to improve shoot traits by uncovering underlying mechanisms and harnessing advantageous genetic factors suitable for improving crop productivity and quality traits under current and future climate conditions.

Facts & Figures 2024 | 2025

Employees

Total	459 | 482
Men	193 | 199
Women	266 | 282
Divers	1
Nationalities	38 | 35

Graduates

Bachelor	6 | 14
Master	20 | 8
Dissertations	7 | 17
Professional Appointments	0

Trainees	24 | 20
Research Groups	31 | 31

Publications

In peer-revevied Journals	168 | 191

Impact Factor

IF>9	29 | 39
6,01-9	19 | 38
4,01-6	62 | 62
<4	58 | 52

Participation

of citizens in the EU project 'INCREASE'

in Europe	28,285 (total)
in Germany	6,530

IPK media contributions

News	23 | 29
Press releases	15 | 19

External media contributions

Online	39 | 23	Print	29 | 51
TV	8 | 5	Radio	12 | 12

Events

Events	15 | 12
Participants at IPK Events	1859 | 3642
Institute tours	35 | 38
Institute visitors	1058 | 1029

Funding (million euro)

Core funding	36,666,129	39,390,169
Third-party funding	14,676,497	15,912,176
Carryovers	1,210,680	1,507,623
Total funding	**52,553,306**	**56,809,968**

Third Party Funding

BMFTR	3,375,391	4,417,618
BMELH	1,707,002	1,551,277
BMWK	112,000	
BMWI	17,233	
EU	3,832,013	2,329,602
DFG	2,279,217	3,076,408
Federal states	2,268,373	3,587,281
Leibniz Association	497,626	429,045
Research cooperation	298,514	344,287
Foundations	105,309	14,778
Contract research	143,886	9,965
Other	39,933	151,841
Total	**14,676,497**	**15,912,176**

Infrastructure

Greenhouse Area	6,470 m^2
Phytochamber surface	220 m^2
Field trial area	84 ha

IPK-PhenoSphere

Rhizoboxes	360
Growth Containers	110

Holdings of the Federal *Ex situ* Genebank in 2025

Accessions	151,775
Species	2,849
Genera	750
Plant Families	94

Genebank deliveries

2024	21.124
2025	22.262

Organigram

Organigramm of the departmental structure shaping research and management at IPK Gatersleben.

Managing Office
Dr. Jens Freitag

Ombudsperson
Dr. Jozefus Schippers

Biological Safety
Dr. Hardy Rolletschek, Dr. Johannes Thiel

Department Genebank

Prof. Dr. Nils Stein

Area	Research Groups
Characterisation and Documentation (Dr. Stephan Weise)	Genomics of Genetic Resources (GGR), Prof. Dr. Nils Stein
	Genebank Documentation (DOK), Dr. Stephan Weise
	In silico Genebank Proteomics (IGP), Young Investigator Group, Dr. Amanda Souza Camara
	Potato Quantitative Genetics (PQG), Dr. Delphine Van Inghelandt
Conservation Management & Evaluation (Prof. Dr. Nils Stein)	Resources Genetics and Reproduction (RGR), Dr. Anna Elisabeth Backhaus
	Cryo- and Stress Biology (CSB), Dr. habil. Manuela Nagel
	Diversity and Collection Management (TEN), Dr. Klaus Dehmer
Taxonomy and Evolution (Dr. Martin Mascher)	Domestication Genomics (DG), Dr. Martin Mascher
	Genetics of Environmental Adaption (GEA), Dr. Laura Dixon

Department Breeding Research

Prof. Dr. Jochen C. Reif

Area	Research Groups
Breeding Informatics (Prof. Dr. Jochen C. Reif)	Quantitative Genetics (QG), Prof. Dr. Jochen C. Reif
	Bioinformatics and Information Technology (BIT), Dr. Uwe Scholz
Chromosome Biology (Prof. Dr. Andreas Houben)	Chromosome Structure and Function (CSF), Prof. Dr. Andreas Houben
	Kinetochore Biology (KB), Dr. Inna Lermontova
Genome Analysis (Prof. Dr. Thorsten Schnurbusch)	Biotrophy and Immunity (BIM), Dr. Dimitar Douchkov (komm.)
	Plant Architecture (PBP), Prof. Dr. Thorsten Schnurbusch
	Agroecological Breeding (AB), Young Investigator Group, Dr. Samira El Hanafí

Department Molecular Genetics

Prof. Dr. Thomas Altmann

Area	Research Groups
Systems Genetics (Prof. Dr. Thomas Altmann)	Heterosis (HET), Prof. Dr. Thomas Altmann
	Network Analysis and Modelling (NAM), Dr. Jędrzej Jakub Szymański
Growth Dynamics (Dr. Kerstin Neumann)	Automated Plant Phenotyping (APP), Dr. Kerstin Neumann
	Metabolic Diversity (MD), Dr. John Charles D'Auria
	Image Analysis (BA), Dr. Evgeny Gladilin
Seed Biology (Dr. Jozefus H. M. Schippers)	Seed Development (SE), Dr. Jozefus H. M. Schippers
	Assimilate Allocation and NMR (AAN), Dr. habil. Hardy Rolletschek

Bioinformatics
Coordination Biodiversity Informatics: Dr. Uwe Scholz | Coordination System Analysis and Modelling: Dr. Jędrzej Jakub Szymański

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Ministry of Science and Economics, Saxony-Anhalt

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Safety at Work
Dr. Martin Giersberg

Equal Opportunities
Dr. Rhonda Meyer

Staff Council
Chair: Thomas Kruse

Department Physiology and Cell Biology

Prof. Dr. Nicolaus von Wirén

Area	Research Groups
Physiology and Biochemistry Prof. Dr. Nicolaus von Wirén	**Molecular Plant Nutrition** (MPE) Prof. Dr. Nicolaus von Wirén/ Dr. Ricardo Giehl
	Genetics and Physiology of Root Development (GPW) Prof. Dr. Hannah Schneider
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
Meiosis (ME) Dr. Stefan Heckmann
Plant Reproductive Genetics (PRG) **Emmy Noether Group, DFG** Dr. Steven Dreissig
Functional Plant Structures (FPS) **Emmy Noether Group, DFG** Dr. Yongyu Huang
Biotechnology and Genome Editing (BGE) Dr. Robert Hoffie

Department Administration and Central Services

Dr. Ingmar Schmidt

Working Groups
Personnel (PW) Dr. Susann Deike
Finances, Knowledge Transfer and Management of third-party funds (FWD) Josefine Köhler
Research Library & Information Services (BIB) Simone Winter
Purchasing (EKF) Sabine Löffler
Campusmanagement and Logistic (CML) Katrin Menzel
Buildings and Equipment (TCH) Steffen Kirsch
Experimental Fields and Nurseries (VuG) Peter Schreiber

As of 31 December 2025

Selected Highlights

2024

January

A New Metalloreductase Keeps Roots Growing

An international research team led by the IPK has shown that the HYP1 protein protects roots from increased iron reactivity during phosphorus deficiency, thereby sustaining root growth. The results have been published in Nature Communications.

February

IPK Welcomes European Parliament

Following the European Commission, the European Parliament has also voted in favour of new rules for New Genomic Techniques. The IPK welcomes the decision, which incorporates numerous recommendations from the scientific community.

March

Key Gene behind a Toxic Barley Alkaloid

Research groups from the IPK and Leibniz University Hannover have decoded the complete biosynthetic pathway of the barley alkaloid gramine. This enables gramine to be produced in model organisms. The study has been published in "Science".

April

A Day to Discover Science and Careers

Pupils from Years 5 to 12 gain insights into the Research Campus Gatersleben during the annual careers' day. They learn about the work of the IPK and the training opportunities available on campus.

May

Northern Genebank Sites Ready for the Future

With support from the state of Mecklenburg-Western Pomerania, the genebank branches in Malchow and Groß Lüsewitz have been comprehensively modernised. The new facilities are inaugurated with an open day in Malchow.

How Barley Builds Its Spike

An international research team led by the IPK has revealed how signals from meristem boundaries regulate spikelet development and thus shape barley inflorescence architecture. The results have been published in "Current Biology".

June

Leibniz at the Federal President's Residence

At the 'Week of the Environment' in the grounds of Bellevue Palace, the home of the Federal President, the Leibniz Biodiversity Research Network presents ideas for advancing environmental, climate, resource and species protection. The IPK is one of 18 participating partners.

INCREASE Wins European Citizen Science Prize

The citizen science part of INCREASE receives the European Union's €60,000 Grand Prize for Citizen Science 2024 in Linz. Nearly 20,000 people across Europe have already taken part in the bean diversity project, which is co-coordinated by the IPK.

2025

January

How Key Proteins Dock at the Centromere

An international research team has investigated how the proteins KNL2 and CENP-C attach to the centromere, a structure essential for cell division, in Arabidopsis thaliana. The study identifies key components of this mechanism and has been published in "Nucleic Acids Research".

March

Bioeconomy beyond Lignite

The new consortium "DiP Saxony-Anhalt — Model region of the bioeconomy" is combining plant research and digitalisation to develop innovative solutions for structural change following the phase-out of lignite mining in southern Saxony-Anhalt. The launch event takes place at the IPK.

April

A Day to Discover Science and Careers

Pupils from Years 5 to 12 gain insights again into the work of the IPK during the annual careers' day. They explore the Research Campus Gatersleben and learn about its training and working opportunities.

May

IPK Joins the CEPLAS Cluster of Excellence

The CEPLAS Cluster of Excellence has succeeded in the third round of Germany's Excellence Strategy. The IPK will join the existing partners in Düsseldorf, Cologne and Jülich as a member of the cluster for plant sciences.

June

Visitors Explore the Research Campus

More than 2,000 visitors attend the Open Day and Festival of Encounters at the Research Campus Gatersleben. In bright summer weather, the IPK and companies based on the campus showcase their work.

A Key Protein for Plant Meiosis

IPK scientists have discovered SCEP3, a previously unknown key protein in plant meiosis. It enables chromosomes to recombine and be distributed accurately during reproduction. The study has been published in "Nature Plants".

Plant Science Student Conference

The Plant Science Student Conference celebrates its 20th anniversary. Organised in alternating years by students from IPK and IPB in Halle, the anniversary edition at Gatersleben attracts more than 100 participants from 19 institutions.

July

Beans Take Centre Stage on Screen

MDR and ARTE premiere their documentary 'Superfood Beans' during the Long Night of the Sciences in Halle. IPK scientist Kerstin Neumann, co-coordinator of the European citizen science project INCREASE, is one of the film's protagonists.

August

A New Joint Group for Potato Research

The IPK and the Julius Kühn Institute are expanding their collaboration in potato research by strengthening the Groß Lüsewitz site. From September, Delphine Van Inghelandt will lead the new joint research group 'Quantitative Genetics and Potato Breeding Methodology'.

September

European Plant Breeders Meet in Leipzig

The European Association for Research on Plant Breeding, EUCARPIA, holds its congress in Leipzig. IPK scientist Andreas Börner chairs the association.

ERC Starting Grant for IPK Root Researcher

IPK root researcher Hannah Schneider receives a Starting Grant from the European Research Council (ERC). Her FATE project on root cortical tissue receives €1.5 million funding from 2024 to 2029.

A New Milestone in Plant MRI

A research team from the IPK and the University of Würzburg has developed a method that uses magnetic resonance imaging (MRI) to observe the metabolism of sugars and amino acids non-invasively in complex storage organs such as seeds. The study has been published in "Science Advances".

Science Meets at Drübeck Abbey

Early-career researchers from the CEPLAS Cluster of Excellence and the IPK meet for five days at the second International Summer School at Drübeck Abbey. Following its success, the format will continue.

November

Inside the Barley Pangenome

An international research team led by the IPK has analysed the barley pangenome using complete genome sequences from 76 wild and cultivated barley accessions and data from a further 1,315 genotypes. The resulting catalogue of variation reveals structurally complex loci for important traits. The findings have been published in "Nature".

Gatersleben Research Awards

Hanna Marie Schilbert from Bielefeld University and Mustafa Bulut from the Max Planck Institute of Molecular Plant Physiology in Potsdam receive the Gatersleben Research Award. The prize is presented by the Society for the Promotion of Crop Plant Research Gatersleben.

Journalists Explore Biodiversity

The Journalists' College on Biodiversity combines lectures, guided tours, discussions, and excursions. The German Centre for Integrative Biodiversity Research (iDiv) is this year's partner of the IPK organising it. The programme follows the recent COP16 in Colombia.

August

From the Classroom to the Laboratory

Fourteen teachers exchange the classroom for the laboratory during a PLANT 2030 training course on genome editing. Following a tour and lecture at the IPK, they conduct their own experiments in the Green Lab ("Grünes Labor Gatersleben" e. V.).

September

Integrative Bioinformatics Returns to Gatersleben

The Gatersleben Research Conference welcomes 74 participants from ten countries to the International Symposium on Integrative Bioinformatics. The three-day programme features seven keynote speakers, 20 talks, eight flash talks and 15 poster pitches. The IPK hosts the symposium for the second time, following its first edition in Gatersleben in 2013.

Barley's Ancestry Revealed

An international study led by the IPK has shown that modern barley originated from several wild populations in the Fertile Crescent and therefore has a 'mosaic ancestry'. The results have been published in "Nature".

October

The Oat Pangenome

An international research team led by the IPK has created an oat pangenome, while a second study has investigated the crop's origins. The results have been published in "Nature" and "Nature Communications".

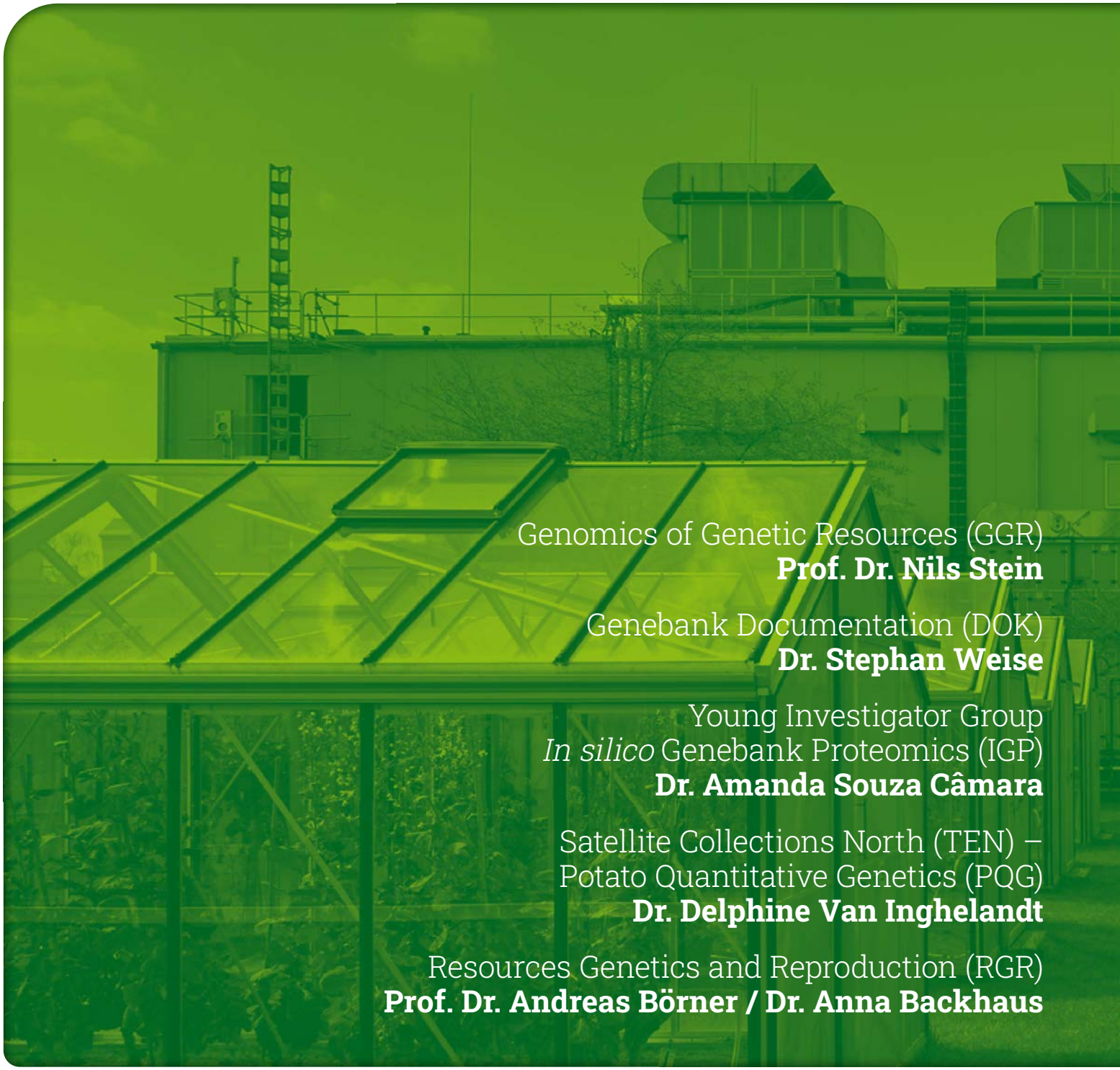
November

Dormancy Control in Barley

New findings from the Carlsberg Research Laboratory show how the MKK3 gene controls dormancy in barley and could help protect crops from climate-related yield losses. The IPK contributed to the study, which has been published in "Science".

Science Award for an IPK Researcher

IPK researcher Narendra Narisetti was awarded the Wernigerode Science Prize at a ceremony in the Town Hall, attended by Saxony-Anhalt's Minister for Science. Nicolaus von Wirén, Managing Director of the IPK, delivered the laudatory address.



Genomics of Genetic Resources (GGR)
Prof. Dr. Nils Stein

Genebank Documentation (DOK)
Dr. Stephan Weise

Young Investigator Group
In silico Genebank Proteomics (IGP)
Dr. Amanda Souza Câmara

Satellite Collections North (TEN) –
Potato Quantitative Genetics (PQG)
Dr. Delphine Van Inghelandt

Resources Genetics and Reproduction (RGR)
Prof. Dr. Andreas Börner / Dr. Anna Backhaus





Cryo- und Stress biology (CSB)
Dr. habil. Manuela Nagel

Satellite Collections North (TEN) –
Diversity and Collection Management (TEN)
Dr. Klaus J. Dehmer

Experimental Taxonomy (ETX)
Dr. Frank Blattner

Domestication Genomics (DG)
Dr. Martin Mascher

Genetics of Environmental Adaptation (GEA)
Dr. Laura Dixon

DEPARTMENT GENEBANK



DEPARTMENT GENEBANK

Heads: Prof. Dr. Nils Stein

Mission

Conserving plant genetic resources (PGR) in the Federal *Ex situ* Genebank is of great societal and scientific importance. These resources provide a foundation for research on the evolution, domestication, and environmental adaptation of crop plants. At the same time, they are essential for addressing current and emerging challenges in crop improvement, thereby supporting food security and helping to counteract the ongoing loss of crop-related agrobiodiversity in temperate agricultural systems.

To fulfil these roles, PGR management and conservation must meet the highest quality standards to ensure long-term preservation; however, preservation alone is not sufficient: the true value of PGR is realised only through active use. It is therefore our responsibility and has become a key priority in both research and collection management to enrich our plant genetic resources with comprehensive molecular, phenotypic, and environmental data and to integrate this information, thus supporting the transformation of the genebank from a passive repository of plant genetic resources into a dynamic and innovative research infrastructure; what we refer to as a Biodigital Resource Centre. This development will enable and facilitate knowledge-based selection and effective utilisation of PGR, advancing research at the scientific frontier and supporting innovative strategies in modern plant breeding.

Conservation Management

The Federal *Ex situ* Genebank is one of the world's largest PGR collections, in both botanical diversity and collection size. As of July 2025, the holdings comprised 151,775 accessions from 94 plant families representing 750 genera and 2,849 species.

The collection is maintained in Gatersleben and the two external sites, Malchow (oil and fodder plants) and Groß Lüsewitz (potato collections). During the reporting period (July 1, 2024 - June 30, 2025), we cultivated 6,963 accessions in the field or greenhouse for seed propagation and carried out 11,731 seed germination tests.

In addition to its living collections, the genebank accommodates several reference collections: (1) a herbarium with 450,400 specimens, (2) 110,394 reference samples of seeds and fruits and (3) 58,559 cereal spikes. In the past two years, we distributed 43,386 samples to researchers, plant breeders, or other interested stakeholders (Table 1). Material is distributed exclusively under the Standard Material Transfer Agreement (SMTA), ensuring compliance with the relevant provisions of the International Treaty on Plant Genetic Resources for Food and Agriculture or the Nagoya Protocol. Since 1948, IPK has provided more than 1.2 million samples to users in Germany and abroad. Table 2 summarises our inventory.

Table 1: *Distribution of plant genetic resources (PGR) to the various user groups in 2024 and 2025.*

User group	Distributed Accessions 2024	Distributed Accessions 2025
Other research institutes	6.844	12.287
Plant breeders	4.212	4.022
IPK researchers	7.158	2.888
Genebanks and botanical gardens	496	697
Non-profit organisations	270	389
Private individuals	2.144	1.979
In total	**21.124**	**22.262**

In addition to the large quantity of seed-based accessions, the IPK operates one of the world's largest cryo-collections for vegetatively preserved plants, currently comprising 2,508 accessions, including 2,094 potato, 157 mint and 253 Allium samples. The potato cryo-collection is continuously growing with the aim of backing up the entire tissue-culture-based clonal cultivar collection in cryo. Such backup is also important for the seed-based collection. IPK safety duplicates hosted at the Svalbard Global Seed Vault of the Crop Trust were increased to 69,673 accessions representing about 46% of the total collection.

To support the coordinated conservation of genetic resources at the national and international level, the Genebank Department interacts closely with the Federal Ministry of Agriculture, Food and Regional Identity (BMLEH), the Alliance of Bioversity International and the International Center for Tropical Agriculture (Alliance), and the Secretariat of the European Cooperative Programme for Plant Genetic Resources (ECPGR). The IPK Genebank department has received a mandate from ECPGR to host and advance the European Search Catalogue for Plant Genetic Resources (EURISCO). The ISO 9001:2015 certificate for the genebank's quality management (QM) was renewed in 2025 until March 2028.

Research

The Genebank department makes substantial contributions to the two IPK research themes, "Activating Genetic Diversity" and "Exploiting Biodigital Plant Data", while the Department Genebank research groups are assigned to one of the three departmental programs: Characterisation and Documentation, Conservation Management and Evaluation, and Taxonomy and Evolution.

The research programme "Characterisation and Documentation" focuses on the description of genebank materials at various levels and at the maintenance and further development of the Genebank Information System (GBIS) as a foundation for the transformation of the genebank into a Bio-digital Resource Centre. This was complemented by the renewal of IPK's mandate to host and further develop the EURISCO catalogue and coordinate the underlying network. This activity also underpinned the EU H2020 project AGENT, which aimed at establishing an active cooperation network between European genebanks. EURISCO played a similarly central role in the Horizon Europe project PRO-GRACE, developing a concept for a European research data infrastructure for PGR. A key focus of EURISCO's further development is integrating passport data with phenotypic and molecular data to characterise biological material. This program was complemented in 2024 by the expertise of two new research groups: In silico Genebank Proteomics (IGP), a young investigator group, capitalising on the barley pangenome resources for AI-assisted modelling of the barley pan-proteoforms, and Potato Quantitative Genetics (PQG), a division of the satellite collections north (TEN), established as a joint research group between the Julius Kühn Institute and IPK to strengthen research on the potato collections.

The research programme "Conservation Management and Evaluation" comprises the core team of research groups responsible for collection management. Here, studies on the genetics of seed longevity were continued. Concerning vegetatively propagated species, the cryo-collections of potato and *Allium* were continuously expanded. The impact and role of endophytes during potato cryopreservation have become a focus of interest. For garlic, an extensive European cooperation is assessing duplication levels in almost 2,000 accessions using reduced representation sequencing, which will provide an important proxy for designing future garlic cryopreservation. *Lemna* is an emerging new species with promising application potential, and IPK has teamed up in international cooperation with emphasis on testing the species' cryopreservation potential and properties.

The research programme "Taxonomy and Evolution" conducts research on phylogenetic classification, as well as speciation, domestication, and adaptation within selected plant genera. The evolution of di- and tetraploid *Hordeum bulbosum*, the secondary gene pool of cultivated barley (*Hordeum vulgare*), was in focus of an IPK flagship project on the sequencing and assembly of the *H. bulbosum* pangenome. The study formed a collaborative nucleus among multiple research groups across the Genebank and other IPK departments and established a genomic resource comprising ten chromosome-scale genome assemblies representing 32 phased haplotypes from diploid and tetraploid accessions (Figure 1). The pangenome provided fundamentally new insights into the evolution of this species. Comparative analyses demonstrated that tetraploid lineages originated multiple times and remained connected to diploid populations through historical gene flow. Beyond its fundamental significance, the project demonstrated how biodiversity collections can be transformed into biodigital resources for crop improvement. H. bulbosum has long been recognised as a valuable source of disease resistance and adaptation traits, yet its use in breeding has been constrained by limited genomic resources. The pangenome now provides a framework for

characterising introgression lines, tracing the inheritance of wild chromatin in breeding material, and accelerating the identification of candidate genes. As a proof of concept, the study resolved the genomic architecture of a major virus-resistance locus and identified candidate genes, thus illustrating the translational value of large-scale genome resources for the utilisation of plant genetic resources.

In 2025, the programme "Taxonomy and Evolution" was restructured by opening a new research group, Genomics of Environmental Adaptation (GEA), and terminating the Experimental Taxonomy (ETX) group due to the retirement of the group leader. The mandate for curating the taxonomy collections, previously part of ETX, has been newly integrated as a section of the research group Domestication Genomics (DG).

Table 2: *Overview of collections from the Genebank by crop species*

Species groups	Accessions
cereals and grasses	**66.397**
wheat	28.322
barley	23.786
oat	4.865
rye	2.582
triticale	1.619
Aegilops	1.513
millets	841
maize	1.531
grasses	1.338
legumes	**27.881**
Phaseolus	9.014
field beans	3.033
soybeans	1.491
other beans	645
pea	5.385
chickpea	527
vetchling	513
vetches	1.845
lupines	2.712
lentils	473
clover	1.971
other legumes	272
Cucurbitaceae	**2.669**
pumpkins	1.052
melons	728
cucumbers	741
other Cucurbitaceae	148
vegetables	**17.836**
tomatoes	3.910
pepper	1.533
eggplants	113
beta beets	2.372
raphanus	766
carrots	507
chicory	670
Allium	1.958
Brassica	2.170
lettuce	1.148
spinach	215
celery	254
Quinoa	953
other vegetables	1.267
oil, fibre and dye plants	**5.469**
flax	2.325
sunflower	677
dye plants	458
fibre plants	190
oil plants	548
other oil, fibre and dye plants	1.271
medicinal and spice plants	**8.244**
poppy	1.135
tobacco	590
other medicinal and spice plants	6.519
mutants	**1.684**
tomato mutants	743
soybean mutants	527
Antirrhinum mutants	414
Satellite Collections North	**21.595**
potatoes	**6.358**
potatoes	6.357
oil and forage crops	**15.238**
rapeseed and feeding kale	2.671
grasses	11.222
red clover and alfalfa	1.345
Total	**151.775**

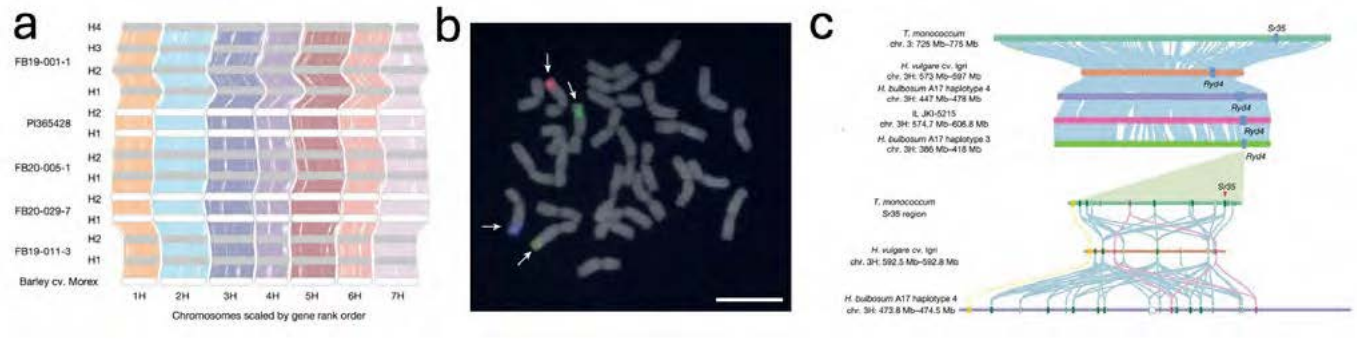


Figure 1: *A haplotype-resolved pangenome of the barley wild relative Hordeum bulbosum. (a) Synteny plot between H. bulbosum haplotypes. Grey bars represent chromosomes and are scaled according to the number of genes with syntenic alignments to other genomes. H1–H4 denote haplotypes 1–4. (b) Structural validation of haplotype-phasing through haplotype-specific oligonucleotide-based FISH in mitotic chromosomes of FB19-028-3. The red, green, blue and yellow probes target haplotypes 1, 2, 3 and 4, respectively, of chromosome 5H. Scale bar, 10 µm. (c) Microsynteny comparison of the Sr35 and Ryd4Hb resistance loci. The upper panel shows long-range synteny among Igri, A17, Triticum monococcum TA10622 and JKI-5215; the lower panel compares local gene order and content between H. vulgare cv. Igri and A17 haplotype 4. Genes are colour-coded: yellow, S-formylglutathione hydrolase-like; purple, ankyrin-repeat proteins; green, complete NLRs; white/green outline, partial NLRs. Sr35 is marked in red. Syntenic links (≥ 80% nucleotide identity) are colour-coded by gene family.*

Research groups in the Genebank Department made highly visible contributions to Agricultural Genomics by providing high-quality genomic resources for the cereal species barley, wheat, rye, and Oats. These activities have been elevated to high-quality pangenomes in all the mentioned species. The pangenome, pantranscriptome and panepigenome of the crop species *Hordeum vulgare* is being continued at an even higher pace and further facilitated through the extension of IPK's central sequencing platform for the most recent state-of-the-art technology (Pacific Biosystems REVIO and NOVASEQ Xplus by Illumina).

Outlook

Building on the expertise accumulated over more than seven decades, the department Genebank stands for research-driven conservation and characterisation of PGR collections. It supports the sustainable preservation of one of the world's largest *Ex situ* collections and drives innovations to enhance its value as infrastructure for research and crop plant improvement.

Advances in genome analysis and plant phenotyping will further accelerate progress toward systematic characterisation of the complete genebank collection. This will include the sequencing-based genotyping of entire crop collections. The availability of sequence information will benefit the conservation of genetic resources in manifold ways. In this context, we will continue the path taken to further develop the genebank 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* Genebank 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 taking the mandate for coordinating EURISCO since 2014, the department has continued to set international standards for the conservation of genetic resources and cemented the value of the genebank as an internationally visible and widely used research infrastructure. By coordinating the H2020 project AGENT, IPK led innovation-driven research to build an actively cooperating genebank network, with the aim of enabling genomic prediction across genebank collections. The Department's scientific focus on molecular genetics and genomics of the Triticeae 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 further advance research into genome diversity, evolution, and crop adaptation.



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

Head: Prof. Dr. Nils Stein

Mission

Our research aims to use state-of-the-art, high-throughput genomic technologies to uncover the pangenomes of cereal crops and their wild relatives. This work provides a new knowledge base for fundamental discovery and, in particular, for documenting the global genomic diversity of major crop species such as barley, wheat, and rye, including accessions held in the Federal *Ex situ* Genebank.

We apply the established concept of genebank genomics, which involves the systematic genotyping of entire genebank collections and the integration of genomic data with passport information as well as characterisation and evaluation (C&E) data. This approach is being extended, through collaboration, to additional crop species conserved in IPK's genebank. Beyond IPK, the concept is also being implemented across other European genebanks, with the goal of establishing an active and collaborative genebank network.

The resulting (pan-)genomic resources in cereals are used in functional genomics studies to identify the genetic basis of important traits. These include resistance to soil- and insect-borne viral diseases in barley, the genetic regulation of barley morphology and plant architecture, and the genes underlying leaf variegation.

To support the implementation of this research programme and to provide institute-wide services, the research group GGR operates and continuously expands a state-of-the-art next-generation DNA sequencing platform.

Results

(Pan-)Genome Analysis

The research group takes a leading role in sequencing and re-sequencing of the genomes of barley, wheat and rye and contributes to genome and pangenome projects in other species (e.g. Oats: Avni *et al.* 2025, potato: Cheng *et al.* 2025). In the focus is the barley pangenome project, coordinated by IPK, including the research groups GGR, DG and BIT, and it involves broad international collaboration. So far, almost 200 barley genome assemblies were generated based on PACBIO Hifi sequencing. An advanced pangenome of 76 assemblies has been published (Jayakodi *et al.* 2024) and the remaining resources are in preparation for publication. GGR contributes to the Hordeum genus pangenome, an effort coordinated by Martin Mascher (DG), with the aim to provide genome assemblies of all ~30 diploid species of the genus *Hordeum*. This activity involved also the *Hordeum bulbosum* pangenome IPK flagship project (Feng *et al.* 2025), coordinated also by M. Mascher (DG) and bringing together research groups of the departments Genebank and Breeding Research (DG, ETX, GGR, BIT, CSF, ACB). The barley pangenome resource is further substantiated through pan-transcriptome (Guo *et al.* 2025) and pan-epigenome (Navratilova *et al.* 2025 and Zhu *et al.* in preparation, Figure 1) data layers. This effort, which aims at laying the foundation for efficient functional analysis in barley, has recently received generous support by BMFTR for the interdisciplinary PPP project PREBreed (2025-2028), bringing together research groups of all IPK scientific departments..

Unlocking crop plant genetic resources

GGR, together with other groups at IPK, demonstrated the feasibility of genotyping entire crop collections of the IPK genebank (Milner *et al.* 2019), a research area coined "genebank genomics" (Mascher *et al.* 2019). By applying this concept broadly to the collections of IPK genebank, a foundational data layer will be generated that is suited to push the transformation of IPK's classical *Ex situ* genebank into a Bio-digital Resource Center. In the BMFTR funded project Genebank2.0/3.0

Selected publications

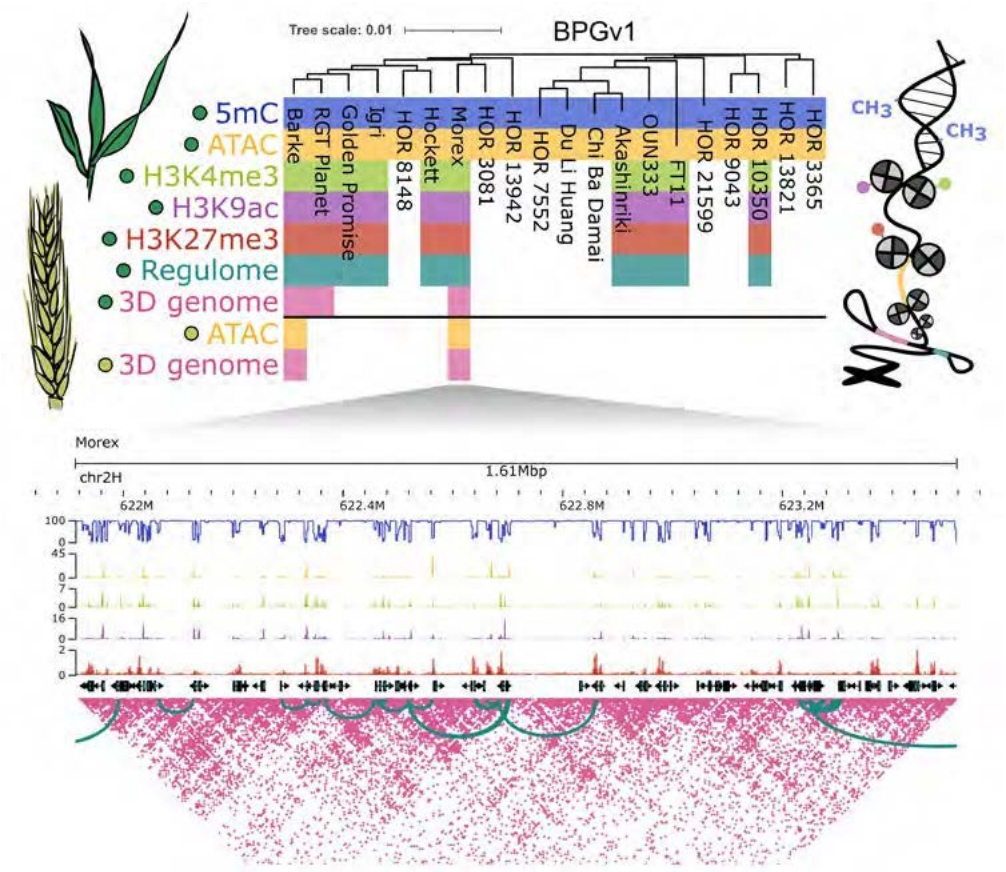
Jayakodi M et al. (2024) Structural variation in the pangenome of wild and domesticated barley. ***Nature*** 636: 654-662.

Mascher M et al. (2024) Promises and challenges of crop translational genomics. ***Nature*** 636: 585-593.

Cheng L et al. (2025) Leveraging a phased pangenome for haplotype design of hybrid potato. ***Nature*** 640:408-417.

Feng J-W et al. (2025) A haplotype-resolved pangenome of the barley wild relative *Hordeum bulbosum*. ***Nature*** 645: 429-438.

Guo W et al. (2025) A barley pan-transcriptome reveals layers of genotype-dependent transcriptional complexity. ***Nat. Genet.*** 57: 441-450.



The pan-epigenome of barley. Functional epigenomic features, including DNA methylation (5mC), chromatin accessibility (ATAC), histone modifications, and chromatin interactions, have been profiled in leaf and inflorescence tissues across up to 20 barley pan-genome version 1 (BPGv1) genotypes. All datasets can be explored through an interactive epigenome browser (example region shown for the genotype Morex; Navratilova et al., 2025).

(phase 1-3), coordinated by Jochen Reif (QG), all cultivated bread wheat accessions and a large proportion of wild relatives were genotyped by reduced-representation sequencing. The barley and wheat genebank genomics activities of IPK were the driving force behind the IPK-coordinated EU H2020 project AGENT; bringing together 18 genebank and genebank-informatics partners from all-over Europe in a 5-year collaborative project with a total budget of 7 million EURO, which has concluded in late 2025. GGR together with TEN continue this strategic development in genebank genomics by starting the systematic GBS-genotyping of the Groß Lüsewitz Potato Collections in frame of the BMFTR funded project POMORROW (2025 – 2028).

Embedding in IPK Research Themes

The research group GGR is contributing mainly to the Research Themes 1 “Activating Genetic Diversity” and 2 “Exploiting Biodigital Plant Data” 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 genebank 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 and expand this strategically to other crop species and crop wild relatives of the collection. This will cover the areas of structural variation, pan-epigenomics, spatial developmental genomics, as well as 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 Revio, Illumina NovaSeq Xplus, ONT Promethion etc.) is providing excellent opportunities for this kind of research and for international collaboration and networking.



RESEARCH GROUP **GENEBANK DOCUMENTATION** (DOK)

Head: Dr. Stephan Weise

Mission

The working group's activities cover a wide range of tasks related to documenting and leveraging plant genetic resources (PGR), as well as managing genebank data. Specifically, the research group develops and operates information systems for PGR. On the one hand, these serve to facilitate the workflows in the genebank. On the other hand, the goal is to enhance the utilisation of plant genetic resources for various users in research and breeding. Integrating and curating data from different areas and sources, as well as harmonising and exchanging data, are thus essential tasks of the group. Moreover, the group provides other groups with extensive expertise.

Results

The Genebank Information System (GBIS) is the institute's central infrastructure for supporting all genebank accession maintenance processes. As with all IT systems, continuous further development of its various components is essential to ensure the performance and efficiency of the system in the long term. In addition to technical adjustments, the system must also be adapted regularly in response to new requirements. This involved, for example, the full redesign of the public search and ordering system (GBIS/I), which was completed at the end of 2025. Another example is the finalisation of a new tablet-based software, PhenoApp, which is used to score accessions during seed regeneration in the genebank. Originally developed by JKI, it was expanded during the reporting period to include a series of specific requirements for genebank work and is now in productive use.

For more than ten years, the Genebank Documentation has been responsible for hosting and further developing the European Search Catalogue for Plant Genetic Resources (EURISCO) on behalf of the European Cooperative Programme for Plant Genetic Resources (ECPGR). Data is becoming increasingly important for the exploitation and utilisation of PGR. IPK therefore applied for this mandate in order to actively support co-operation in this area. Since taking on the mandate, the number of accessions documented in EURISCO has increased from 1.1 million to over 2.1 million, which are preserved in more than 430 *Ex situ* and almost 40 *in situ* CWR collections in 43 countries. EURISCO thus represents one of the most important international aggregator systems and makes an important contribution to the utilisation of this great genetic diversity. Thanks to the close links with other international systems and partners, it has been possible to raise a considerable amount of additional third-party funding and increase IPK's overall visibility. The institute has therefore successfully endeavoured to extend the hosting mandate for a further (now third) five-year phase (currently until the end of 2028).

In recent years, the research group has been involved in several Horizon 2020 projects. Two of these, AGENT (2020-2025) and INCREASE (2020-2026), were continued or completed during the reporting period, respectively. AGENT was a concerted action to activate genebanks, aiming to facilitate access to wheat and barley genetic resources for breeders and farmers through standardised protocols for data generation, documentation and delivery to users. The INCREASE project, in turn, aims to advance the conservation of European plant genetic resources of four legume crops, and to promote their use and valorisation. In both projects, the research group was and is involved in work packages focusing on the development of guidelines and formats for data generation, data exchange and data presentation, and on the development of infrastructure for the management, presentation and analysis of data on genetic resources.

From January 2023 to October 2025, the working group participated in the PRO-GRACE research project as part of the Horizon Europe funding programme. The aim of PRO-GRACE was to develop a concept for a large European research infrastructure for plant genetic resources. In this context, the working group was responsible for leading a work package on the inventory of PGR-related data and systems as well as information standards. All activities were successfully accomplished and are the subject of ongoing publication plans.

Selected publications

Berkner MO et al. (2024) Genomic prediction reveals unexplored variation in grain protein and lysine content across a vast winter wheat genebank collection. ***Front. Plant Sci.*** 14: 1270298.

Maxted N et al. (2025) A significantly enhanced role for plant genetic resource centres in linking *in situ* and *ex situ* conservation to aid user germplasm access. ***Genetic Resources*** S2: 203-223.

Selby P et al. (2025) BrAPI v2: real-world applications for data integration and collaboration in the breeding and genetics community. ***Database*** 2025: baaf048.

Tanwar UK et al. (2025) Establishment and phenotypic characterization of genetically diverse core collections of *Lupinus albus*. ***BMC Plant Biol.*** 25: 1256.

Weise S et al. (2025) The German Federal Ex Situ Genebank for Agricultural and Horticultural Crops – Conservation, exploitation and steps towards a bio-digital resource centre. ***Genetic Resources*** S2: 91-105.

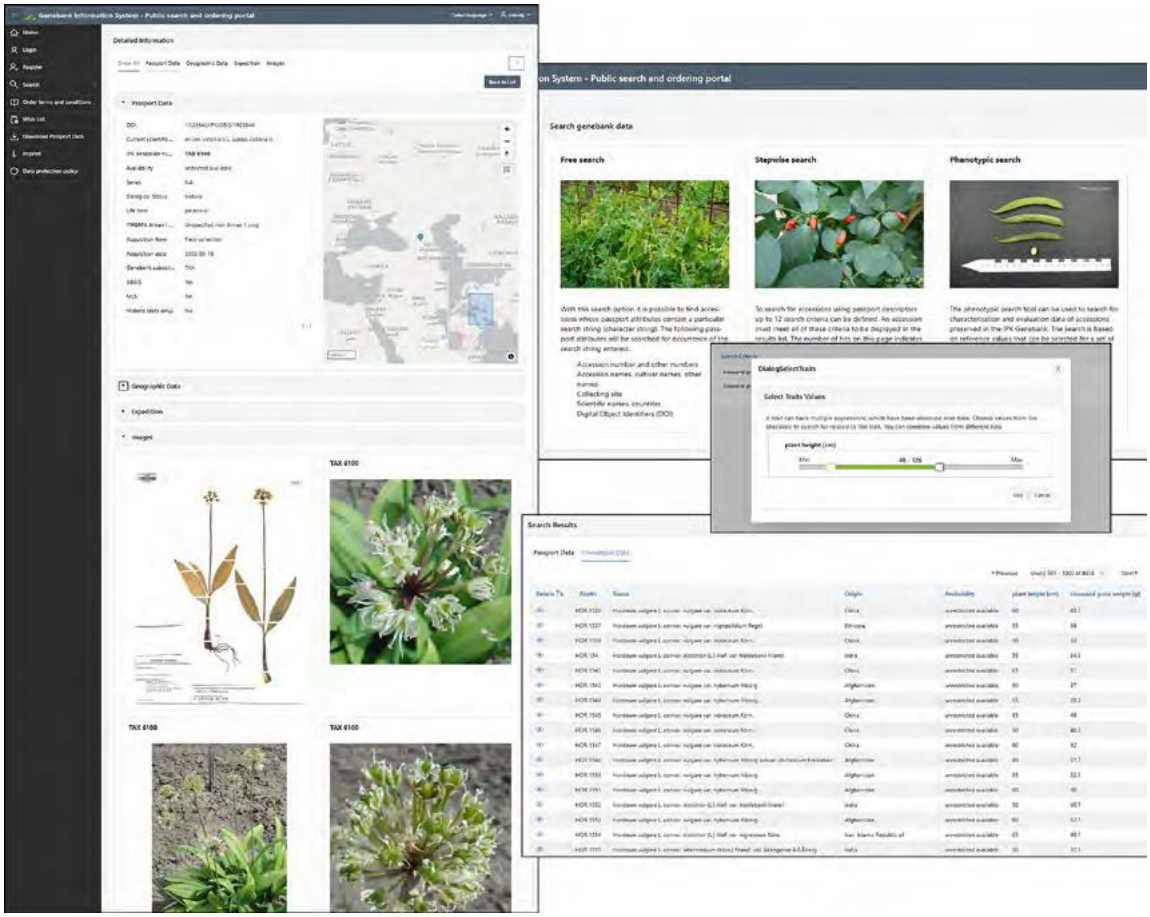


Figure 1: *Web-based interface of the newly developed search and ordering system GBIS/I.*

In addition, since January 2024, the research group has been involved in the COUSIN consortium (Horizon Europe programme, 2024-2028). COUSIN aims at developing and implementing a roadmap for the use of crop wild relatives for breeding and farming. The working group is responsible for leading a work package on the provision of high-quality data.

The continuous management, curation and analysis of both historical and current genebank accession data is one of the research group's fundamental, permanent tasks. The continuous improvement and complementation of passport and phenotypic data has significantly increased the quality and quantity of information available on genebank accessions.

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 activities of the working group largely constitute a service for the Genebank department. GBIS forms the IT basis for most of the preservation processes in the genebank collection. The data managed in this system comprises information at various levels, which serves as a starting point for selecting materials of scientific or breeding interest from the genebanks PGR resources.

In cooperation with other bioinformatics groups of the institute, the activities of the research group are part of the strategy to transform the genebank into a bio-digital resources centre in the frame of Research Theme 2 "Generating and Exploiting Bio-Digital Plant Data".

Outlook

Looking ahead, the group prioritises the continued development and operation of GBIS, including its core components (GBIS/M, the internal management system, and GBIS/I, the online search and ordering system), and EURISCO to ensure long-term availability of comprehensive PGR data. Strengthened cooperation with national and international information networks will be pursued. Future work will focus on establishing metrics for data quality and processes to improve it – critical for enhancing the FAIRness of PGR data. The group will deepen collaboration with other bioinformatics groups to advance the interfacing of information systems. The aim is to offer users of bio-digital data various entry points into systems that communicate with each other via APIs, depending on the specific question at hand.



YOUNG INVESTIGATOR GROUP **IN *SILICO* GENEBANK PROTEOMICS** (IGP)

Head: Dr. Amanda Souza Câmara

Mission

This research group aims to resolve molecular mechanisms, that are key to plant adaptation, by modelling macromolecular structures – proteins and chromatin -, their dynamics and interactions in the three-dimensional space. The group has two main goals: i) leveraging vast genetic resources of barley, we explore the structural variability in its panproteome to identify genetic variants that affect protein function; and ii) understand basic questions on how genetic information is transmitted in different plant species by modelling the physical forces that shape the genome organisation and its compaction through the cell cycle.

Results

This group began activities in January 2024 starting a new project on protein structure variation over the pangenome of barley. This project leverages the recent developments on Artificial Intelligence - specially on protein structure prediction – and on pangenome sequencing in IPK, and proposes to inspect which sequence variations cause protein structural variation and consequent disfunction and phenotype variability. Funded by the "Ministerium für Wissenschaft, Energie, Klimaschutz und Umwelt des Landes Sachsen Anhalt", the group has one Postdoc working in this project. Over the last two years, he has stablished a protein structure prediction routine with local installations of AlphaFold2 and, most recently, AlphaFold3, predicting ~380 structures per day. To analyse this vast number of proteins, we are developing a clustering pipeline sensitive to folding variations. Investigating how these protein structures cluster and distribute across 76 genotypes of barley, we aim to identify structural and sequence variations that most probably confer different functional roles. Besides this main project, the expertise of the group on protein structure has allowed collaboration with different groups of IPK, using further computational tools, like molecular dynamics, to better understand the function of specific candidate genes, like the synaptonemal complex central element SCEP3 (Feng *et al.* 2025), the kinetochore null2 (Yadala *et al.* 2024) and the orthologous wheat frizzy panicle and barley compositum 2.

Continuing under DFG funding acquired for the individual position of Amanda Camara while she was a postdoc in the Domestication Genomics group, the second project of this group tries to answer how chromosomes compact during the mitotic cell cycle, helping to understand how genetic information is transmitted. It follows a previous project between the Domestication Genomics and Chromosome Structure and Function groups, which found a helical organisation in mitotic chromosomes of barley gathering Hi-C sequencing data, super-resolution microscopy and polymer simulations. Three review papers also derived from this study in the past two years, where we highlight the use of these techniques for understanding chromatin organisation (Figure 1) and review the history of the chromonema (a compact form of chromatin), its existence across species and hypotheses for its coiling dynamics.

Selected publications

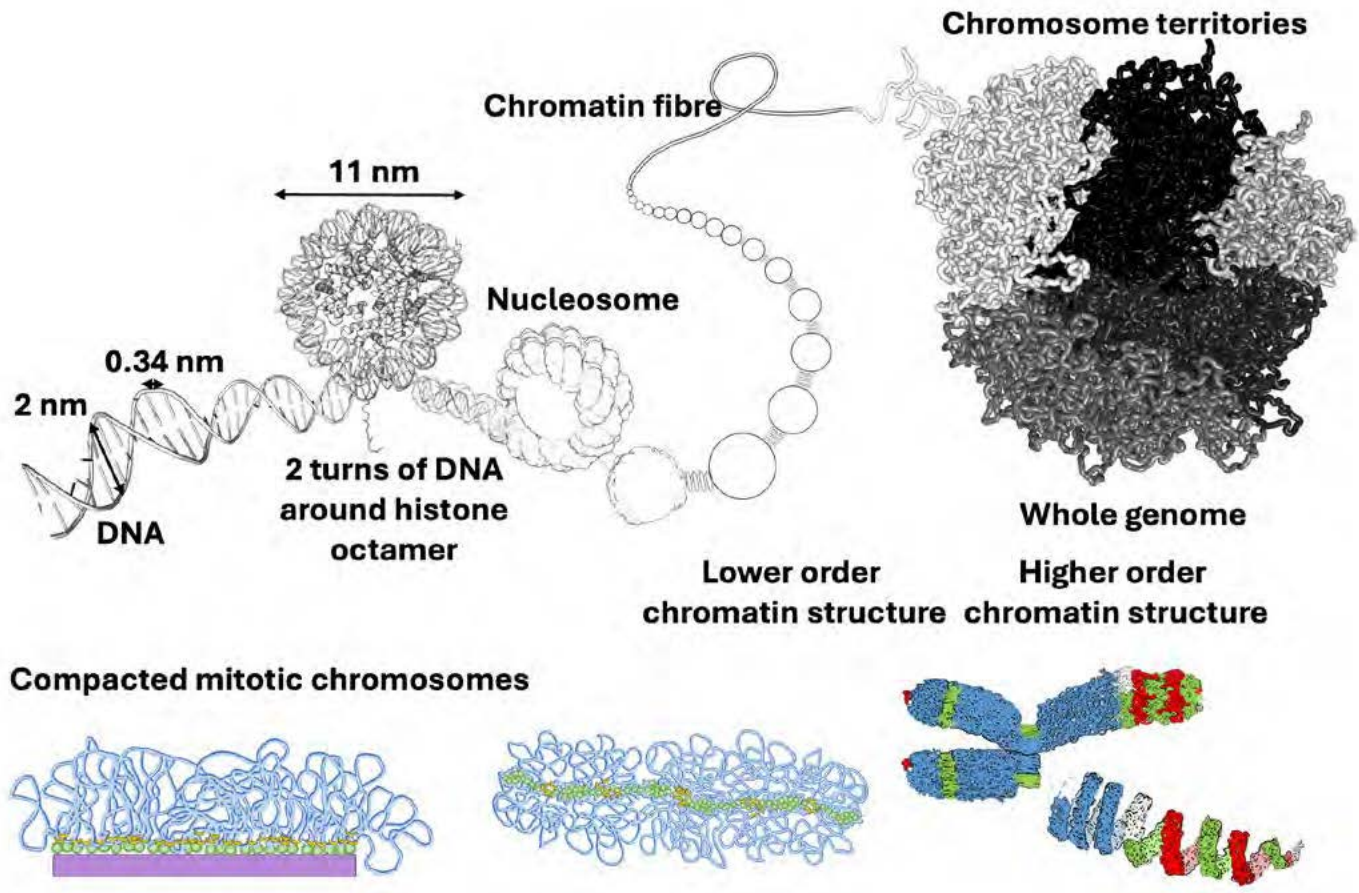
Câmara AS, Kubalová I, Schubert V (2024) Helical chromonema coiling is conserved in eukaryotes. ***Plant J.*** 118: 1284-1300.

Šimková H, Câmara AS, Mascher M (2024) Hi-C techniques: from genome assemblies to transcription regulation. ***J. Exp. Bot.*** 75: 5357-5365.

Câmara AS, Mascher M (2025) Understanding and simulating the dynamics of a polymer-like chromatin. In: Baroux C, Tatout C (Eds.): Methods for plant nucleus and chromatin studies: methods and protocols. (Series: Methods in molecular biology, Vol. 2873) New York: Humana Press. 283-302.

Feng C et al. (2025) The synaptonemal complex central element SCEP3 interlinks synapsis initiation and crossover formation in *Arabidopsis thaliana*. ***Nat. Plants*** 11: 1353-1366.

Nogueira VHR et al. (2025) Fuzz testing molecular representation using deep variational anomaly generation. ***J. Chem. Inf. Model.*** 65: 1911-1927.



Embedding in IPK Research Themes The research on the panproteome adds a new layer to the digitisation of the genebank, in line with Research Themes 1 and 2. It provides structure-based hypothesis to specific proteins of roots, shoots or chromosome organisation in collaboration with diverse groups in IPK in line with Research Themes 4, 5 and 3. Last, the research on chromosome compaction aligns with Research Theme 3, offering testable hypothesis and models of chromatin polymer for different plants at different stages of the cell cycle.

Figure 1: *On top, a scheme of polymer models to simulate chromatin dynamics, indicating different organizational levels, and, at the bottom, models that we have previously proposed for differently compacted mitotic chromosomes – general holocentric chromosomes; chromosomes of C. japonica, with few but large centromere units; and barley chromosomes, showing a helical coiling of the chromonema (from left to right; Câmara and Mascher, 2025).*

Outlook

We intend to submit our innovative analyses of hundreds of proteins and its distribution inside the panproteome of barley to high-impact journals within the coming year, demonstrating the value of large-scale structural predictions. Likewise, we plan to propose and publish a coiling mechanism for mitotic chromosomes, so far unknown for any species. To continue and expand this work, Amanda Câmara has applied for an ERC Starting Grant. The proposed project focuses on linking protein sequence variation to phase separation mechanisms affecting chromatin organisation and transcription. This direction builds on the group's expertise and aligns with IPK's strategy to understand molecular mechanisms underlying plant adaptation to changing environments.



RESEARCH GROUP **SATELLITE COLLECTIONS NORTH – POTATO QUANTITATIVE GENETICS** (PQG)

Head: Dr. Delphine Van Inghelandt

Mission

The joint IPK-JKI research group, newly established in 2024, develops quantitative genetic methods to identify and characterise positive alleles and allele combinations in genetic resources of potato as well as accumulate them in the breeding process. The overarching aim of the working group is to optimally exploit the genetic resources that are e.g. stored in the IPK genebank for breeding purpose to increase genetic gain in potato breeding. To achieve this goal, we pursue various approaches, including quantitative genetic analyses of experimental datasets, computer simulations, and quantitative genetic theory that considers the specificities of polyploid species.

Results

Implementation of genomic selection in potato breeding, its effect on long-term genetic gain and evaluation of the transferability of its prediction models across market segments.

Our group evaluated the effectiveness of different cross-selection (CS) methods incorporating genomic selection (GS) in autotetraploid potato breeding compared to traditional phenotypic selection (PS) (Wu *et al.* 2025). Simulation results implicated that GS with optimally selected proportions increased both short- and long-term genetic gain relative to PS. Among mean-based CS methods, MEGV-0, which considers additive and dominance effects when predicting progeny mean, achieved the highest long-term gain. A method combining the usefulness criteria and genome-wide diversity (EUCD) maintained similar genetic gain while preserving a higher genetic diversity and reducing the number of fixed QTL (Figure 1). This implies a more efficient conversion of diversity into genetic gain. These findings provide practical guidance for improving potato breeding strategies through GS and CS.

While we showed that genomic prediction (GP) can help increase the efficiency of breeding programmes, this procedure is, however, not yet routine in commercial breeding programmes in tetraploid organisms like potato. Therefore, our group collaborated to estimate the prediction accuracy for 26 different traits in a panel of about 1000 potato genotypes, evaluate the influence of the size and constitution of the training set, and investigate the effect of selection in the later (Thelen *et al.* 2025). In this study, a training set of 280–480 clones and 10,000 markers was sufficient to reach high prediction accuracies. Prediction within a specific market segment led to a higher prediction accuracy compared to adding clones from other market segments or to predicting between different market segments. Lastly, a higher prediction accuracy was found when in a training set of selected clones (clones with high trait values), 20% of the clones were replaced by sampled clones showing the lowest 10% trait values.

Harnessing natural variation of potatoes

As the genetic diversity of wild Solanum species remains underexplored, efforts to construct a pangenome were crucial for advancing potato improvement. We published a spotlight article that highlight studies published early 2025 presenting the results of an impressive amount of genomic, transcriptomic, and genetic data and providing different resources and scientific insights that

Selected publications

Arlt C et al. (2025) Assessment of genomic prediction capabilities of transcriptome data in a barley multi-parent RIL population. ***Theor. Appl. Genet.*** 138: 247.

Thelen K et al. (2025) Transferability of genomic prediction models across market segments in potato and the effect of selection. ***Theor. Appl. Genet.*** 138: 219.

Van Inghelandt D, Stich B (2025) Potatome - harnessing natural variation of potatoes. ***Mol. Plant*** 18: 1109-1111.

Wu P-Y et al. (2025) Optimal implementation of genomic selection in clone breeding programs exemplified in potato: II. Effect of selection strategy and cross-selection method on long-term genetic gain. ***Plant Genome*** 18: e70000.

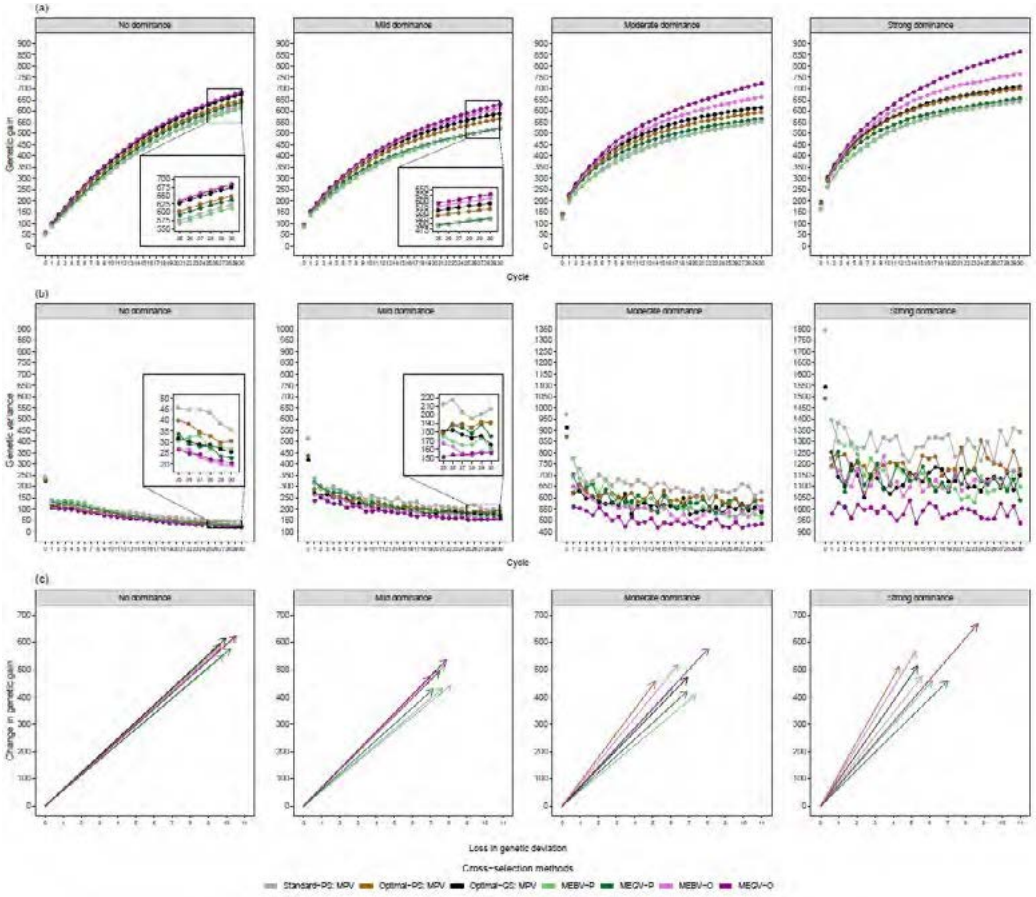


Figure 1: *The evolution of genetic gain (a) and genetic variance (b) for a target trait along 30 breeding cycles on average across 30 simulation runs. The efficiency of converting genetic diversity into genetic gain (c) by regressing the change of genetic gain on the loss of genetic standard deviation between cycle 0 and cycle 30. The three parameters were assessed at D clone stage for different selection strategies (Standard-PS, Optimal-PS, and Optimal-GS), different mean-based cross-selection methods (mean phenotypic values of the two parents [MPV], mean estimated breeding values of the two parents [MEBV-P], mean estimated genetic values of the two parents [MEGV-P], mean estimated breeding values among simulated offspring [MEBV-O], and mean estimated genetic values among simulated offspring [MEGV-O]), and different genetic architectures of the target trait (no, mild, moderate, and strong dominance effects).*

support and facilitate the breeding process of potato (Van Inghelandt & Stich 2025).

Embedding in IPK Research Themes With the development of phenomic and genomic prediction methods and phenotyping resources to facilitate the characterisation of the potato genetic resources (PGR), the research group is contributing mainly to the Research Theme 1: Activating Genetic Diversity. These aspects completely integrate in the goal of characterisation and documentation of PGR to contribute to the Bio-digital Resource Centre. The generated data will be used for quantitative genetic analyses applied to the genebank accessions to harness the genetic basis of target traits. The knowledge gained will help proposing targets for genome editing (Research Theme 3: Engineering Genomes and Chromosomes) and contribute thereby to the enhancement of Plant Shoot Performance (Research Theme 5).

Outlook

In the coming research period, the research group PQG will continue/finalise its activity on the theoretical assessment of segregation variance in autotetraploid species. An accurate information on genetic variance among offspring is essential for breeders to identify optimal crosses, increasing the probability for superior progenies and a higher crop performance. Therefore, our group is currently developing algebraic formulae to estimate genetic variance in autotetraploid crops such as potato, for which such derivations are not available. Further, the group will intensify the activities initiated in September 2024 to characterise the diversity of the IPK potato genebank (GL-KS) at different levels relying on national and international collaborations. This work will address not only the tuber-based clonally propagated collection but also on the long term the seed-based wild relatives. This will be developed in the POMORROW project (BMFTR, 2025-2028). Further, the group will pursue its work in the PotatoPredict project and elaborate new modelling strategies for genotype*environment predictions.





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

Heads: Prof. Dr. Andreas Börner /
Dr. Anna Backhaus

Mission

The research group is responsible for the management of the Gatersleben genebank collection, which entails the long-term storage, regeneration, and distribution of the germplasm comprising a wide spectrum of ca. 300 different crop species. Central to the group's research is how this unique plant diversity can be preserved and utilised more accurately, efficiently, and widely. Especially the access to and use of crop wild relatives is currently limited by a lack of genomic and phenotypic data, as well as the costly and technically challenging transfer of genetic information between these and cultivated species. The group investigates how modern genetic tools can be leveraged to unlock beneficial genes from thus far untapped genepools. The long-term goal is to identify and transfer genetic factors that will contribute novel traits to future climate resilient crops. Until August 2025, the group worked on comprehensive phenotypic evaluation and genetic characterisation of agronomic traits, as well as seed longevity, in cereals and legumes. While the work on legumes, in particular lupins, beans, lentils, and peas will continue, the research on seed longevity will be wound down.

Results

The collection of the IPK Genebank maintained in Gatersleben comprises over 130,000 samples. Safety duplicates located in the Global Seed Vault in Svalbard are available for 69,673 accessions (about 47 % of the whole collection). As part of the routine activities, germination tests have been performed for 18,748 accessions and circa 20,000 accessions have been distributed yearly. About 7,000 accessions per season were grown for regeneration, evaluation, demonstration and research. Furthermore, a collection of about 1,000 Allium species has been comprised out of the genebank and taxonomic collections and these have been translocated to a new field site. At any moment, circa another 100 perennial species are maintained in the permanent crop garden.

Studies on seed longevity were continued. Seeds of five agriculturally relevant legume species (*Phaseolus vulgaris* L., *Lathyrus sativus* L., *Cicer arietinum* L., *Pisum sativum* L., and *Vicia faba* L.), stored at different conditions (room temperature or -18 °C) for several years, were analysed using a LIANA© prototype to collect data regarding ultra-weak photon emission and delayed luminescence after UV excitation (Figure 1). The obtained data were integrated with germination parameters which underline species-specific behaviours in response to storage conditions. The prediction models show variable efficiency in classifying seeds based on germination which underline species-dependent links between photon emission and seed quality. Therefore, these measurements represent novel, non-invasive, and rapid approaches to evaluate seed quality.

Research to improve the utilisation of genebank collections is focused on agronomic traits of cereals. The two key traits grain protein content (GPC) and thousand kernel weight (TKW) were investigated across 179 contemporary and historic varieties and landraces across three growing seasons. Significant phenotypic variation existed for both traits among genotypes and seasons, and no discernible difference was evident between the old and modern accessiFons. To understand the genetic basis of the traits, we conducted a genome-wide association study using genotypic data from the 25K Infinium iSelect array. As a result, we detected 16 quantitative trait nucleotides (QTNs) associated with GPC and 15 associated with TKW. While some loci confirmed previously published associations, four QTNs linked to GPC on chromosomes 2A, 7A, and 7B, as well as two QTNs related to TKW on chromosomes 1B and 6A, may represent novel associations. Annotations for proteins involved in the senescence-associated nutrient remobilization and in the following build-up of resources required for seed germination have been found for selected putative candidate genes.

Selected publications

Griffo A et al. (2024) Non-invasive methods to assess seed quality based on ultra-weak photon emission and delayed luminescence. ***Sci. Rep.*** 14: 26838.

Schierenbeck M et al. (2024) Natural allelic variation confers diversity in the regulation of flag leaf traits in wheat. ***Sci. Rep.*** 14: 13316.

Griffo A et al. (2025) Application of machine learning models for non-invasive seed quality detection. ***Curr. Plant Biol.*** 44: 100557.

Puchta-Jasińska M et al. (2025) Comprehensive profiling of the miRNome and degradome reveals regulatory signatures of seed aging and germination. ***Int. J. Mol. Sci.*** 26: 9292.

Zhang H et al. (2024) Optimization of Genotyping-by-Sequencing (GBS) for germplasm fingerprinting and trait mapping in faba bean. ***Legume Sci.*** 6: e254.

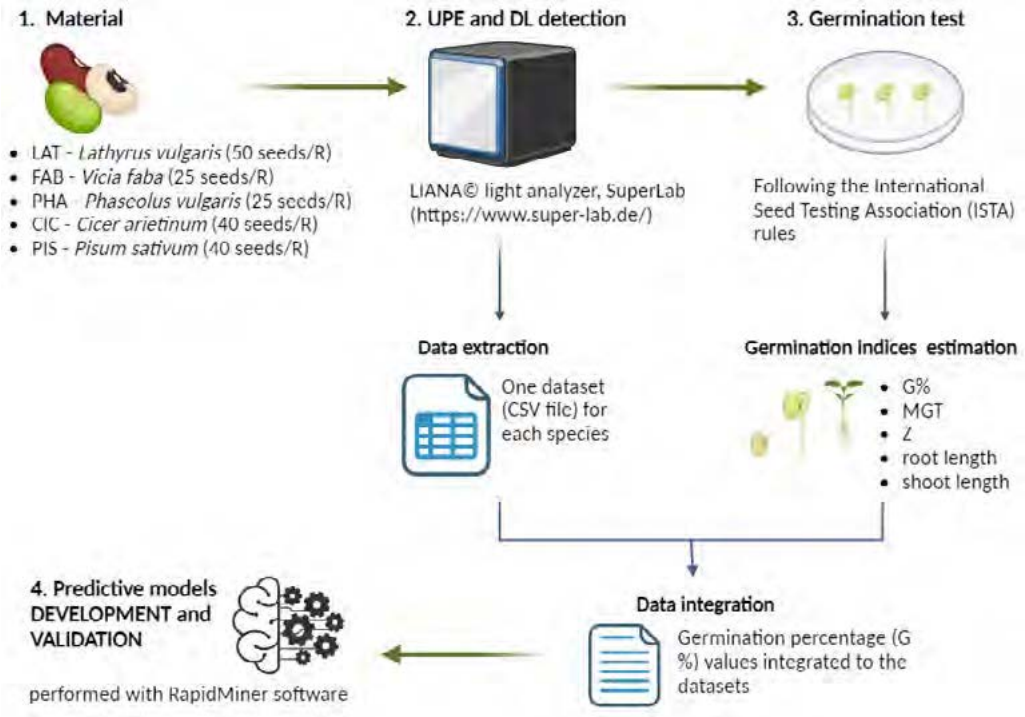


Figure 1: *Schematic representation of the experimental system. Multiple accessions of seeds of five legume species stored at room temperature (Ambient) or -18 °C (Cold) for more than ten years were ordered in different biological replicates based on their size. The replicates were analysed with the LIANA© light analyser and subsequently used for germination test.*

Embedding in IPK Research Themes

The experimental work in 2024/2025 belonged to the IPK Research Theme 1: "Activating Genetic Diversity", in collaboration with other research groups within and outside the Genebank department. While Research Theme 1 will remain at the centre of all activities, we will also interact with Research Theme 3 ("Mechanisms of Plant Reproduction") in the future.

Outlook

With the appointment of a new lead of the group RGR, Dr. Anna E. Backhaus, the main priority for the research group RGR will be to redirect and refocus research activities while keeping an internationally competitive and recognised research profile. This will partly rely on strategic collaborations with the OneCGIAR, Crop Trust, and national partners, such as CEPLAS.

RGR is dedicated to keep up the visibility of IPK genebank as a leader in high-quality management of PGRFA, supported by continuous innovation flow into the genebank collection management.

A major focus will be initiated on establishing innovation for the transfer of useful allelic diversity from barley's secondary gene pool, *Hordeum bulbosum*, to cultivated barley (*Hordeum vulgare* ssp. *vulgare*). A limited set of introgressions obtained in the 1980s is available, comprising multiple unique biotic stress resistance genes already discovered among the derived accessions. Methods and protocols are being optimised and new triploid hybrids have been obtained. As these are being back-crossed, we establish molecular marker-based screening protocols for cheap and fast introgression tracking. Furthermore, we established a comprehensive collection of *Bulbosum* plants at IPK, allowing us to phenotype within species diversity for unique traits such as biotic resistances, bulb formation, and perennialism, but also crossabiltiy with *Hordeum vulgare*.



RESEARCH GROUP **CRYO AND STRESS BIOLOGY** (CSB)

Head: Dr. habil. Manuela Nagel

Mission

The CSB group is an integrative part of the Federal *Ex situ* Gene Bank (Figure 1) and responsible for the medium-term conservation and distribution of 236 *in vitro* accessions of mint, Brassica and Antirrhinum, as well as the long-term cryopreservation of one of the world's largest cryo-collections with 2,569 (updated November 2025) clonally propagated potato, mint and Allium accessions. In recent years, the cryo-collection has been reorganized and stored in triplicate, with two sets housed at Gatersleben and one at the half-automated tanks at DSMZ in Braunschweig. This strategic approach has significantly increased the overall data and sample security level of the cryo-collection. Furthermore, ongoing research projects on chloroplast development and endophytic microorganisms during cryopreservation, as well as the characterisation and evaluation of Allium accession including duplicate identification are crucial components of the CSB mission to ensure the long-term preservation of clonal crops.

Results

Impact of endophytes during potato cryopreservation (DFG PotEND)

Endophytic microorganisms significantly influence the regrowth performance of shoot tips after cryopreservation. To elucidate the specific plant-endophyte relationship following potato cryopreservation, RNA was extracted from 382 accessions with high and low regrowth potential, and endophytic bacterial diversity was mapped in collaboration with the AIT (Austria). The 16S rRNA fragment amplicon sequencing revealed that potato accessions with high bacterial relative abundance belonged to groups with low or no regrowth potential, with the most abundant types in the low regrowth accessions being the bacteria order Micrococcales. To modulate the endophytic biome, 52 bacterial isolates were obtained from *in vitro* cultures of potato accessions rewarmed after cryopreservation. Based on siderophore, auxin, and ACC deaminase synthesis, phosphate solubilization, and potential osmolyte production, four strains were selected and inoculated onto four potato accessions, two with low regrowth after cryopreservation and two with high regrowth after cryopreservation. Notably, experimental inoculation of potato explants led to a decrease or complete inhibition of regrowth after cryopreservation, indicating that the abundance of microorganisms is generally detrimental and that interactions between accessions and microbiota are highly specific.

Importance of chloroplast abundance for cryopreservation

High regrowth of shoot tips after cryopreservation is dependent on the tolerance towards multiple stress conditions, including dehydration, that are exposed during cryopreservation. Given that most organelles of the vegetative tissue are highly desiccation-sensitive, particularly chloroplasts and their developmental stage play important role for regrowth. To investigate this further, we used duckweed fronds as a model and reduced the number of mature chloroplasts by pre-cultivating fronds of Lemna japonica on glucose-containing nutrition media and under limitation of light. This approach resulted in increased regrowth after cryopreservation. The importance of the photosynthetic apparatus and chloroplast development will be further investigated.

Conservation strategy for European garlic (ECPGR Garli-CCS)

Garlic is an important crop in Europe, with approximately 3,200 accessions maintained in European field genebanks. The project aimed to develop an efficient conservation strategy for European garlic accessions. Therefore, DNA was extracted from 2,434 garlic accessions from 16 European and one international genebanks and genotyping-by-sequencing (GBS) applied. From the 2,493 DNA samples, 122 million SNPs were generated and distributed across the eight garlic chromosomes. Preliminary phylogenetic analysis, principal component analysis (PCA), and model-based clustering analysis revealed six clusters that correspond to the six infraspecific Allium sativum groups: Longi-

Selected publications

Hojsgaard D et al. (2024) New frontiers in potato breeding: tinkering with reproductive genes and apomixis. ***Biomolecules*** 14: 614.

Nagel M et al. (2024) Plant cryopreservation: principles, applications, and challenges of banking plant diversity at ultralow temperatures. ***Annu. Rev. Plant Biol.*** 75: 797-824.

Martín C et al. (2025) Genetic and epigenetic fidelity of garlic cryopreserved plant material compared to field collections. ***Sci. Hortic.*** 345: 114132.

Weise S et al. (2025) The German Federal Ex Situ Genebank for Agricultural and Horticultural Crops – Conservation, exploitation and steps towards a bio-digital resource centre. ***Genetic Resources*** S2: 91-105.

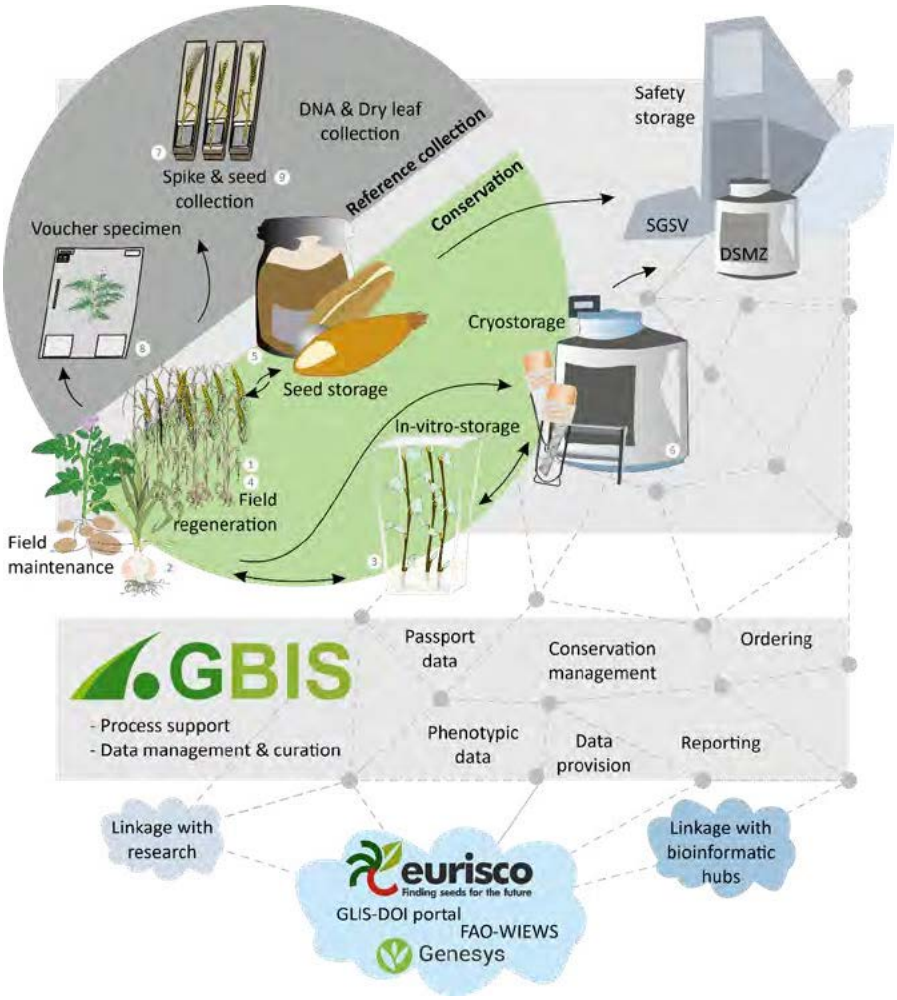


Figure 1: *Integrative genebank management for conservation of seed and clonal accessions including safety storage of seeds at the Svalbard Global Seed Vault (SGSV) and of cryosamples at the German Collection of Microorganisms and Cell Cultures (DSMZ). Arrows indicate the direction of the main workflows. The Genebank Information System (GBIS) provides process support including management and curation of data, allowing users to specifically select and order material, and is linked to international information systems, bioinformatics hubs and research projects. 1,2,4 Regeneration of seed and clonal accessions in the fields of Gatersleben, Groß Lüsewitz and Malchow/Poel; 3, In vitro slow-growth storage of potato (Solanum tuberosum L.) in Groß Lüsewitz; 5, Active and basic seed storage in Gatersleben and Malchow/Poel; 6, Long-term cryostorage of clonal accessions; 7, Spike reference collection; 8, Voucher specimen (IPK Herbarium); 9, Seed reference collection in Gatersleben. Source: Weise et al. (2025) https://doi.org/10.46265/genresj.GYDY5145*

cuspis, Pekinense, Ophioscorodon, Subtropical, Sativum bolting, and Sativum non-bolting. A preliminary Identity-by-State (IBS) analysis identified approximately 16% of the total samples as potential duplicates. Additionally, phenotypic data for 1,731 garlic accessions were provided and will be utilised for quantitative genetic analysis. As final outcome, all data are used to prioritise important genotypes for cryopreservation, to create a European garlic core collection with a centralized access point for garlic breeders and researchers and to develop a conservation strategy ensuring the long-term conservation and utilisation of European garlic accessions.

Embedding in IPK Research Themes

The research activities of members of Cryo and Stress Biology group comprise the two IPK Research Themes 1 “Activating Genetic Diversity” (conservation strategies for garlic and microbiomes of potato), and 5 “Enhancing Plant Shoot Performance” (investigations of complex stresses during cryopreservation). We actively collaborate with various IPK research groups (HET, MD, PBP, SZB, MPE, CSF) coordinate material exchange, field multiplication and data management for securing and cryopreserving vegetatively propagated accessions (RGR, TEN, DOK, DG).

Outlook

The significance of cryopreservation has increased in the last years. Due to the high cost efficacy, genetic stability and survival of material compared to field or *in vitro* preservation, plant cryopreservation will become even more important in the future. For this reason, the CSB will provide further cryopreservation training for European and international guests and scientists, which is also supported from the ECPGR network. In addition, integrative conservation management of garlic genetic resources will be discussed within ECPGR community and will support the decision-making process at IPK. Overall, the challenge is to balance genebank services, training workshops, and important research activities. We plan to continue research on the principles of cryopreservation, including the role of endophytes, chloroplasts, specific genes, and transcription factors during cryopreservation in various species.



RESEARCH GROUP **SATELLITE COLLECTIONS NORTH – DIVERSITY AND COLLECTION MANAGEMENT** (TEN)

Head: Dr. Klaus J. Dehmer

Mission

The Satellite Collections North (TEN) maintain plant genetic resources of potatoes, oil and forage crops at IPK's Gross Luesewitz and Malchow/Poel sites. Our research aims at the adding value to the collections by characterising genetic diversity, resistance/tolerance to diseases and drought, the content of valuable ingredients, and nutrient use efficiency. In respect to traditional genebank work, TEN is responsible for the collection, preservation, characterisation, evaluation, documentation and distribution of seeds, tubers or *in vitro* plantlets (with corresponding data) of more than 21,000 accessions.

Results

Phenotyping and genotyping in forage legumes, grasses and potatoes

Seed treatment with cold atmospheric plasma (CAP) did not lead to significantly increased germination rates in different accessions and seed lots of *Poa pratensis* and *Trifolium pratense*, although germination speed was increased to a certain degree. Therefore, CAP cannot be used in genebank management as standard operating procedure for increasing germination rates.

Drought stress response within perennial ryegrass (*Lolium perenne*) accessions was found to be variable per plant. After two years growth in a rain-out shelter, accessions previously considered as tolerant recovered overall stronger after drought stress periods.

GBS genotyping of all 1,236 entries of IPK's *Medicago* collection provided one of the first genus-wide insights into the genetic relationships between cultivated and wild species. Distinct clusters corresponded mostly to sections within the genus and separated the cultivated crop species *M. sativa* and *M.* x *varia* together with their progenitor species *M. falcata* from the wild species. This study provides valuable insights for genebank management. Screening of diverse alfalfa entries in respect to phosphorus efficiency and field performance revealed a high variation for biomass formation.

Hydroponics-based screenings of 225 table potato accessions for both nitrogen (N) and phosphorus (P) efficiency revealed a large variation for both traits. In respect to N, a good correlation to yield in field trials could be shown. In general, especially genotypes from the Andean subcollection of the Gross Luesewitz potato collections (GLKS) displayed high efficiencies (Figure 1 left, green columns), while regarding P uptake efficiency, accessions from the cultivated potato subcollection were also among the best performers (Figure 1 right, orange columns).

Collection management and enhanced evaluations

At Gross Luesewitz, the collections contain 6,357 accessions from 140 tuber bearing *Solanum* species. At Malchow/Poel, 15,230 oil and forage crop entries from 20 genera and 134 species are maintained.

In 2024 and 2025, material from 2,836 accessions was provided to 162 users. Germination rates were determined for 8,646 seed lots, and 15,034 or 83% of the seed propagated accessions are saved at the Svalbard Global Seed Vault. 2,072 potato accessions are cryopreserved at Gatersleben (cooperation with CSB Group).

1,717 accessions were regenerated. At Malchow, C&E data were collected for 994 entries. Potato accessions were evaluated for *Globodera pallida* (11 accs./70 genotypes) and potato wart resistance (128 accs.), as well as for tuber dormancy (271 accs.).

Selected publications

Hu Y et al. (2024) Assessment of inter- and intraspecific P efficiency in forage legumes as affected by recycling fertiliser. ***Agronomy*** 14: 901.

Bachmann-Pfabe* S, Kavka* M et al. (2025) Phenotypic traits in natural perennial ryegrass populations and relations to climate conditions at sites of origins across Europe. ***Genetic Resources*** 6: 99-114.

Hazarika M et al. (2025) Phenotypic variability and genome-wide association studies in potato (*Solanum tuberosum* L.) for phosphorus efficiency. ***BMC Plant Biol.*** 25: 1012.

Kavka M et al. (2025) Influence of cold atmospheric pressure plasma treatment on germination and plant biomass of *Trifolium pratense* L. ***PLoS One*** 20: e0332166.

Sun H et al. (2025) The phased pan-genome of tetraploid European potato. ***Nature*** 642: 389-397.

** Joint first authorship*

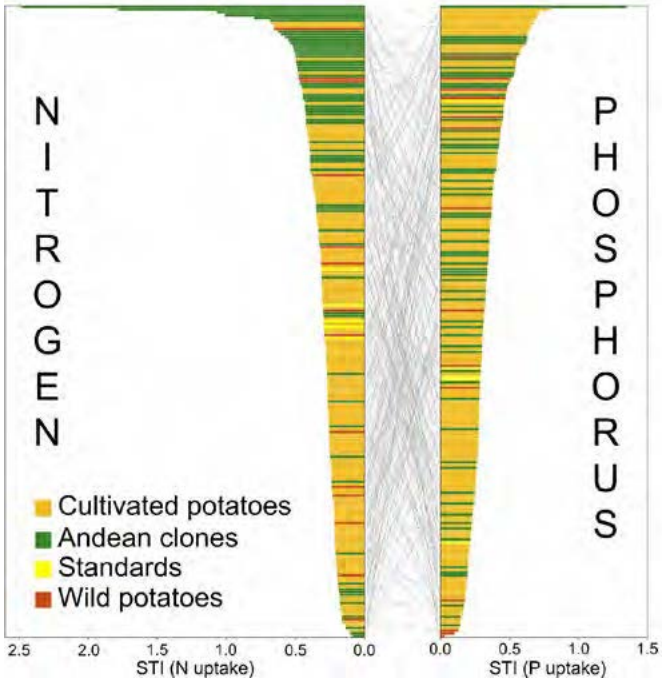


Figure 1: *Stress tolerance indices (STI) for N (left) and P uptake efficiency (right) for 225 GLKS entries plus correlating lines between both traits of the individual genotypes.*

Embedding in IPK Research Themes

TEN contributes to both the research and the service work areas of the Genebank department. Our activities perfectly integrate into the characterisation & evaluation area of the department. Focusing on potatoes, oil and forage crops, TEN oversees the maintenance of almost 15% of all IPK Genebank accessions. During their regeneration and/or multiplication, our accessions are characterised for all relevant crop descriptors. In third-party funded projects and in cooperation with external partners, evaluations are being conducted and documented within IPK's GBIS database. By focusing on general and functional diversity in its potato, oil crop and forage collections and by providing the respective data via GBIS to its users, TEN research feeds into the IPK Research Theme 1 "Activating Genetic Diversity".

Outlook

Within the POMORROW project, the entire GLKS collections will be genotyped by sequencing at IPK, with the generated GBS data being used for the establishment of a representative POMORROW core collection. The latter will be screened by POMORROW partners for agronomically relevant traits. Here, TEN will focus on nutrient efficiency. Besides, further TEN entries will be phenotyped for drought tolerance. *In vitro* and seed management will be improved continuously. Combined with our ISO 9001 quality management, this will further ensure high-quality material being delivered to our users. Safe guarding a sustainable conservation management, the TEN infrastructures at Malchow plus the Gross Luesewitz greenhouse were substantially modernised in 2023. A similar improvement of the office and laboratory building at Gross Luesewitz is still pending. These measures, however, will warrant a continued high-quality conservation of PGR and permit an intensified, application-oriented research.



RESEARCH GROUP **EXPERIMENTAL TAXONOMY** (ETX)

Head: Dr. Frank Blattner

Mission

The working group focuses on the phylogenetic classification and evolution of crops and their wild relatives. We use experimental studies to link molecular markers and phylogenetic data with ecological, 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 nomenclatural suitable treatments of crops and their wild relatives. These latter tasks together with running projects in the genus Crocus (under lead of Dr. Dörte Harpke) were transferred to the Domestication Genomics group after Frank Blattner retired in summer 2025 and ETX was closed.

Results

In Hordeum we clarified the evolution of *Hordeum bulbosum*, the closest relative of barley (*H. vulgare*). Based on our collections in the Mediterranean together with genebank materials for western Asian tetraploid cytotypes, phylogeographic and population genetic analyses laid the groundwork to identify samples representative for the species. They were used in a haplotype-resolved pangenome analysis of *H. bulbosum* (Feng *et al.* 2025). A surprising outcome of the population genetic analyses was the strong differentiation that Libyan genotypes showed in comparison to all other populations of the species, and that these Libyan diploids contributed extensively to the initial formation of autotetraploids. This tetraploid cytotype was afterwards introgressed from diploids in certain geographic areas when they came into contact. Moreover, in the Greek Peloponnese we could identify a second and independent formation of tetraploids from local diploids and show their merging with the stock of older tetraploids from this area. This research was part of an IPK flagship project conducted together with the research groups Domestication Genomics, Genomics of Genetic Resources, and Chromosome Structure and Function.

Chromosome-number changes play a fundamental role in plant evolution, yet the mechanisms linking whole-genome duplication (WGD), genome restructuring, and dysploidy remain poorly understood. Crocuses exhibit exceptionally diverse chromosome numbers and karyotypes even within closely related species. Within the framework of the DFG-funded project (Project number: 465449547; 04/2022-08/2025), we demonstrated that extreme chromosome-number reduction in the genus Crocus is tightly linked to WGD and subsequent genome restructuring. By generating long-read genome assemblies from key lineages and analysing duplicated genes, we identified one WGD preceding the diversification of *Crocus* and additional nested WGDs later in its evolution. We further showed that these WGDs triggered lineage-specific repeat bursts, consistent with a shared repeat "library" hypothesis. Comparative repeatome analyses based on low-coverage short read genome skimming data of c. 200 individuals, anchored in a robust phylogeny, allowed us to link repeat dynamics to chromosome rearrangements underlying descending dysploidy (Figure 1). Overall, we aimed to unravel *Crocus* chromosome evolution, clarify the role of dysploidy in plant diversification, and establish the genus as a model for mechanisms regulating dysploidy in monocentric plants. The project is continued under the lead of Nomar E. Waminal (DFG own position; project number 559280114). There, we aim to determine whether WGD is required for repeat bursts and cladogenesis in Crocus or whether similar patterns of diversification can arise without it, to identify specific repeats or chromosomal regions that predispose chromosomes to descending dysploidy, and to evaluate the extent to which dysploid chromosome changes contribute to reproductive isolation.

From our international network of *Crocus* researchers, Almila Ciftci (University of Istanbul, Turkiye) and Andrija Bogdanovic (University of Niš, Serbia) visited the working group in the reporting period to conduct shared research and learn NGS and cytogenetic analyses, which they now implement in their home universities. Results out of these cooperations contribute to the taxonomic revision of Crocus, where the first volume is now nearly finished.

Selected publications

Maylandt C et al. (2024) Phylogeography of the Euro-Siberian steppe plant *Astragalus austriacus*: Late Pleistocene climate fluctuations fuelled formation and expansion of two main lineages from a Pontic-Pannonian area of origin. ***Perspect. Plant Ecol. Evol. Syst.*** 64: 125800.

Nemati Z et al. (2024) Metabolomic and transcriptomic analyses of yellow-flowered crocuses to infer alternative sources of saffron metabolites. ***BMC Plant Biol.*** 24: 369.

Ala N et al. (2025) Phylogenomics of Western Eurasian *Tilia*: merging GBS datasets to place the Hyrcanian forest limes. ***BMC Plant Biol.*** 25: 1370.

Feng J-W et al. (2025) A haplotype-resolved pangenome of the barley wild relative *Hordeum bulbosum*. ***Nature*** 645: 429-438.

Herklotz V et al. (2025) Bimodal centromeres in pentaploid dogroses shed light on their unique meiosis. ***Nature*** 643: 148-157.

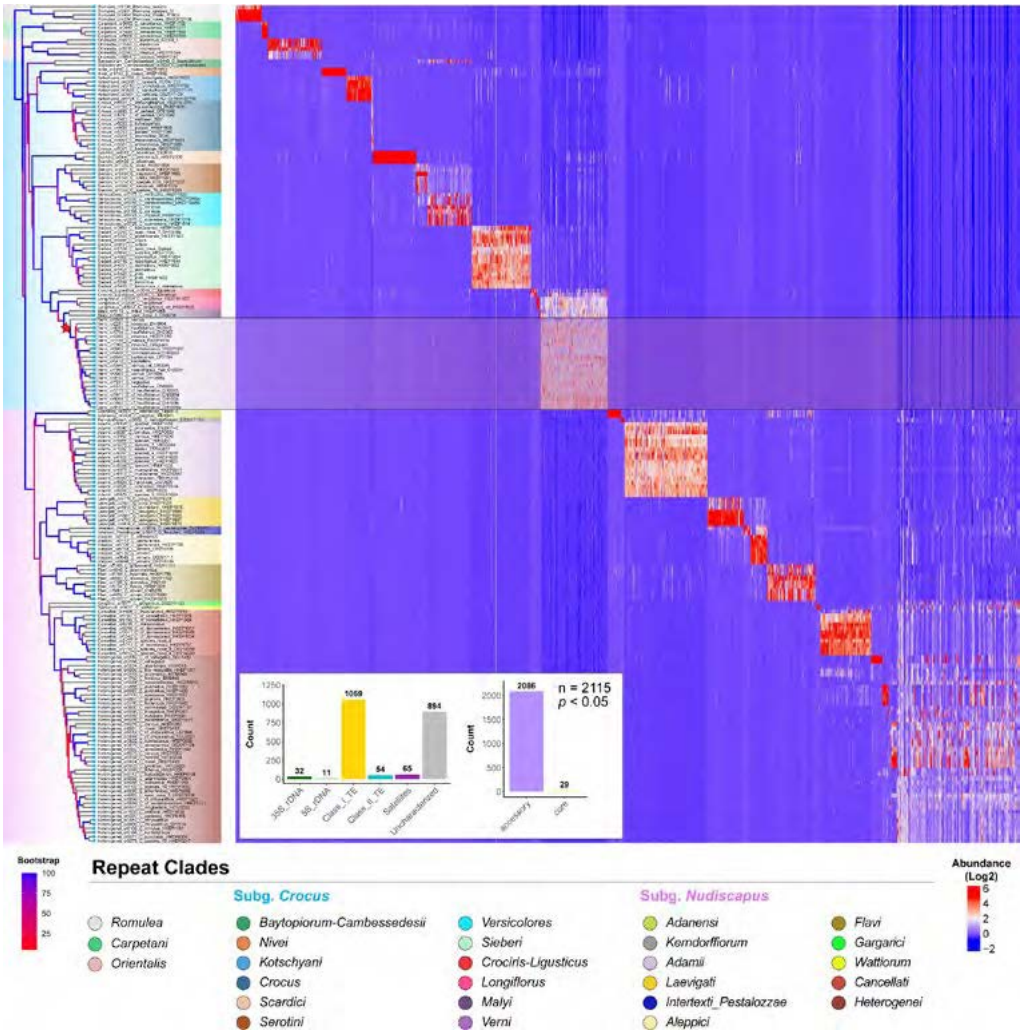


Figure 1: *The Crocus panrepeatome analysis showed phylogenetic signal of repeat dynamics. The shared dynamics of repeats among closely related taxa indicate shared evolutionary trajectory.*

Another cooperation with colleagues from Iran resulted in a re-evaluation of the limes occurring in the Hyrcanian Forest biodiversity hotspot of northern Iran. Here between one and seven *Tilia* species were assumed to occur. Our analyses showed that all *Tilia* populations of this area belong to just one species, *T. dasystyla*, and that the Hyrcanian Forest was, in contrast to many other taxa, no ice-age refugium for the European limes.

The herbarium of the IPK currently holds a collection of about 450,000 specimens, 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 mostly of reference materials of genebank accessions and for individuals with published sequence data, 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 is going on (79053 scans).

Embedding in IPK Research Themes

Our work is mostly connected to Research Theme 1 "Activating Genetic Diversity". Here we contributed to the IPK flagship project on the evolution of Hordeum bulbosum, the international pan-Hordeum project, the ERC project on phylogenomics of the genus Hordeum, and cooperate closely with the cytogenetics groups regarding karyotype evolution.
Our project on karyotype evolution in crocuses focusing on understanding the mechanisms linking WGD, genome restructuring, and dysploidy is also connected to Research Theme 3 "Engineering Genomes and Chromosomes".

Outlook

No plans, as the group was terminated in 2025.



RESEARCH GROUP **DOMESTICATION GENOMICS** (DG)

Head: Dr. Martin Mascher

Mission

The research group Domestication Genomics studies how domestication and adaptation have shaped genetic diversity in crops and their wild relatives. Our main research systems are the temperate cereals barley, wheat, rye and oats, complemented by selected grain legumes. Our research goals are: (i) to clarify the relationship between crops and their progenitors and wild relatives; (ii) to trace the demographic trajectories of crops as they moved from their centres of origin into Europe and beyond; and (iii) to understand the molecular consequences of domestication and adaptation on patterns of sequence diversity, gene expression and gene regulation. We apply methods of population genetics, genome informatics and functional genomics. A central component of our work is the development of (pan-)genomic and transcriptomic resources that enable comparative analyses across species and ploidy levels and provide long-term value to the research and breeding communities.

Results

Over the reporting period, the Domestication Genomics group has established pangenomics as a central framework for understanding genome evolution, structural variation and adaptation in temperate cereals and their wild relatives. A major milestone was the completion of a high-resolution barley pangenome comprising long-read genome assemblies of 76 wild and domesticated accessions, complemented by short-read data from more than 1,300 genotypes. This resource substantially expands the catalogue of structural variants in barley and reveals extensive gene copy number variation at agronomically relevant loci. Case studies on disease resistance, plant architecture, grain traits and malting quality demonstrate that allelic diversity at structurally complex loci has played an important role in crop adaptation under agricultural selection.

Building on barley genomic resources developed in the past 15 years, we reconstructed key aspects of barley's evolutionary history using haplotype-based analyses of whole-genome sequences from modern genebank accessions and archaeological specimens. Our results support a model of prolonged pre-domestication cultivation in the Fertile Crescent, followed by repeated gene flow from diverse wild populations into domesticated lineages. The pronounced haplotype differentiation among barley populations provides new insights into the challenges of mapping adaptive loci and has direct implications for association studies and pre-breeding.

To unlock the potential of crop–wild introgressions, we generated a pangenome of Hordeum bulbosum, barley's closest wild relative, based on phased genome assemblies representing 32 haplotypes. Comparative analyses revealed multiple origins of autotetraploid cytotypes and extensive gene flow between ploidy levels. Differences in genome size between barley and H. bulbosum were traced to lineage-specific transposable element dynamics. The translational value of this resource was demonstrated by mapping non-host resistance to a viral pathogen to a structurally complex immune-related gene cluster.

At a broader evolutionary scale, we contributed to a genus-wide *Hordeum* pangenome based on chromosome-scale assemblies of all diploid species and selected tetraploids. This dataset uncovered large-scale structural rearrangements, deep interspecific hybridisation events, introgressions, and widespread horizontal gene transfer from other grass lineages. While protein-coding genes remain largely conserved, regulatory elements show rapid turnover, providing a substrate for phenotypic diversification.

Beyond barley, we coordinated the development of an oat (*Avena sativa*) pangenome comprising 33 chromosome-scale assemblies and a comprehensive atlas of gene expression across tissues, accessions and subgenomes. Analyses revealed how subgenome divergence constrains compensatory gene regulation and how recent chromosomal rearrangements have shaped elite oat breeding germplasm.

Selected publications

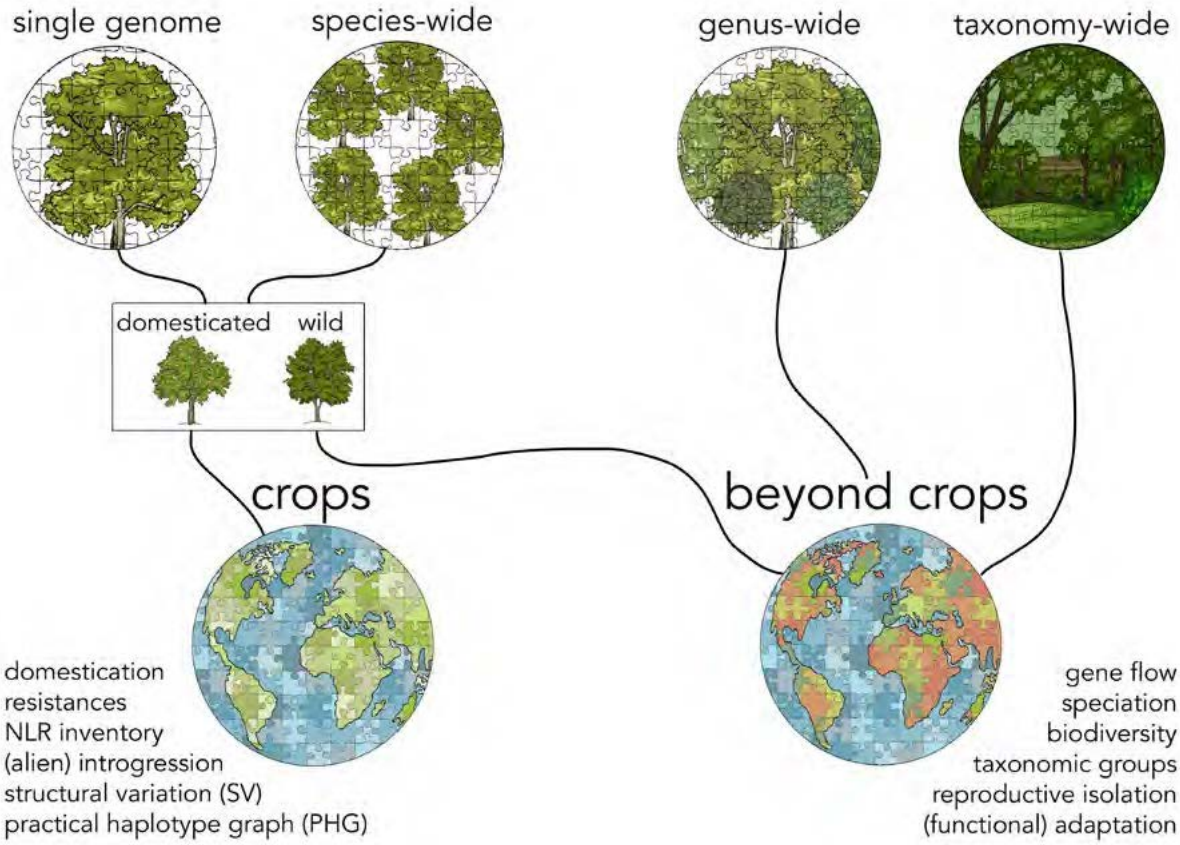
Jayakodi M et al. (2024) Structural variation in the pangenome of wild and domesticated barley. ***Nature*** 636: 654-662.

Mascher M et al. (2024) Promises and challenges of crop translational genomics. ***Nature*** 636: 585-593.

Schreiber M et al. (2024) Plant pangenomes for crop improvement, biodiversity and evolution. ***Nat. Rev. Genet.*** 25: 563-577.

Feng J-W et al. (2025) A haplotype-resolved pangenome of the barley wild relative *Hordeum bulbosum*. ***Nature*** 645: 429-438.

Guo Y et al. (2025) A haplotype-based evolutionary history of barley domestication. ***Nature*** 647: 680-688.



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Figure 1: *Pangenomics at different taxonomic levels. Reference sequences can be assembled for the genomes of both wild and domesticated plants. Diversity panels employed in pangenome studies may span different taxonomic levels, from single species to the tree of life. The term 'super-pangenome' is a useful shorthand to refer to pangenomics beyond the species level. Analysis methods differ according to whether the observed genomic variants segregate in a population of interfertile individuals or represent fixed differences between reproductively isolated species. Broadly speaking, intraspecific diversity fuels genetic mapping and breeding, whereas super-pangenomes hold answers to taxonomic and evolutionary questions. At higher taxonomic levels, taxon sampling cannot but look beyond crops, as the species that farmers attend to are in a minority.*

Embedding in IPK Research Themes

During the reporting period, our work focused on expanding pangenomic resources for cereals and extending these efforts towards genus-wide and cross-species comparative frameworks. These activities were tightly integrated with IPK-wide initiatives and carried out in close collaboration with the research groups GGR, ETX, RGR, BR and BIT, as well as with numerous national and international partners. In line with the IPK Research Strategy 2025–2030, our research directly contributes to Research Theme 1 (*Activating genetic diversity*) by systematically capturing and characterising genomic variation across crops and their wild relatives, and to Research Theme 2 (*Exploiting bio-digital plant data*) through the development of scalable pangenomic datasets, analytical pipelines and data infrastructures that enable downstream functional and translational research.

Outlook

Our future work will focus on consolidating pangenomics as a functional and translational framework for crop research. In barley and wheat, we will expand biological case studies that link structural variation to phenotype, in close collaboration with IPK partners. Together with the BIT group, we aim to develop computational tools and user-friendly interfaces that make complex pangenome resources broadly accessible. This work is supported by the BMFTR-funded PRBreed initiative.
Genebank genomics will be extended through deep whole-genome sequencing of additional representative accessions in wheat, barley and oat. These data will be used to refine models of crop evolution, identify underutilized diversity and support genomics-informed pre-breeding across institutions.

A major focus will be the systematic exploitation of crop wild relatives. We will develop a pan-transcriptome of the genus *Hordeum* and, in DFG-funded projects, establish pangenome resources for wheat wild relatives such as *Aegilops longissima* to accelerate resistance gene cloning.

In addition, the group will contribute comparative genomics expertise to emerging legume pangenome initiatives, including faba bean, pea and bitter vetch, supported by the BMFTR projects FABALOUS and DIPISUM.

A key challenge will be the integration and long-term sustainability of increasingly complex datasets across projects and partner institutions.



RESEARCH GROUP
GENETICS OF ENVIRONMENTAL ADAPTATION (GEA)

Head: Dr. Laura Dixon

Mission

The Genetics of Environmental Adaptation group was established in November 2024 and aims to identify, characterise and deploy allelic information to enable cereal crop adaptation to specific environmental signals. This can either be via targeted responses to the environment or through robustness to multiple conditions. To enable this understanding the research team uses naturally occurred adaptation in variety of cereal species with the aim of translating this understanding to cultivated cereals.

Results

We have completed a series of large phenotyping experiments which provide the foundation for the groups research activities. This includes a panel of near isogenic lines to aid identifying the genetic region underpinning our previously identified speed vernalization response. Regarding understanding the classic vernalization response, we conducted developmental phenotyping of transgenic *VRN2* under controlled conditions as well as in the small glasshouses and identified a further role for one of the *VRN2* genes. This has been supported through molecular analysis of the protein interactions of *VRN2*s and constructs have been developed for protein interaction assays and CRISPR knockouts in hexaploid wheat.

To understand the allelic requirements to control cereal developmental stages we have conducted a series of staggered vernalization experiments and have a staggered drill field trial underway. These results are being supported through marker development for all identified alleles in the major growth habit genes, gene expression profiling and germplasm development to answer specific hypothesis (Figure 1).

Multi-environment phenotyping was conducted splicing responses. This was supported through a multi-environment RNA-seq time-series. This data provides the basis for the molecular targets as well as understanding the role of temperature-mediated alternative splicing in seasonal responses. We have also started construct development for CRISPR lines in hexaploid wheat.

We have utilised the move to IPK to diversify the cereal species we research to enable the identification of the molecular components which underpin unusual but possibly useful developmental characteristics. We have started with the molecular genetic dissection of a perennial rye ("Mountain rye"). Here we have sequenced and assemble an example plant's genome, phenotyped a population and started to conduct hypothesis driven experiments relating to cold tolerance. This is in collaboration with the DG group and external collaborators in Australia and Denmark.

The second novel group species is *Hordeum bulbosum* where we are interested in understanding the role of the bulb structure in the plant's resilience to environmental challenges. We have conducted developmental time courses and microscope imaging, in collaboration with SZB, of bulb formation. We have also determined interesting bulbosum introgression lines (BILs) regarding flowering phenology.

Selected publications

*Gauley A et al. (2024) *Photoperiod-1* regulates the wheat inflorescence transcriptome to influence spikelet architecture and flowering time. ***Curr. Biol.*** 34: 2330-2343.

Gauley A et al. (2025) Fine tuning wheat development for the winter to spring transition. ***Plant Commun.*** 6: 101501.

Rohde A et al. (2025) New genomic resources to boost research in reproductive biology to enable cost-effective hybrid seed production. ***Plant Genome*** 18: e70092.

**This publication is based on work that has been carried out at the John Innes Centre, Norwich, UK and the University of Leeds, UK.*

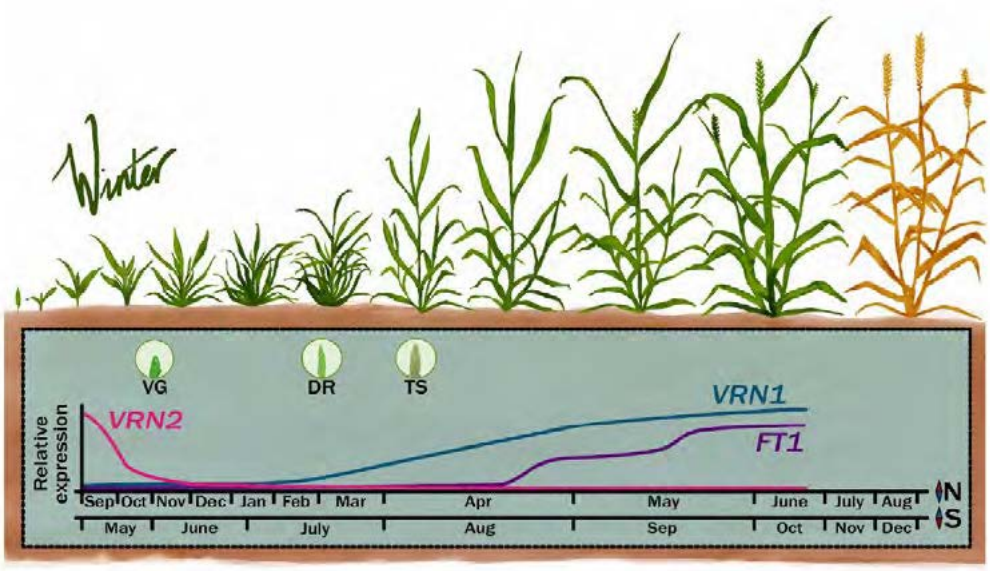


Figure 1: *Schematic showing the developmental timing of winter wheat under field conditions. The expression profiles of the three major vernalization genes are shown. VERNALIZATION 2 (VRN2; pink line) is repressed during autumn enabling the increase in expression of VRN1 (blue line) and FLOWERING LOCUS T (FT1; purple line) highlighting periods of major developmental changes which are not influenced by these genes. The inflorescence development stages are depicted above the expression profiles where VG = vegetative; DR = double ridge and TS = terminal spikelet.*

Embedding in the IPK research priorities

The GEA group links directly with IPKs research priorities of utilising genetic diversity through the generation of a bio-digital resource centre. The importance of enabling improved crop adaptation through understanding genetic diversity is a focus for IPK moving forward. GEA is a highly collaborative group and has already established collaborations within the Genebank department (DG, IGP and RGR) and more widely within IPK, including SZB, GPW and MPE.

Outlook

We will continue our molecular genetic dissection of the vernalization response in hexaploid wheat. We have advanced genetically refined germplasm to characterise the response and this will be conducted by a post-doc in the group. Specifically focusing on alleles which can be used to regulate developmental timing of the floral transition.

The second focus will be on identifying targets of temperature-mediated alternative splicing in hexaploid wheat. This will require establishing the bioinformatic pipelines required to robustly identify these rare events and use this as a tool to characterise the targets.

Finally, we will continue to develop germplasm to understand the targets for temperature and photoperiod signaling responses in wheat, mountain rye and *Hordeum bulbosum*.



BREEDING
RESEARCH

Quantitative Genetics (QG)
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

Plant Architecture (PBP)
Prof. Dr. Thorsten Schnurbusch

Young Investigator Group:
Agroecological Breeding (AB)
Dr. Samira El Hanafi

DEPARTMENT BREEDING RESEARCH



DEPARTMENT BREEDING RESEARCH

Head: Prof. Dr. Jochen C. Reif

Mission

The Breeding Research department advances knowledge and develops innovative approaches to exploit crop genetic diversity more effectively. Its research covers the entire breeding process, from creating genetic variation and selecting parental lines to identifying superior genotypes and maintaining elite varieties. While primarily focusing on major cereal species and legumes, the department also includes model species in its work, integrating breeding informatics, genome analysis and chromosome biology.

Research

Leveraging rapid advances in 'omics' technologies, the department's researchers are developing plant breeding data ecosystems to harness big data for predicting the performance of agriculturally important traits and unravelling their genetic architecture. This includes identifying, validating and analysing candidate genes for key traits such as inflorescence growth and development, and disease resistance. In-depth studies are being undertaken to assess genetic and epigenetic components relevant to the regulation of chromosome segregation and chromosomal regions, recombination manipulation, and genetic variation fixation by haploidisation. Research activities within the Breeding Research Department take place within the following research groups: Quantitative Genetics (QG), Bioinformatics and Information Technology (BIT), Chromosome Structure and Function (CSF), Kinetochore Biology (KB), Biotrophy and Immunity (BIM), Agroecological Breeding (AB) and Plant Architecture (PBP). The following scientific achievements are considered highlights for the 2024/25 period:

The genetic mechanism of B chromosome drive in rye illuminated by chromosome-scale assembly

The genomes of many plants, animals, and fungi often harbour dispensable B chromosomes that rely on various chromosomal drive mechanisms to counteract the tendency of non-essential genetic elements to be purged over time. The B chromosome of rye - a model system species for nearly a century - undergoes targeted nondisjunction during the first pollen mitosis, favouring segregation into the generative nucleus, thus increasing its numbers over generations. However, the genetic mechanisms underlying this process are poorly understood. Using a newly assembled, ~430 Mb-long rye B chromosome pseudomolecule, we identified five candidate genes whose roles as trans-acting moderators of the chromosomal drive are supported by karyotyping, chromosome-drive analysis, and comparative RNA-seq. The DCR28 gene family is a neo-functionalised, serially duplicated rye gene, with 15 B-located copies that are uniquely highly expressed during the first pollen mitosis. We show that DCR28 is a microtubule-associated protein involved in cell division (Figure 1; Chen *et al.*, 2024).

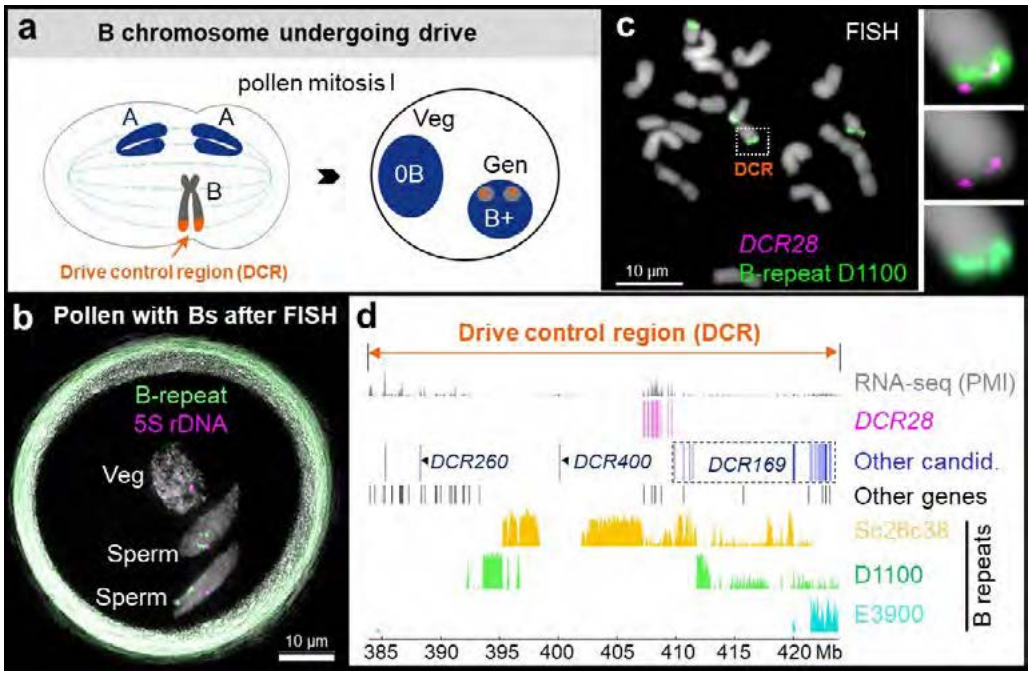


***Figure 1: The drive of the rye B chromosome (B)**. (a) Segregation behaviour of the B undergoing nondisjunction and accumulation in the generative nucleus during the first pollen mitosis. (b) Pollen-FISH combined with super-resolution microscopy to determine the distribution of Bs in mature pollen. (c) Mitotic metaphase of rye with Bs showing DCR28- and D1100-specific FISH signals. (d) The drive control region (383.9 to 423.8 Mb) of the B. The different tracks indicate: 1. expression of RNA-seq data from anthers undergoing the first pollen mitosis, 2. The DCR28 gene cluster, 3. other candidate genes in this region, 4. as well as genes that do not belong to the differentially expressed candidate list. The last three tracks show the distribution of the B-specific repeats Sc26c38, D1100, and E3900.*

Non-cell-autonomous signalling associated with barley ALOG1 specifies spikelet meristem determinacy.

Inflorescence architecture and crop productivity are often tightly coupled in our major cereal crops. However, the underlying genetic mechanisms controlling cereal inflorescence development remain poorly understood. Here, we identified recessive alleles of barley (*Hordeum vulgare* L.) HvALOG1 (*Arabidopsis thaliana* LSH1 and Oryza G1) that produce non-canonical extra spikelets and fused glumes abaxially to the central spikelet from the upper-mid portion until the tip of the inflorescence. Notably, we found that HvALOG1 exhibits a boundary-specific expression pattern that specifically excludes reproductive meristems, implying the involvement of previously proposed localised signalling centres for branch regulation. Importantly, during early spikelet formation, non-cell-autonomous signals associated with HvALOG1 expression may specify spikelet meristem determinacy, while boundary formation of floret organs appears to be coordinated in a cell-autonomous manner. Moreover, barley ALOG family members synergistically modulate inflorescence morphology, with HvALOG1 predominantly governing meristem maintenance and floral organ development. We further propose that spatiotemporal redundancies of expressed HvALOG members specifically in the basal inflorescence may be accountable for proper patterning of spikelet formation in mutant plants. Our research offers new perspectives on regulatory signalling roles of ALOG transcription factors during the development of reproductive meristems in cereal inflorescences (Figure 2; from Jiang *et al.*, 2024).

More yield through heterosis: Decoding gene interactions.

When two lines with distinct traits are crossed, their offspring often exhibit enhanced growth, yield and resilience, a phenomenon known as heterosis. Heterosis has long been exploited in crop breeding, but the underlying genetic mechanisms have remained poorly understood. Traditional approaches assumed that a few dominant genes were responsible for the performance boost. However, recent research reveals a more complex reality: heterosis is primarily driven not by individual genes, but by the coordinated interaction of numerous genes working together in a network. To reveal these hidden genetic relationships, a novel statistical method called hQTL-ODS was developed. Unlike conventional methods, which test gene combinations individually and often require years of computation, hQTL-ODS evaluates the collective influence of all genes simultaneously. This advancement enabled the analysis of over 5,000 wheat hybrids. The findings show that heterosis is not determined by a few strong genes, but by the cumulative effect of many weak gene interactions. These subtle signals are now detectable thanks to the advanced mathematical framework of hQTL-ODS, which is specifically designed for large-scale whole-genome sequencing data.

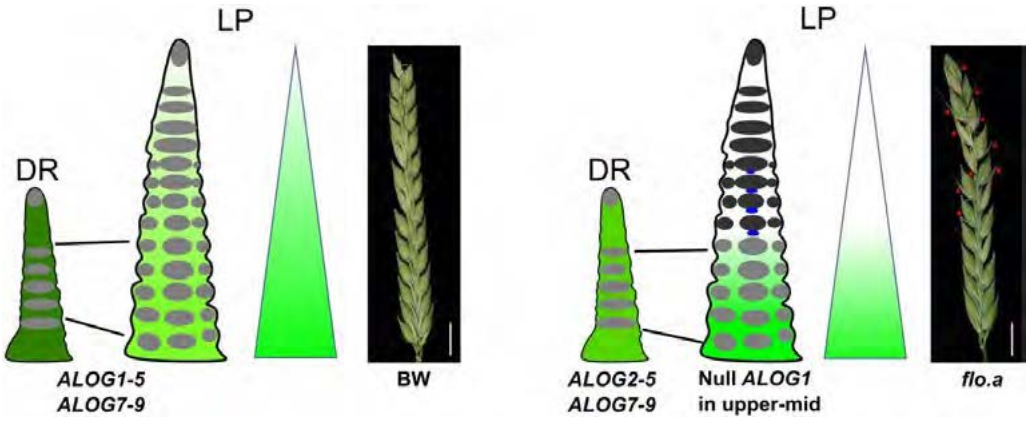


Figure 2: The proposed regulatory mechanism of ALOG family members for mediating spikelet mersitem determinacy. *Different degrees of green indicate expression levels of ALOG members in spike tissues. The red triangles indicate the additional spikelet events. Light and dark grey ovals represent unaffected and affected reproductive meristems, respectively. Blue ovals represent additional spikelet meristems. DR, double ridge; LP, lemma primordium. Scale bar, 1 cm.*

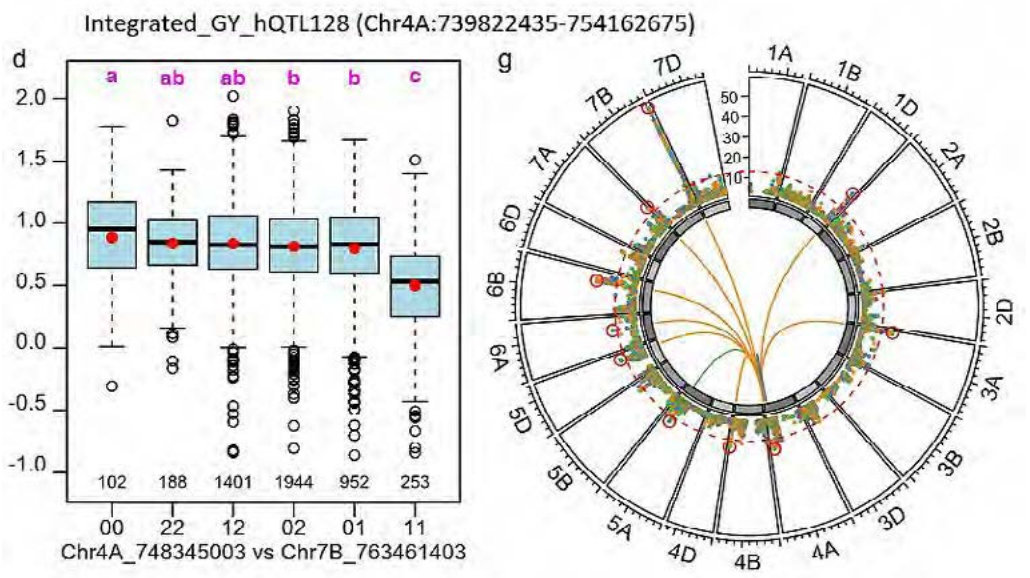


Figure 3: *Heterotic QTL detected for grain yield on chromosome 4A (Integrated_GY_hQTL128). The phenotypic distribution of grain yield MPH for hybrids with distinct genotype combinations of the peak SNP within hQTL and the SNP showing the most significant epistatic interaction effect with the peak SNP. Circled Manhattan plot of epistatic effects between the peak SNP of hQTL and all other SNPs.*

Outlook

The department is advancing crop data science by combining expertise in data management, genomics, and quantitative genetics. These activities benefit from national and international research infrastructures, such as NFDI4Biodiversity, FAIRagro, DataPLANT, de.NBI and ELIXIR, which are FAIR and AI-ready data ecosystems. Researchers are also addressing the genetic challenges posed by diverse cropping systems, including varietal and crop mixtures. The aim is to improve our understanding of plant–plant interactions, broad-spectrum resistance, and architectural traits, with the ultimate goal of enhancing resilience and yield. In parallel, cutting-edge studies on chromosomal biology, meiotic recombination and chromosome segregation are driving innovations in haploidisation.



RESEARCH GROUP
QUANTITATIVE GENETICS (QG)

Head: Prof. Dr. Jochen C. Reif

Mission

Agronomically relevant traits are often genetically complex and typically controlled by multiple genes that interact. The Quantitative Genetic's research group is exploring new approaches to elucidate the genetic architecture and predict complex agronomic traits, thereby facilitating omics-based (pre)breeding strategies and enhancing selection gain. Our model crops are wheat and pea, with other species such as barley, common bean, and Arabidopsis being used for specific research questions. With its expertise in biometrics, the research group provides support to other research groups at the IPK in the analysis of their data, with a focus on the implementation of complex statistical genomic approaches.

Results

Stronger Together

New data approach makes plant predictions more accurate. In its role as data trustee, the QG research group collaborated closely with the BIT research group to overcome data barriers across several wheat breeding companies. The result was a comprehensive training dataset comprising nearly 25,000 wheat lines and combining wheat trial data from over 12 years and 168 different environments (Figure 1). The research group used this data to enhance genome-wide predictions of traits such as grain yield, plant height and flowering time. Despite the differences in how the data was collected, advanced imputation techniques were employed to ensure the results were interoperable and of a high quality. This demonstrates that combining data from multiple sources can significantly enhance prediction accuracy. The researchers concluded that sharing data between companies is an effective way to unlock the full potential of big data and machine learning in breeding, paving the way for the faster development of better, more resilient varieties.

Heritable microbiome variation and local adaption.

The importance of beneficial interactions with microorganisms for crop performance and resilience is widely recognised. However, it has remained unclear to what extent the microbiome is heritable in relation to the host plant genotype, and how host genetic mechanisms can modulate plant–microbiota interactions under environmental stress. In cooperation with partners from the University of Bonn, a quantitative genetic toolbox was developed and applied to analyse 3,168 root and rhizosphere microbiome samples from 129 locally adapted Zea accessions, which were collected from diverse habitats and grown under control conditions and various stresses. The effects of stress treatment and host genotype on the microbiome were quantified, revealing that plant genotype and source environment predict microbiome abundance. Genome-wide association analysis identified host genetic variants associated with both rhizosphere microbiome abundance and source environment. In controlled experiments, transposon insertions in a candidate gene were found to be linked to the abundance of the keystone bacterium Massilia and to total soil nitrogen in the source environment. Isolating and controlling the inoculation of Massilia was shown to contribute to root development, whole-plant biomass production and adaptation to low nitrogen availability. It was concluded that locally adapted maize varieties exert genetic control over their root and rhizosphere microbiomes in a manner that corresponds to variation in their home environments, thereby supporting a role in stress tolerance.

Selected publications

Berkner MO et al. (2024) Genomic prediction reveals unexplored variation in grain protein and lysine content across a vast winter wheat genebank collection. ***Front. Plant Sci.*** 14: 1270298.

He* X, Wang* D, Jiang* Y, Li* M, Delgado-Baquerizo * M et al. (2024) Heritable microbiome variation is correlated with source environment in locally adapted maize varieties. ***Nat. Plants*** 10: 598-617.

Gogna A et al. (2025) Order from entropy: big data from FAIR data cohorts in the digital age of plant breeding. ***Theor. Appl. Genet.*** 138: 257.

Lell M et al. (2025) Breaking down data silos across companies to train genome-wide predictions: A feasibility study in wheat. ***Plant Biotechnol. J.*** 23: 2704-2719.

Li G et al. (2025) Powerful one-dimensional scan to detect heterotic quantitative trait loci. ***Nat. Commun.*** 16: 9697.

** Joint first authorship*

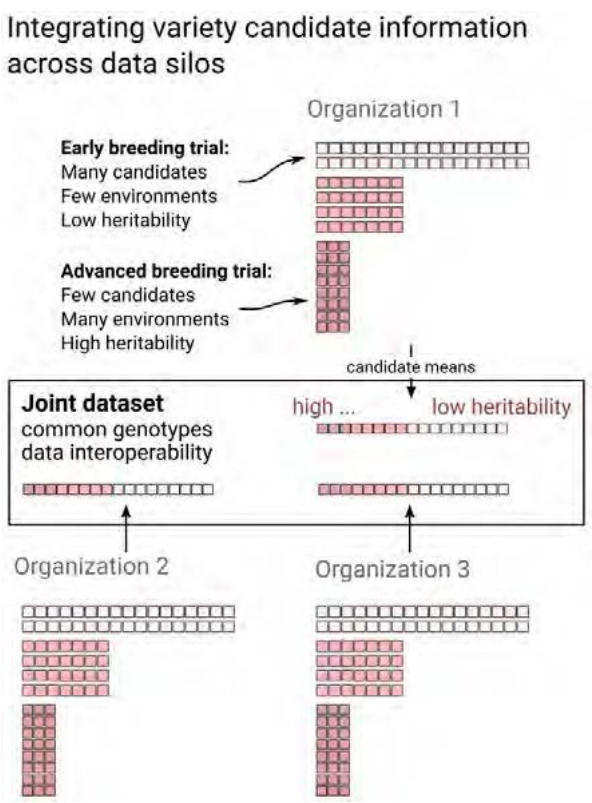


Figure 1: *By integrating data sources with an academic data trustee, more genotypes with high-quality observations can be used for performance prediction.*

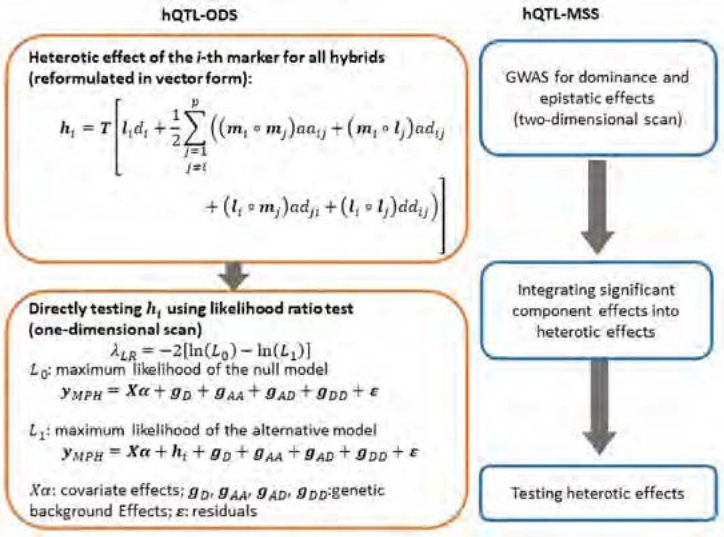


Figure 2: *Overview of the principle of the one-dimensional scan (hQTL-ODS) developed for heterotic QTL, compared to the existing multi-step approach (hQTL-MSS).*

New association mapping approach to map heterotic loci

The phenomenon of heterosis substantially increases yields in many crops, despite the underlying genetic basis being unclear. However, progress has been made over the last decade in describing this basis, leading to the development of a quantitative genetic framework that considers both dominance and epistasis effects to explain heterosis. Nevertheless, including all pairwise epistasis interactions are computationally challenging due to the extensive sequencing depth and population sizes required to identify the genes responsible for complex traits. In a pioneering study, the research group QG has developed a one-dimensional scanning method that directly evaluates the net contribution of each quantitative trait locus to heterosis (Figure 2). Simulations show that this hQTL-ODS approach, as it is known, reduces computation time while offering higher performance and a lower false positive rate. We have applied this method to a population of 5,243 wheat hybrids with sequenced whole-genome profiles, revealing important epistatic hubs that play a crucial role in determining heterosis.

Embedding in IPK Research Themes

The research of the RG QG contributes mainly to the Research theme 1 “Strategies for the Valorisation of Plant Genetic Resources”.

Outlook

Our goal is to investigate new approaches to elucidate the genetic architecture and predict complex agronomic traits. To achieve this objective, we propose leveraging the momentum to establish a wheat data hub that integrates genotypic, phenotypic, and environmental data, and explore in-depth utilisation of artificial intelligence. The resulting big data, combined with AI, has the potential to significantly enhance prediction ability, increase QTL detection power, and improve resolution, making it a crucial component of research theme 2 ‘Exploiting biodigital plant data’. Furthermore, we will continue to drive research on designing and testing new trait-targeted pre-breeding strategies, which is a key component of research theme 1 ‘Activating genetic diversity’.



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

Head: Dr. Uwe Scholz

Mission

BIT provides services alongside the research data life cycle. This includes stewardship, data process engineering, data housing and publication as well as software development to feature FAIR phenomics and genomics data. Highlights with impact are web applications for interactive data exploration and application programming interfaces (APIs), such as BrAPI. Furthermore, the group support scientists to publishing research data in compliance with standard formats (e.g. ISA-Tab) and description standards (e.g. MIAPPE). The group leads the Plant Bioinformatics Service Centre at the German ELIXIR node de.NBI and is co-applicant of the NFDI consortia FAIRagro, NFDI4Biodiversity, and DataPLANT.

Results

The results described in the following are a selection and represent the wide range of ongoing projects during the reporting period.

The Plant Genomics & Phenomics Research Data Repository (e!DAL-PGP) has developed successfully and is actively used (end of December 2025: 327 DOIs, accesses from more than 1.5 million unique IP addresses with a total download volume of 3.9 Petabyte). e!DAL-PGP provides FAIR access to datasets, which have been referenced in several research articles. A detailed overview of usage can be found at this website: https://doi.ipk-gatersleben.de/report.

In collaboration with the IPK research groups DG and GGR as well as the external partner from the HMGU Munich, the Crop Analysis Tool Suite – CATS (https://cats.ipk-gatersleben.de) is being actively managed and extended.

The CATS sub-tool IPK Galaxy Web Blast Server's data resources have been expanded to include pan-genomes from wheat, rye, vicia faba, oat, *Hordeum bulbosum* and various Hordeum species as well as the version 2 of the barley pan-genome.

MISA-web as another CATS tool continues to enjoy strong community adoption, with over 2,283 citations recorded on Google Scholar (accessed 30 December 2025).

Now CATS also provides the new PanBARLEX web portal (https://panbarlex.ipk-gatersleben.de) as a comprehensive resource of gene annotations of the barley pan-genome (see Figure1). It offers convenient access to gene annotations and orthologous gene groups of 76 different barley genotypes that together define a pangenome. The portal encompasses a total of 3,797,824 annotated genes and features versatile entry points, including the ability to locate genes by their IDs, conduct searches based on functional annotations and perform gene queries through a BLAST search. Additionally, reference-free synteny visualisations anchored by single-copy core genes and rendered with Bézier curves, as well as pan-proteome landscapes derived from ProtBERT embeddings projected via UMAP are available. All these features enable the identification of conserved syntenic blocks, rearrangements informed by presence–absence variations (PAVs), gene family clusters, and outliers for functional annotation.

In frame of BMFTR funded national research project INTEGRA, a CEPH objectstore with 5 nodes and more than 100TB for highly parallel operations was set up. The multi-layer object buckets were designed to implement FAIR digital objects by merging data and meta data and its universal access using the universal S3 protocol. This features a backend to serve HPC at BIT SLURM compute cluster for data analysis in high throughput phenotyping and genotyping applications.

Selected publications

Jayakodi M et al. (2024) Structural variation in the pangenome of wild and domesticated barley. ***Nature*** 636: 654-662.

König P et al. (2024) blast2galaxy: a CLI and Python API for BLAST+ and DIAMOND searches on Galaxy Servers. ***Bioinform. Adv.*** 4: vbae185.

Lück S, Scholz U, Douchkov D (2024) Introducing GWAStic: A user-friendly, cross-platform solution for genome-wide association studies and genomic prediction. ***Bioinform. Adv.*** 4: vbae177.

Schüler* D, Lange* M et al. (2025) Data management in balance – a decade of balancing pragmatism, sustainability and innovation at plant research center IPK Gatersleben. ***J. Integr. Bioinform.*** 22: 20250012.

Selby P et al. (2025) BrAPI v2: real-world applications for data integration and collaboration in the breeding and genetics community. ***Database*** 2025: baaf048.

** Joint first authorship*

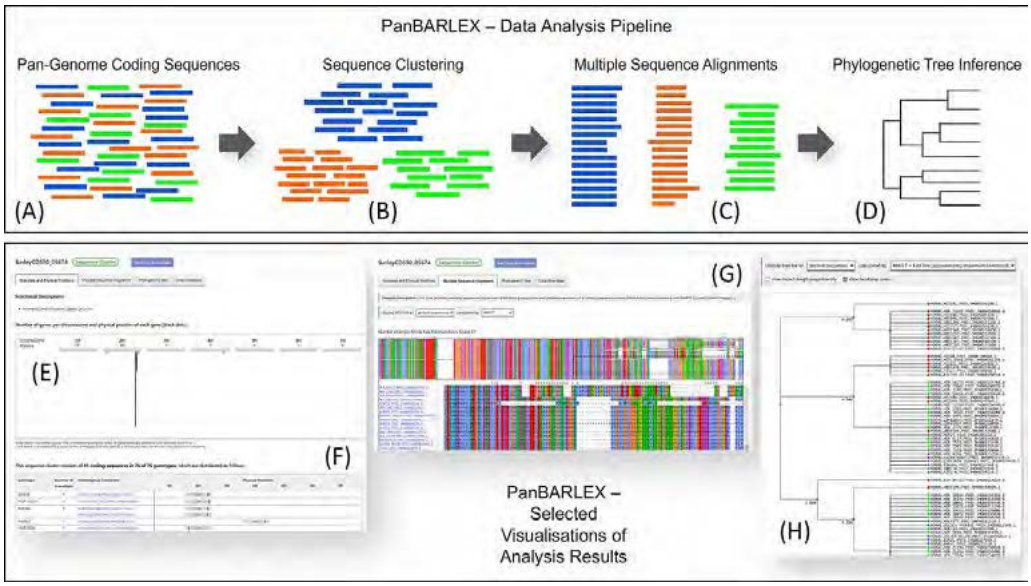


Figure 1: *Overview about the PanBARLEX data analysis pipeline (A – D) and selected visualisations of the analysis results (E – H). As input the pan-genome coding sequences of 3,797,824 annotated genes were used (A). Using MMseqs2 a sequence clustering was carried out (B). The results were used as input to precompute multiple sequence alignments using MAFFT and Clustal Omega (C). These results are used as input to compute phylogenetic tree inferences using FastTree and Clustal Omega (D). Sequence cluster visualisation using the example of the cluster of the gene "Vrs1" are visualised in part (E – F) where (E) recognises the spatial distribution of homologous genes across all chromosomes and (F) shows the presence-absence variation and copy number variation of homologous genes for all 76 genotypes. (G) illustrated the online viewer for the precalculated multiple sequence alignments for selected sequences clusters generated in step (C). The results of step (D) are visualised in an interactive phylogenetic tree viewer (H).*

The central laboratory information management system (LIMS) was extended to include an electronic laboratory notebook (ELN). In addition, a module for processing geodata and maps was implemented. The export function of the LIMS was also extended to allow data to be exported in ISA-Tab format, supporting data publications.

Embedding in IPK Research Themes

With the research on data management along the complete data life cycle and development of application programming interfaces the group contributes to the Research Theme "Exploiting biodigital plant data" and supports the Research Theme "Activating genetic diversity". The group also contributes to Research Themes "Engineering genomes and chromosomes", "Roots for resource-efficient crops" and "Enhancing shoot performance", providing consultancy services regarding fulfilling the FAIR principles.

Outlook

Over the next few years, the group will be conducting research into interfaces between information systems and tools. The aim is to provide users of biodigital data with various access points to systems that communicate with each other via APIs. The development of uniform IPK-wide material and sample management systems to enable the traceability of plant genetic resource usage will be a key area of research in the coming years. This work is closely linked to the DOK group. While the DOK group focuses on data relating to genebank material, the BIT group concentrates on material derived from this. These research efforts primarily deal with molecular and phenotypic data.



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

Head: Prof. Dr. Andreas Houben

Mission

The research group deciphers the regulation, organisation, segregation, and evolution of mitotic, meiotic, and interphase chromosomes to unravel the fundamental mechanisms of chromosome biology in model, wild, and crop species. The knowledge gained will be utilised to accelerate and optimise the breeding process of crop plants, as well as to develop novel tools for chromosome analysis and manipulation.

Results

Kinetochore mutations and histone phosphorylation pattern changes are associated with holo- and macro-monocentromere evolution

While chromosomes of most species are monocentric with a single centromere, a minority exhibit holocentricity, with a centromere along the chromatid length. To explore the origin of holocentromeres, we compared the centromere and (epi)genome organisation of two sister genera with contrasting centromere types. We identified genomic, epigenetic, and kinetochore composition changes underlying the process of mono- to holocentric transition. A complex interplay exists between centromere size, number and distribution of centromere units (mono- versus holocentromeres), and chromatid cohesion in shaping chromosome morphology (Figure 1, Kuo *et al.* 2025).

Consequences of CRISPR/Cas9-engineered chromosome translocations, inversions and fusions on the epigenome and transcriptome

To unravel the effect of chromosomal inversions, translocations and fusions on the epigenetic state of chromatin and the activity of genes in *A. thaliana*, in a collaborative effort (H. Puchta, KIT, Karlsruhe), we employed CRISPR/Cas-assisted chromosome engineering for the generation of chromosomal inversions and fusions in *A. thaliana*. The epigenetic state of these lines was compared to wild-type plants. Finally, the effect of the chromosomal rearrangements on the activity of genes was analysed. The findings demonstrate the robustness of the epigenome and transcriptome following CRISPR/Cas-induced chromosomal restructuring (Khosravi *et al.* 2025). Directed chromosome number changes and structural reorganizations will enable new breeding strategies, redefining linkage groups and establishing genetic barriers (Rönspies *et al.* 2025).

Expanding the CRISPR-FISH toolbox for understanding chromosome biology.

Understanding the spatial organisation of genomes within chromatin is crucial for deciphering gene regulation. Unlike standard fluorescence *in situ* hybridisation (FISH), CRISPR–FISH eliminates the need for global DNA denaturation, thereby enabling superior preservation of chromatin structure. We further improved the CRISPR–FISH method by engineering a recombinant dCas9 protein with an ALFA-tag, thereby enhancing efficiency. The dCas9–ALFA-tag system was also instrumental for live-cell telomere imaging in *Nicotiana benthamiana* (Potlapalli *et al.* 2024). In addition, we developed a non-fluorescent CRISPR-ISH method. This approach uses 3' biotin-labelled guide RNA. The subsequent application of streptavidin-alkaline phosphatase or horseradish peroxidase generates chromogenic, target-specific signals that can be analysed with conventional bright-field microscopes. This advancement makes *in situ* DNA detection techniques more accessible to researchers, diagnostic applications, and educational institutions in resource-limited settings. (Potlapalli *et al.* 2025).

Selected publications

Chen J et al. (2024) The genetic mechanism of B chromosome drive in rye illuminated by chromosome-scale assembly. ***Nat. Commun.*** 15: 9686.

Khosravi S et al. (2025) Epigenetic state and gene expression remain stable after CRISPR/Cas-mediated chromosomal inversions. ***New Phytol.*** 245: 2527-2539.

Kuo Y-T et al. (2025) Kinetochore mutations and histone phosphorylation pattern changes accompany holo- and macro-monocentromere evolution. ***Nat. Commun.*** 16: 11332.

Rönspies M et al. (2025) CRISPR-Cas-mediated heritable chromosome fusions in *Arabidopsis*. ***Science*** 390: 843-848.

Stepanenko A et al. (2025) Genome diversity and evolution of the duckweed section *Alatae* comprising diploids, polyploids, and interspecific hybrids. ***Plant J.*** 122: e70158.

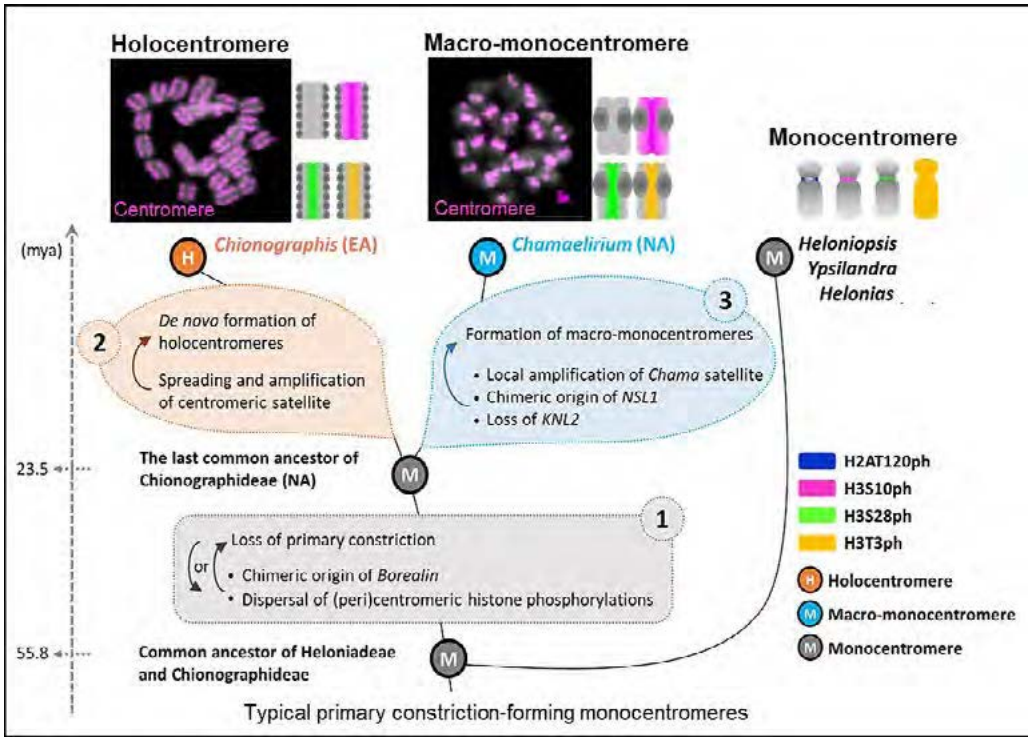


Figure 1: *Model explaining the divergent evolution of holo- and macro-monocentromeres in Chionographideae. The sister tribes Heloniadeae and Chionographideae, which diverged ~55 million years ago (mya), exhibit intercontinental disjunctions between eastern Asia and eastern North America. Chionographis and Chamaelirium possess primary constriction-free chromosomes with holocentromeres and macro-monocentromeres, respectively. In contrast, the monocentromeres of Heloniadeae species possess a primary constriction, suggesting that the loss of this chromosome constriction occurred before the divergence of holocentric Chionographis and macro-monocentric Chamaelirium ~23.5 mya. (1) A Borealin mutation likely acted as an evolutionary trigger, causing the chromosome-wide distribution of histone phosphorylation and sister chromatid cohesion. This ultimately drove the evolution of primary constriction-free chromosomes in the plant tribe Chionographideae. Alternatively, constriction-free chromosomes may have arisen first, followed by selection for the new Borealin variant. (2) The evolution of both macro-monocentromeres in Cha. luteum and holocentromeres in Chi. japonica was driven by the amplification of centromeric repeats. However, in Chionographis, this repeat amplification by non-allelic gene conversion was accompanied by the chromosome-wide spread of centromere units, leading to the formation of a holocentromere. (3) In Cha. luteum, local centromere expansion resulted in macro-monocentromeres. However, the relationship between loss of KNL2 and the chimeric origin of NSL1 and the local centromere expansion remains unclear (Kuo et al. 2025).*

Intrageneric cryptic hybridisation and polyploidization are crucial for duckweed evolution

The aquatic, organ-reduced and mainly vegetatively propagating monocot family *Lemnaceae* are the fastest-growing flowering plants and an emerging multipurpose crop. For 3 of the 5 genera, phylogeny and systematics are unclear. Applying genomic, cytogenetic and molecular marker techniques, we uncovered genomic diversity, systematics and evolution within the genus *Lemna* (Ernst *et al.* 2025, Stepanenko *et al.* 2025, Lee *et al.* 2025). We showed that polyploidization, cryptic hybridisations and backcrosses led to species complexes and paved the way for future breeding efforts.

Embedding in IPK Research Themes

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

Outlook

- To enable the CENH3-degradation-based approach to generate haploid wild-type plants and to increase the frequency of haploids, novel types of male and female haploid inducers will be generated.
- Analysis of candidate genes and repeats regulating the rye B chromosome drive.
- To determine how B chromosomes evolved – Are they a product of chromoanagenesis and a subsequent stepwise sequence accumulation process?
- To address whether the evolutionary transition to holocentricity alter meiotic processes and the recombination landscape
- After deciphering that the chromatids of barley metaphase chromosomes are formed by helically coiled chromatid threads called chromonemata, we plan to analyse the lower chromatin organisation within the chromonema by applying oligo-FSH and super-resolution microscopy. The same methods will be applied to clarify the ultrastructural organisation of barley monocentromeres.
- To further elucidate duckweed diversity and to provide tools for breeding efforts, we will focus on the phylogeny of the economically important genus *Wolffia* and on the generation of synthetic hybrids.



RESEARCH GROUP **KINETOCHORE BIOLOGY** (KB)

Head: Dr. Inna Lermontova

Mission

The research group Kinetochore Biology studies the molecular mechanisms underlying centromere identity, kinetochore assembly, and faithful chromosome segregation in plants. The group focuses on the regulation of the centromeric histone CENH3, the function of centromere licensing factors, and the consequences of disturbed kinetochore function for genome stability and fertility.

The primary research goals are:

1. To elucidate mechanisms of kinetochore assembly and centromere maintenance.
2. To investigate regulatory pathways controlling CENH3 deposition and kinetochore protein dynamics.
3. To analyse centromere-mediated genome instability relevant for haploid induction.
4. To assess genetic and environmental effects on centromere integrity.

Results

Accurate segregation of chromosomes during mitosis and meiosis is essential for plant development and fertility. This process depends on the kinetochore; a multiprotein complex assembled at centromeres that mediates spindle attachment and coordinates chromosome movement. Impairment of kinetochore assembly or centromere integrity results in chromosome mis-segregation, genome instability, and reduced reproductive success.

Regulation of αKNL2 abundance and activity

During the reporting period, a major focus was the regulation of the centromere licensing factor KINETOCHORE NULL 2 (KNL2), which is required for proper loading and maintenance of the centromeric histone variant CENH3. We demonstrated that the *Arabidopsis* αKNL2 protein is regulated by ubiquitin-dependent proteolysis mediated by the anaphase-promoting complex/cyclosome (APC/C) and its activator CDC20 (Figure 1A). αKNL2 undergoes polyubiquitination and proteasomal degradation during mitosis, and interference with this pathway resulted in abnormal protein accumulation, impaired mitotic progression, chromosome mis-segregation, and reduced fertility (Kalidass *et al.*, 2025a). These results show that precise temporal control of αKNL2 abundance is critical for centromere integrity and mitotic fidelity.

In addition to ubiquitin-mediated degradation, we identified SUMOylation as an important post-translational mechanism regulating αKNL2 function. SUMOylation of specific lysine residues in the C-terminal region of αKNL2 was required for its centromeric localisation, stable interaction with CENH3, and appropriate protein turnover (Figure 1B). αKNL2 variants impaired in SUMOylation displayed defects in kinetochore assembly, chromosome alignment, and plant fertility, demonstrating that coordinated post-translational regulation is essential for αKNL2 activity (Kalidass *et al.*, 2025b).

Mechanisms of centromere targeting

We further analysed the molecular requirements for centromeric localisation of αKNL2 and the inner kinetochore protein CENP-C. Our results showed that the conserved centromere-targeting motifs (CENPC-k and CENPC motifs) alone are insufficient for stable centromere association. Instead, adjacent DNA-binding regions that interact with centromeric DNA in a sequence-independent manner are required to reinforce centromere anchoring. Deletion of these regions reduced centromeric localisation, whereas their presence significantly enhanced targeting efficiency. These findings provide mechanistic insight into how kinetochore proteins recognise and associate with highly variable centromeric DNA (Yalagapati *et al.*, 2025).

Selected publications

Crhak Khaitova L et al. (2024) Heat stress impairs centromere structure and segregation of meiotic chromosomes in *Arabidopsis*. ***eLife*** 12: e90253.

Ramakrishnan Chandra J et al.(2024) The role of centromeric repeats and transcripts in kinetochore assembly and function. ***Plant J.*** 118: 982-996.

Kalidass M et al. (2025) Ubiquitin-dependent proteolysis of KNL2 driven by APC/C^{CDC20} is critical for centromere integrity and mitotic fidelity. ***Plant Cell*** 37: koaf164.

Yalagapati SP et al. (2025) Centromeric localization of αKNL_2 and CENP-C proteins in plants depends on their centromere-targeting domain and DNA-binding regions. ***Nucleic Acids Res.*** 53: gkae1242.

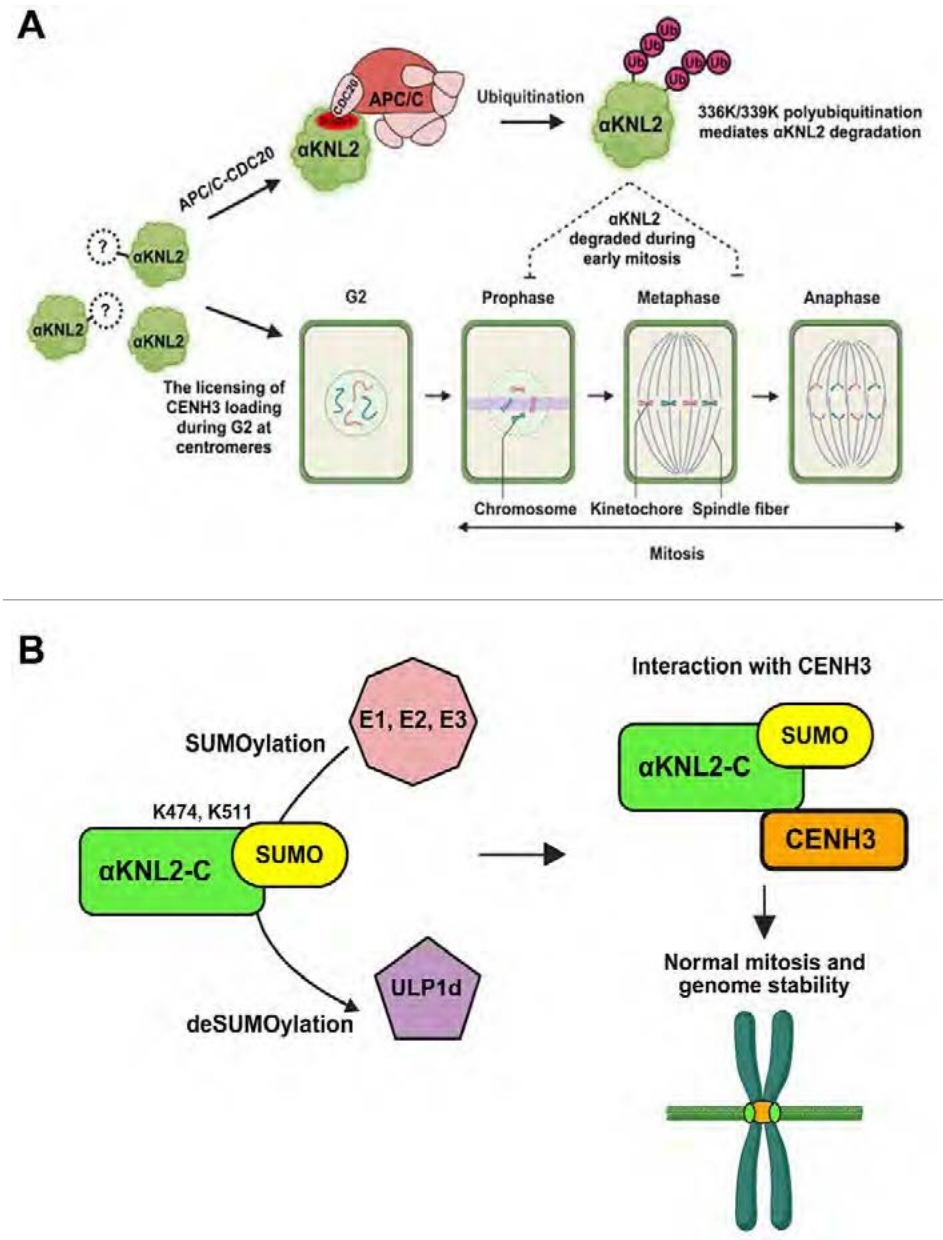


Figure 1: Post-translational regulation of αKNL2 controlling centromere function and genome stability. *(A) Schematic model illustrating APC/C-dependent regulation of αKNL2 abundance in Arabidopsis thaliana. The APC/C complex targets excess αKNL2 for ubiquitin-mediated degradation, ensuring timely removal of the protein during early mitosis and thereby supporting accurate cell division. (B) Schematic model of SUMOylation-dependent regulation of the C-terminal region of αKNL2 (αKNL2-C). SUMO1 and SUMO3 are conjugated to lysine residues K474 and K511 by the SUMO E1-E2-E3 enzymatic machinery, followed by dynamic deSUMOylation mediated by the SUMO protease ULP1d. This SUMO cycle is required for proper αKNL2-C function, efficient centromeric loading of CENH3, normal mitotic progression, and maintenance of genome stability.*

Centromere integrity under elevated temperature

The robustness of centromere function under environmental stress was addressed in a joint study on the effects of elevated temperature on meiotic chromosome segregation in *Arabidopsis thaliana*. Elevated temperature was shown to reduce centromeric CENH3 levels and the abundance of the kinetochore protein BMF1 during male meiosis, leading to chromosome mis-segregation and reduced fertility. These results indicate that meiotic centromeres are particularly sensitive to temperature stress and represent a potential vulnerability point under changing environmental conditions (Crhak Khaitova *et al.*, 2024).

Outlook

Future work of the Kinetochore Biology group will focus on further dissecting post-translational regulation of kinetochore proteins and its role in maintaining centromere stability during cell division. Particular emphasis will be placed on understanding how ubiquitination and SUMOylation pathways fine-tune the abundance, localisation, and activity of centromere licensing factors. Building on mechanistic insights obtained in *Arabidopsis*, we aim to extend selected analyses to crop species to assess the conservation and functional relevance of kinetochore regulatory pathways. In parallel, we plan to investigate how genetic perturbations of kinetochore components affect chromosome segregation fidelity, genome stability, and centromere-mediated haploid induction efficiency under standard and stress conditions. These approaches will contribute to a deeper understanding of how centromere integrity constrains plant fertility and will provide a foundation for future applications in plant breeding.



RESEARCH GROUP **BIOTROPHY AND IMMUNITY** (BIM)

Head: Dr. Dimitar Douchkov

Mission

The group focuses on identifying and exploiting durable, quantitative disease resistance mechanisms in cereals, with an emphasis on resistance types that remain largely inaccessible to conventional breeding. Using wheat and barley as complementary systems, we combine plant pathology, genetics, and high-resolution phenotyping to resolve resistance mechanisms at the level where they are biologically effective. A central objective is the translation of mechanistic insights into genetically defined resources that can be directly used for wheat improvement.

Results

Nonhost resistance as a genetically tractable breeding target

Nonhost resistance represents the most stable and broad-spectrum form of plant immunity, yet it has traditionally been considered genetically intractable due to the absence of macroscopic phenotypic variation. By applying microphenomics, we demonstrate that NHR exhibits quantitative, heritable variation at the microscopic scale, which can be measured reproducibly across large genotype panels.

We quantify early infection traits such as penetration success, haustorium formation, and colony establishment. These data enable genome-wide association analyses, including k-mer-based GWAS (Figure 1), which avoid reference bias and capture structurally complex loci. This approach identifies multiple genomic regions contributing to quantitative NHR components, including loci that are not detectable using SNP-based methods.

Development and extension of Microphenomics platforms

We continuously expand the Microphenomics framework to additional pathosystems and stress contexts. Microphenomics assays for wheat stripe rust in both wheat and barley have been established, enabling quantitative comparison of host, near-host, and nonhost interactions under strictly controlled conditions. Experiments are performed on detached tissues, which allows precise pathogen exposure while keeping whole plants uninfected. This setup ensures high reproducibility, minimises environmental noise, and enables parallel experimentation across laboratories.

By integrating microphenomics with high-throughput plant phenotyping, disease progression dynamics can be captured across biological scales, from single infection sites to whole-plant responses. This methodological development enables the analysis of complex resistance phenotypes that are not accessible using conventional phenotyping approaches.

Expanding genetic resources for wheat improvement

A central strategic activity of the group is the activation and expansion of genetic resources for wheat improvement. We are systematically developing the Triticum araraticum gene pool through coordinated sequencing, phenotyping, and the construction of a genetically informed core collection. This work aims to unlock novel resistance alleles and adaptive traits that are absent from elite wheat germplasm and to make them accessible for genetic analysis and pre-breeding. In parallel, we work on a broad range of alien introgressions in wheat, focusing on resistance traits derived from wild relatives and secondary gene pool species. By combining precise phenotyping with advanced genomic analyses, we aim to resolve beneficial introgressed segments at high resolution and to facilitate their targeted use in breeding programmes.

Selected publications

Lück S, Scholz U, Douchkov D (2024) Introducing GWAStic: A user-friendly, cross-platform solution for genome-wide association studies and genomic prediction. ***Bioinform. Adv.*** 4: vbae177.

Kaur H et al. (2025) Isolation and characterization of fungi associated with wheat heads and leaf blotch symptoms in Sweden. ***Eur. J. Plant Pathol.*** 173: 809-823.

Lück S, Bourras S, Douchkov D (2025) Deep phenotyping platform for microscopic plant-pathogen interactions. ***Front. Plant Sci.*** 16: 1462694.

Lück S et al. (2025) Accelerated haustoria segmentation enables rapid gene function analysis in cereal-powdery mildew pathosystems. ***Mol. Plant Microbe Interact.*** 38: 825-833.

Ulrich M et al. (2025) Foliar disease resistance phenomics of fungal pathogens: image-based approaches for mapping quantitative resistance in cereal germplasm. ***Theor. Appl. Genet.*** 138: 232.

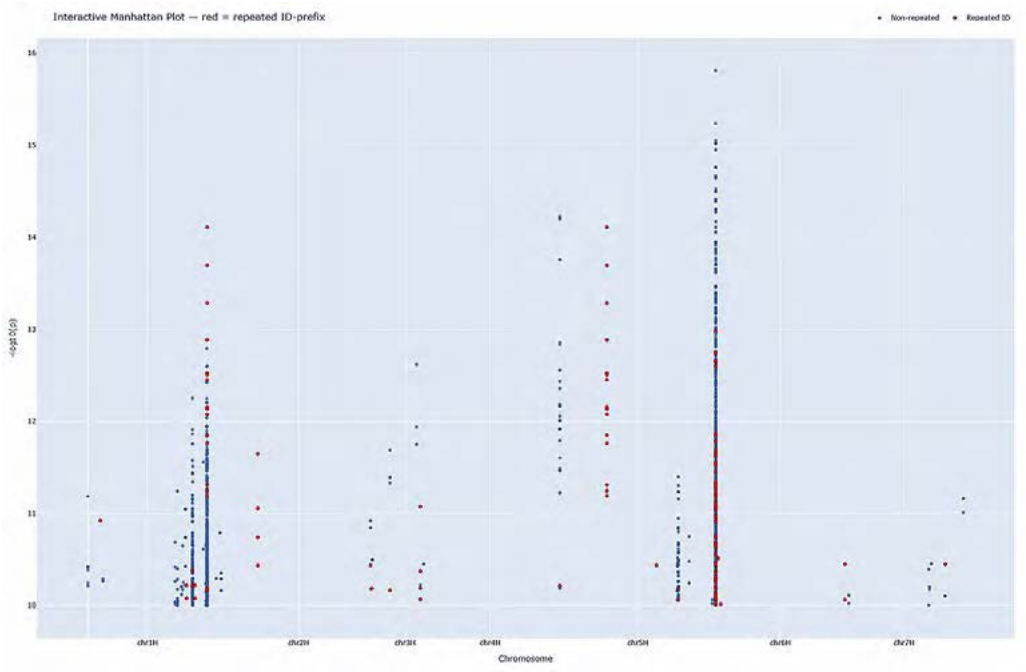


Figure 1: *k-mer GWAS for nonhost resistance of barley to wheat powdery mildew based on colony count phenotyping. Manhattan plot showing the genomic distribution of significantly associated k-mers mapped to the barley reference genome (Morex v3). Each point represents a k-mer assigned to a genomic position and plotted by chromosome (x-axis) and association strength as –log10(P) (y-axis). The phenotype used for association analysis is powdery mildew colony count, quantified by microphenomics. Blue dots indicate uniquely mapped k-mers, while red dots indicate multiply mapped k-mers with non-unique genomic positions. Clusters of significant k-mers delineate candidate genomic regions contributing to quantitative variation in nonhost resistance.*

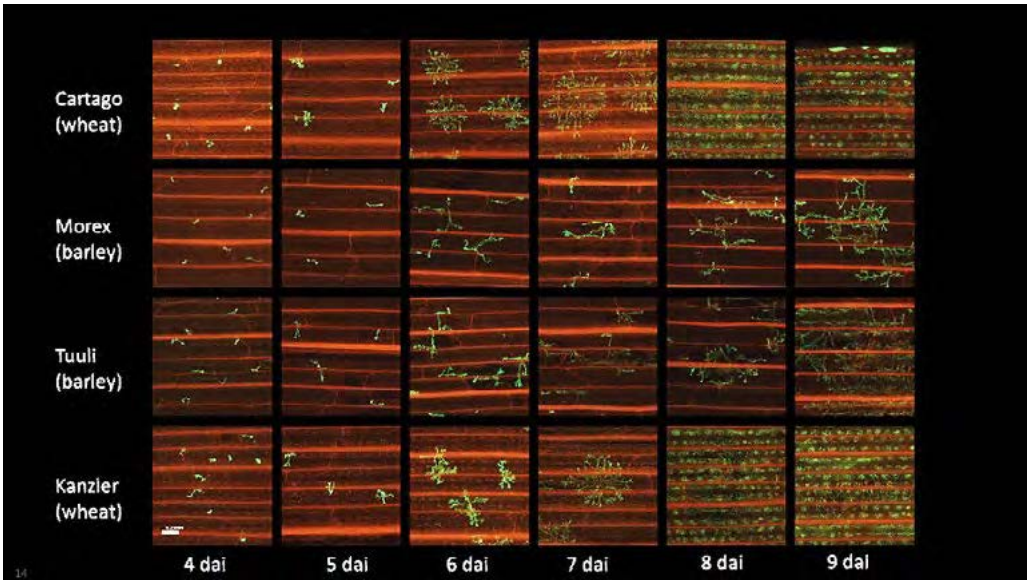


Figure 2: *Infection progression of wheat stripe rust on barley and wheat accessions over time. Fluorescence microscopy images show the development of wheat stripe rust on two barley accessions, Morex and Tuuli, and two wheat cultivars, Cartago and Kanzler, at 4 to 9 days after infection. Green fluorescence marks fungal structures, and orange marks host propidium iodide-stained tissue. The images illustrate apparent differences in infection pattern and progression among accessions, with wheat generally supporting dense microcolony formation and sporulation, while barley shows more restricted or dispersed fungal growth.*

Embedding in IPK Research Themes

The work of the research group Biotrophy and Immunity contributes mainly to Research Theme #1 (Activating Genetic Diversity) and Research Theme #2 (Exploiting Biodigital Plant Data).

Outlook

Future activities focus on making nonhost resistance accessible for breeding. This includes systematic exploration of secondary and tertiary gene pools, expansion of alien introgression resources, and further development of microphenomics-based phenotyping pipelines. Methodologically, we will deepen the integration of k-mer genomics, high-resolution imaging, and predictive models to resolve complex resistance architectures. Strategically, the group aims to establish itself as a reference centre for quantitative NHR research and microphenomics-driven resistance discovery in cereals.



RESEARCH GROUP **PLANT ARCHITECTURE** (PBP)

Head: Prof. Dr. Thorsten Schnurbusch

Mission

In the Plant Architecture Lab, we are undertaking a comprehensive exploration of natural variations and induced mutants in wheat and barley to unravel the intricate genetic, molecular, and biochemical mechanisms underlying developmental traits, particularly variations in grain number per spike.

Research Report

Research Statement and Major Achievements: **Towards a better understanding of the genetic and molecular determinants of spikelet architecture and survival in cereal crops (Nat. Commun. 16, 3937; Curr. Biol. 34, 2344-2358; Annu. Rev. Plant Biol. 75, 427-458)** The establishment, maintenance, and signaling of inflorescence meristems (IM) in cereal crops are not well understood. There is a significant lack of knowledge regarding the cellular positioning of the stem cell niche, organising cells, and the peripheral zone in important crops like barley (Hordeum vulgare L.). To better understand barley spike formation, exploring the cellular patterning of the shoot apex is essential. As part of the DFG-funded Research Unit (FOR5235) Cereal Stem Cell Systems (CSCS) and in collaboration with the Simon Lab, we investigated the CLAVATA pathway that regulates meristem size and inflorescence architecture in grasses; however, how individual meristems integrate to form specific inflorescences is unclear. In barley, the receptor-like kinase HvCLV1 and CLE-family peptide HvFCP1 control distinct meristem activities. Their interaction promotes spikelet formation while restricting inflorescence meristem and rachilla growth. Mutants of Hvfcp1 or Hvclv1 produce extra spikelet rows and florets due to extended rachilla activity. This signaling pathway coordinates meristem function by regulating trehalose-6-phosphate levels, offering a strategy to engineer inflorescence architecture through targeted meristem regulation. Moreover, we identified recessive alleles of barley HvALOG1 that cause extra spikelets and fused glumes on the abaxial side of central spikelets from the upper-mid inflorescence to the tip. HvALOG1 shows boundary-specific expression, excluding reproductive meristems, suggesting localised signaling centres regulate branching. Early spikelet formation involves non-cell-autonomous signals from HvALOG1 for meristem determinacy, while floret organ boundaries form cell-autonomously. Barley ALOG family members work together to shape inflorescence, with HvALOG1 mainly controlling meristem maintenance and floral development. Spatiotemporal redundancy among HvALOGs in the basal inflorescence likely ensures proper spikelet patterning, revealing new roles for ALOG factors in cereal reproductive development.

One promising avenue for improving grain yield of cereal crops, including wheat (Triticum spp.) and barley, involves reducing floral mortality. Florets, the grain-bearing units of cereal spike-type inflorescences, usually form in excess and subsequently degenerate during development a phenomenon known as pre-anthesis tip degeneration (PTD; Figure 1). It starts with growth arrest of the inflorescence meristem dome, which is followed basipetally by the degeneration of floral primordia and the central axis. Importantly, increased spikelet survival is linked to increased numbers of grains per spike; therefore, reducing spikelet mortality is an intriguing approach to improve grain yield. Both internal and external factors can cause premature floral organ death, leading to reproductive failure. Our review summarises current understanding of floral development and death, especially in Triticeae crops, emphasising the roles of vascular patterning and photosynthesis. It calls for deeper agroecological insights into the balance between floral birth and death for crop success.

Selected publications

Abbai R et al. (2024) Grain yield trade-offs in spike-branching wheat can be mitigated by elite alleles affecting sink capacity and post-anthesis source activity. ***J. Exp. Bot.*** 75: 88-102.

Golan G et al. (2024) Agroecological genetics of biomass allocation in wheat uncovers genotype interactions with canopy shade and plant size. ***New Phytol.*** 242: 107-120.

Huang Y, Schnurbusch T (2024) The birth and death of floral organs in cereal crops. ***Annu. Rev. Plant Biol.*** 75: 427-458.

Jiang G et al. (2024) Non-cell-autonomous signaling associated with barley ALOG1 specifies spikelet meristem determinacy. ***Curr. Biol.*** 34: 2344-2358.

Vardanega I et al. (2025) CLAVATA signalling shapes barley inflorescence by controlling activity and determinacy of shoot meristem and rachilla. ***Nat. Commun.*** 16: 3937.

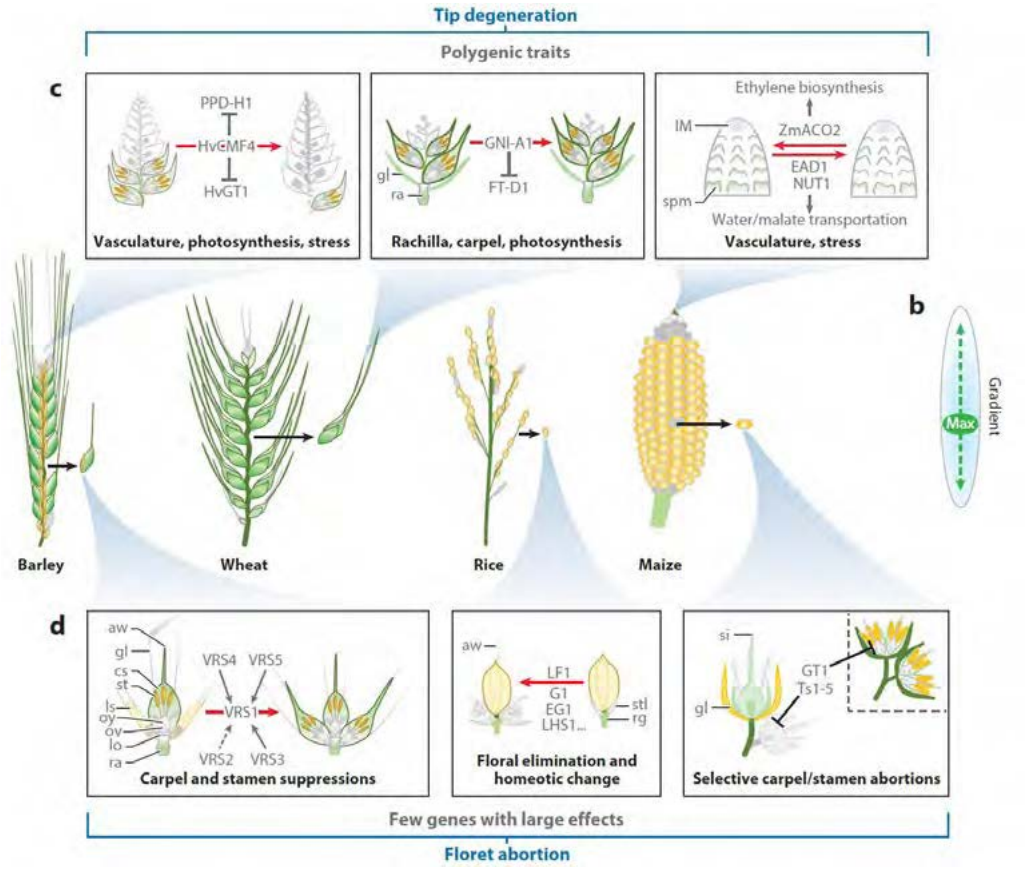


Figure 1: *Tip degeneration as a feature of grass inflorescence development in comparison with abortive floral processes. The widespread oval-shaped floral maturation pattern among the four inflorescences. (c, d) Major floral death. A major phenotypic consequence for (c) tip degeneration is the elimination of both florets and the floral axis (grey), which is common in indeterminate growth and highly quantitative among naturally diverse populations. The identified regulators and the synthesized keywords summarising their functionalities are highlighted. Red arrows point to the phenotypic direction where genes have loss-of-function mutations. (d) Floret abortion is due to the specific shutdown of floret developmental programmes, such as the sexual organs carpel and stamen.*

Agroecological genetics of biomass allocation in wheat uncovers genotype interactions with canopy shade and plant size. (New Phytol. 242, 107-120).
Another facet of the research focuses on how resource allocation entails trade-offs between the growth and function of various organs, which subsequently influences fitness and investment strategies in temperate cereals. Plant biomass distribution affects resource use, reproduction, and interactions, crucial for ecology, evolution, and agriculture, yet its genetic regulation under environmental change is poorly understood. Here, we studied wheat recombinant lines grown in sunlight and simulated shade to analyse genotype-by-environment effects on biomass allocation to leaves, stems, spikes, and grains. Using size-corrected mass fractions and allometric slopes, we identified light-responsive alleles linked to crop adaptation. Notably, DELLA protein polymorphism influenced shade response and size, with gibberellin-sensitive alleles affecting stem and reproductive allocation differently under shade. Our approach provides a basis for exploring the genetic determinants underlying investment strategies in the face of different resource constraints and will be useful in predicting social behaviours of individuals in a crop community.

Embedding in IPK Research Themes

Work within the Research Group Plant Architecture (PBP) relates predominantly to the research focal point area 4 “Growth & 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.



YOUNG INVESTIGATOR GROUP: **AGROECOLOGICAL BREEDING** (AB)

Head: Dr. Samira El Hanafi

Mission

The Agroecological Breeding research group aims to refine and optimise breeding strategies that exploit intra- and interspecific complementarities in variety and crop mixtures. The research objectives are to (1) integrate advanced quantitative genetic frameworks to quantify and partition mixture performance into genetic components across environments enabling reliable inference on complementarity and stability in diversified stands, (2) dissect the genetic basis of overyielding and uncover mechanisms of disease suppression, and (3) develop predictive models that accelerate breeding progress for diversified systems.

Results

Linking quantitative genetic approaches with community-level performance.

Wheat variety mixtures demonstrated that mixing can improve yield and yield stability, but benefits depend strongly on the specific partner combination and environmental context. Overyielding, including transgressive overyielding in particular combinations, points to complementarity or facilitation beyond simple sampling effects. However, ecological and trait-based approaches, including differences in individual functional traits among mixture components, failed to explain this variation consistently. We therefore aimed to dissect the genetic basis of overyielding by treating mixture performance as a community-level phenotype. Building on quantitative-genetic approaches successfully used to study heterosis in wheat, we developed and applied this framework in Arabidopsis thaliana mixtures, where the results indicated a prominent role of epistasis-like genetic effects in overyielding (Figure 1). At individual loci, these analyses further revealed links between overyielding and component traits, providing specific entry points for biological interpretation and follow-up studies. The framework is now being transferred to the substantially enlarged wheat variety-mixture population to identify genetic determinants of overyielding and to develop predictive models for superior genotype combinations. Available proxies for component choice can support initial screening, but remain less informative for interaction-driven gains, which are likely to underlie transgressive overyielding. In parallel, leaf and yellow rusts, the most prevalent diseases in the region, showed that mixing does not consistently confer disease suppression. However, pronounced reductions occurred in specific combinations, particularly when mixtures combined contrasting levels of resistance, indicating that disease suppression depends strongly on mixture composition. The central challenge is therefore to distinguish mixture benefits driven by generally strong components from those that emerge only from particular genotype combinations, and to predict the latter reliably.

Component-based metrics support scalable wheat screening for wheat–pea mixtures.

We used the wheat-fraction Net Equivalent Ratio (wNER) as a baseline metric to benchmark wheat performance in mixed stands by comparing the wheat component yield in mixture to its proportional expectation. Across environments, many wheat entries showed wNER > 1, indicating above-proportional wheat contribution in mixtures. Partitioning mixture performance further suggested that most variation is attributable to the wheat genotype's own contribution in mixture (general mixing ability/producer effect), whereas consistent pea partner effects were comparatively limited under the present design. Practically, this supports screening wheat lines for mixture suitability using scalable proxies, while recognising that cross-environment stability remains the key constraint and must be addressed through multi-environment validation and prediction-oriented modelling.

Selected publications

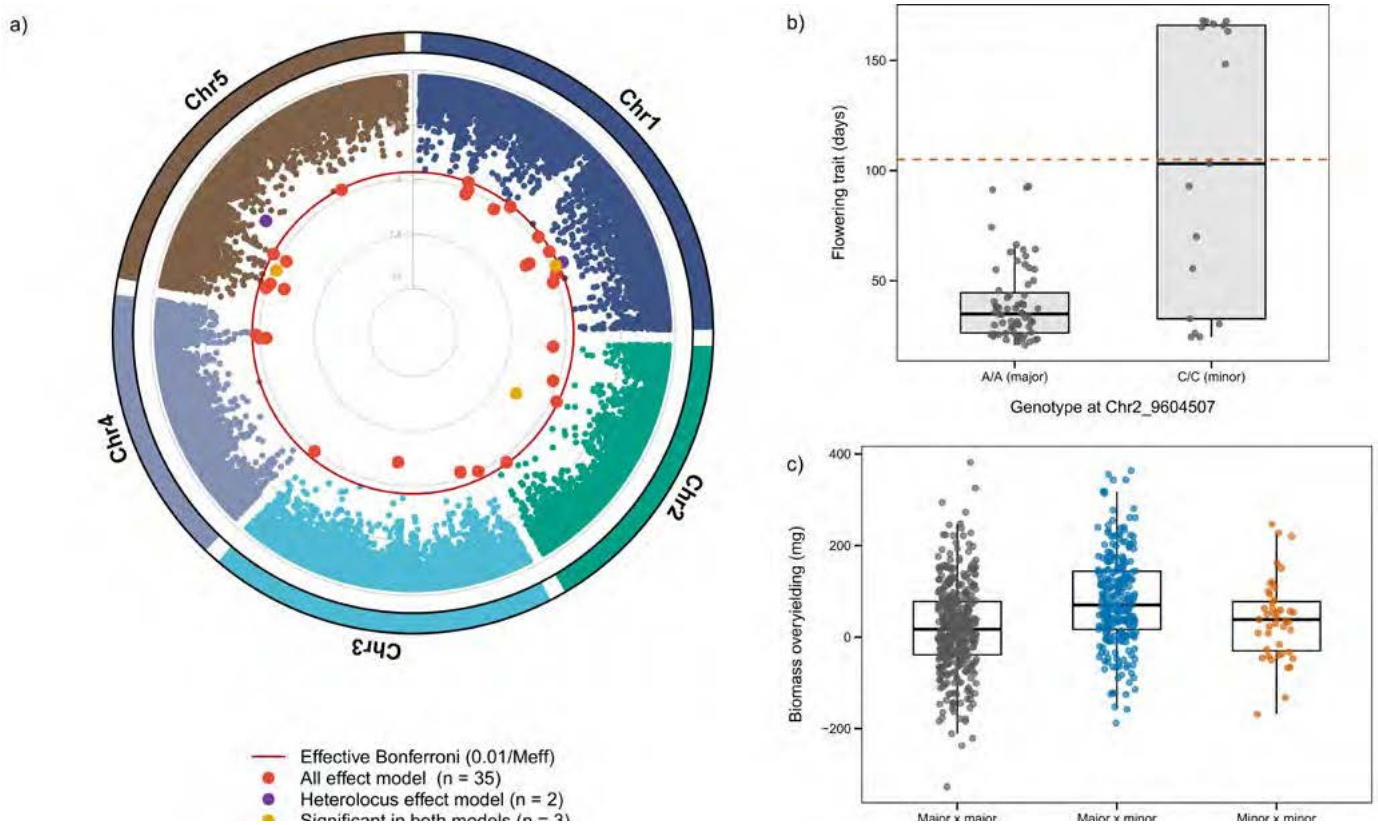
Yuan Z et al. (2024) Capitalizing genebank core collections for rare and novel disease resistance loci to enhance barley resilience. ***J. Exp. Bot.*** 75: 5940-5954.

Niels L et al. (2025) Harnessing historical genebank data to accelerate pea breeding. ***Theor. Appl. Genet.*** 138: 243.

Yuan Z et al. (2025) High-quality phenotypic and genotypic dataset of barley genebank core-collection to unlock untapped genetic diversity. ***GigaScience*** 14: giae121.

Yuan Z et al. (2025) Diseases resistance of 300 barley plant genetic resources across four environments. ***e!DAL - Plant Genomics and Phenomics Research Data Repository (PGP), IPK Gatersleben*** https://dx.doi.org/10.5447/IPK/2025/9

Zapata SL et al. (2025) Disentangling the genetic architecture of key traits for wheat hybrid seed production. ***J. Exp. Bot.*** 76: 5320-5336.



Embedding in IPK Research Themes

The research group's work contributes to all five Research Themes of the IPK Research Strategy.

Outlook

We will continue to focus on (1) translating variety and crop mixtures into a predictable breeding target for yield, yield stability and disease suppression, (2) dissecting the genetic basis of overyielding and disease suppression in wheat mixtures, and (3) integrating ecological mechanisms of complementarity with quantitative genetic and prediction-oriented modelling across environments. To this end, we joined consortium with Swiss partners to quantify how ecological interaction mechanisms in mixtures can simultaneously raise productivity and reduce epidemic growth under contrasting environments. The genetic basis of both overyielding and disease suppression for certain diseases including Septoria, yellow and leaf rust will be tackled in two complementary pillars: PreDiMIX (DFG funded project HA 10835/1-1), leveraging a diversity panel to capture broad allelic and resistance level variation across environments, and a submitted Emmy Noether proposal using biparental populations to enable controlled dissection and validation of key loci and interaction effects.

Figure 1: *Genetic dissection of overyielding in Arabidopsis thaliana mixtures; Using a heterosis-inspired QTL framework, overyielding was decomposed into dominance-like (Heterolocus effect model) and epistasis-like effects (All effect model). Genome-wide associations identified loci underlying these components (a). Chr2_9604507 emerged as a shared locus for flowering time (FT) and overyielding (OY). The FT-increasing allele was enriched among very-late-flowering accessions (b), while mixtures with contrasting component alleles exhibited the greatest biomass overyielding (c).*



MOLECULAR GENETICS

Heterosis (HET)
Prof. Dr. Thomas Altmann

Network Analysis and Modelling (NAM)
Dr. Jędrzej Jakub Szymański

Automated Plant Phenotyping (APP)
Dr. Kerstin Neumann

Metabolic Diversity (MD)
Dr. John D'Auria

Image Analysis (BA)
Dr. Evgeny Gladilin

Seed Development (SE)
Dr. Jozefus H. M. Schippers

Assimilate Allocation and NMR (AAN)
Dr. Ljudmilla Borisjuk
and Dr. Hardy Rolletschek

Young Investigator Group
"Integrated Mechanistic Models" (IMM)
Dr. Mary-Ann Ebeling

DEPARTMENT MOLECULAR GENETICS



DEPARTMENT MOLECULAR GENETICS

Head: Prof. Dr. Thomas Altmann

Mission

Sustainable production of food, feed, renewable raw materials, and energy sources of adequate quantity and quality bears great challenges in a world with continuous population growth and severe environmental burdens and changes. Therefore, the central aim of the Molecular Genetics (MOG) department is to gain detailed information on the molecular processes that determine plant performance in changing environments. 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

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", an integrative approach is taken, combining plant genetics and omics to understand and model plant performance and its associated regulation at the cellular, organ, and whole-plant levels. Supporting novel technology platforms and methodologies are developed and used, including unique phenotyping infrastructures such as the IPK-PhenoSphere, MRI of living plant organs, automated image analysis and image-based modelling, high-throughput metabolomics, spatial transcriptomics, genome-wide transcription factor binding assays, and the latest deep learning and modelling approaches. 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 IPK's research themes 5, Enhancing Plant Shoot Performance, 4, Roots for Resource-efficient Crops, and 2, Exploiting Biodigital Plant Data, MOG addresses the central strategic IPK goals to uncover fundamental processes of plant adaptation and performance and to advance the knowledge required to tailor crop plants to improve resilience-, yield-, and sustainability-related traits. Using its core competences, MOG supports the IPK-wide research expertise and infrastructure by the coordination of IPK's Plant Phenotyping Platform management and use, and of the Bioinformatics Area of `Systems Analyses and Modelling´.

With seven permanently installed Research Groups and a third party-funded Young Investigator's Group (Integrated Mechanistic Models – IMM; until September 2025), that combine complementary expertise, the MOG department is fully enabled to address its goals and to carry out its major tasks.

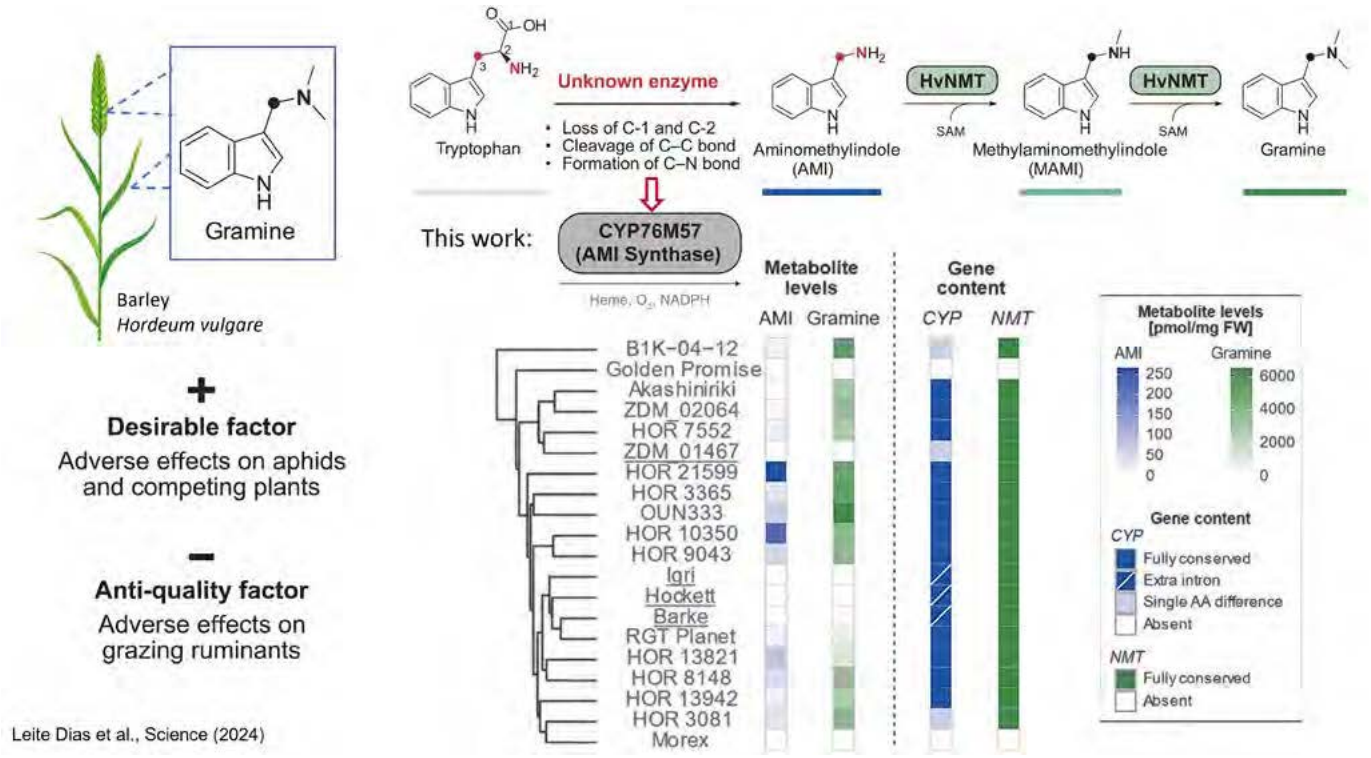


Figure 1: *Elucidation of the Gramine biosynthetic pathway in barley and variation of gene content and corresponding metabolite levels (Leite Dias et al., Science 2024).*

The scientific expertise and the technical skills of the MOG research groups (RGs) are integrated in three tightly interlinked research programmes: Growth Dynamics - investigating vegetative growth and development under the influence of dynamically changing, field-like conditions, Seed Biology - addressing developmental and metabolic processes that control cell, tissue, and organ formation in seeds as well as seed filling and maturation, and Systems Genetics - elucidating molecular-genetic mechanisms and elaborating improvement strategies through dynamic multi-omic QTL detection, functional network analysis, and modelling of regulatory and metabolic processes.

Major highlights of the MOG research work performed in 2024 and 2025 relate to important scientific advances addressing plant performance-related processes, improvements and use of research infrastructures, and the development of novel research tools:

Scientific research highlights include the demonstration that the sets of detected genetic factors affecting expression of plant growth-related traits are predominantly specific for particular environmental scenarios, which can be mildly contrasting such as constant vs. fluctuating illumination or drasticly deviating as in the case of combined heat and drought stress vs. favourable (control) conditions (Heuermann *et al.* 2024, Physiol. Plant.; Shi *et al.*, 2025, Plant Stress). This indicates the importance of specific sets of genes with complementary allelic effects in plant performance in particular environmental conditions.

The complete biosynthetic route of the allelopathic alkaloid gramine in barley was resolved including the demonstration of a cryptic oxidative rearrangement, the identification of a cardinal biosynthetic gene, and providing enzyme-level evidence for each step (Leite Dias *et al.*, Science 2024). Heterologous reconstruction in yeast and Nicotiana demonstrated the completeness of the biosynthetic pathway and opened novel opportunities to investigate ecological interactions and biochemical properties such as substrate specificities.

A Genome-wide characterisation of two-component system (TCS) elements in barley, that serve as common intracellular signal transduction pathway implicated in various processes of plant development and response to abiotic stress, enabled the identification of grain-specific phosphorelay genes (Hertig *et al.*, BMC Plant Biol. 2025) and to attribute selected TCS genes to different maternal and filial cell types in the endosperm transfer cell (ETC) region.

Mechanical constraints were shown to play a decisive role in triggering seed maturation beyond biochemical and molecular regulation (Rolletschek *et al.*, New Phytol 2024). Combining MRI-based 3D reconstruction with molecular, cellular, and metabolic analyses of *B. napus* embryos grown *in*

DEPARTMENT MOLECULAR GENETICS

vivo and *in vitro* under experimentally manipulated spatial constraints, it was shown that mechanical restriction accelerates the transition from cell proliferation to storage accumulation. These observations established mechanical signaling as an important driver of embryo maturation.

The development of deep learning approaches to decode cis-regulatory DNA resulted in a key achievement in understanding gene regulation at the genome-scale (Peleke *et al.* Nat. Commun. 2024). Convolutional neural networks trained on regulatory sequences were shown to accurately predict gene expression across model plant species and revealed sequence features underlying tissue- and condition-specific transcription. Interpretable model components enabled the identification of regulatory elements mediating the effects of non-coding sequence variation.

Combining information about QTL colocalisation across omics layers, correlations between omics features, and network approaches revealed prime candidate genes for metabolic and vegetative growth variation in rapeseed, regulatory modules, and subgenome-specific contributions to biomass accumulation (Knoch *et al.*, Plant J. 2024).

Research infrastructure advances and research tool developments were achieved by implementing and evaluating theoretical non-photochemical quenching (NPQ(T)) as a high-throughput proxy for conventional NPQ to assess photosynthetic performance of chickpea under drought stress (Lauterberg *et al.*, Sci. Rep. 2024).



Figure 2: *Automated detection (middle) and segmentation (right) of spikes in a Barley shoot image (left) using FRCNN and U-net DNN models (Ullah et al. (2024) Plant Phenomics).*

Robust software tools for quantitative phenotyping of grain development in the course of plant shoot growth were developed through systematic investigations of different AI approaches to detect and segment spike/awns in images of wheat and barley plants (Ullah *et al.*, Plant Phenomics 2024; Ullah *et al.*, Plant Methods 2025). Furthermore, novel AI frameworks for automated image generation and end-to-end (i.e. image-to-trait) computation were established (Gladilin *et al.*, Agronomy 2025).

In the MRI platform for non-invasive visualisation of the internal structures and biochemical compositions of plants, the chemical exchange saturation transfer (CEST) methodology was developed and implemented for plant systems. This enables sensitive *in vivo* detection of sugars and amino acids in metabolically active sink organs, including seeds, fruits, tubers, and taproots of major crops and provides unprecedented spatial and temporal insight into assimilate distribution and dynamics (Mayer *et al.*, Sci. Adv. 2024).

Outlook

Advancing its three research programmes, the MOG department is further dedicated to the identification of genes and favourable variants (alleles) affecting performance and resilience traits and to make key conceptual and tangible contributions to the long-term goal of enabling genome sequence variation-based prediction of crop plant performance in certain environmental scenarios. In the investigations, major priority will be given to the integration of spatially and temporally resolved phenotype and molecular omics analyses under specifically designed environmental conditions that will be combined with genetic mapping (systems mapping), network analyses, and process modelling. The generated data will support the gain of the necessary comprehensive knowledge of molecular mechanisms that govern important regulatory and metabolic processes in plants and of the involved genes, which will be required to estimate consequences of sequence variation. Integral will be the experimental testing of the predictions from mathematical modelling as well as ML / AI approaches on performance characteristics of certain sets of defined genotypes exposed to relevant and informative environmental regimes. To enable this, MOG will continue to operate, enhance, and use research infrastructures such as the IPK-PhenoSphere and the MRI facility, in particular to study dynamic processes in plants. Furthermore, it will pursue joint projects that establish mechanistic links between genomic sequence variation, environmental factors, and phenotypic expression of plant performance-related traits as done e.g. in the AVATARS project (BMFTR) and its expanded follow-up project, INTEGRA (BMFTR). The ongoing collaborations with Leibniz (IPB, ZALF, IGZ), university (MLU, JLU, CAU, LUH, HHU, Univ. Cologne), research institute (FZJ, MPI-PZ), and industry (NPZ/NPZi, KWS, BASF) partners will be extended and deepened including joint efforts within major initiatives such as CEPLAS or dip.



RESEARCH GROUP **HETEROSIS** (HET)

Head: Prof. Dr. Thomas Altmann

Mission

The research group Heterosis (HET) studies plant performance, chiefly in the crops rapeseed, barley, wheat and maize, and in the model *Arabidopsis*. The primary goal is the identification and characterisation of developmental processes, physiological mechanisms, (epi)genetic factors, and molecular networks that determine vegetative growth dynamics under varying environmental conditions that are relevant currently and in future weather scenarios. The research extends to plant organ interactions and plant performance predictor identification, and combines systems biology approaches with high-throughput non-invasive phenotyping techniques applied to plants cultivated in sophisticated controlled environment facilities. The achieved insights will support crop improvement strategies to enhance and secure crop yields and quality in the face of climate change.

Results

In 2024-2025, substantial contributions were made to the detection of prime candidate genes and metabolic pathways involved in plant (growth) performance and development: Combining information about QTL colocalisation across omics layers and correlations between omics features enabled the discovery of prime candidate genes for metabolic and vegetative growth variation in rapeseed (Knoch *et al.*, 2024, Plant J.). Jointly with further candidate genes identified in other projects such as AVATARS (BMFTR), they are now investigated for their crop improvement potential in the new INTEGRA project (BMFTR).

Combining time-resolved high-throughput phenotyping with genome-wide association analyses identified a QTL associated with root and shoot resilience to boron limitation in *Arabidopsis thaliana* (Alcock *et al.*, 2025, New Phytol.) and demonstrated that the sets of detected genetic factors affecting plant growth are predominantly specific for particular environmental scenarios (Heuermann *et al.* 2024, Physiol. Plant.; Shi *et al.*, 2025, Plant Stress). This opens novel perspectives on the action of natural genetic variants and their utilisation strategies including the enhanced prediction of genotype-specific trait dynamics with genetic markers (Hobby *et al.* 2025, Nat. Plants).

A combination of multi-omic profiling and epigenetic mapping strategies in a large panel of Arabidopsis F1 epigenetic hybrids showed that differentially methylated regions in parental pericentromeres are associated with hybrid methylation remodeling events at thousands of target regions throughout the genome (Kakoulidou *et al.*, 2024, Life Sci. Alliance).

Detailed molecular analyses revealed the involvement of the transcriptional regulators HOX1 (VRS1) and HOX2 in barley spike architecture (Thirulogachandar *et al.*, 2024, JXB).

Jointly with the Automated Plant Phenotyping (APP) and Image Analysis (BA) groups, the Heterosis group manages and optimises the use of IPK's plant phenotyping infrastructures accessible for collaborative research (Lauterberg *et al.*, 2024, Sci. Rep.; Gladilin *et al.*, 2025, Agronomy; Ulla *et al.*, 2025, Plant Methods), thus enabling the generation of unique data sets of highest quality (Knoch *et al.* 2025, Sci. Data; Shi et al, 2025, Data in Brief). The phenotyping infrastructure is key for numerous collaborative 3rd party funded projects, such as STRESS-STOPP (BMLEH), DRIVE (BMFTR), INTEGRA (BMFTR).

Embedding in IPK Research Themes

The group predominantly addressed the 'Systems Genetics' and 'Growth Dynamics' research programs within the Molecular Genetics (MOG) department, with an emphasis on vegetative development under varying environmental conditions. Through its involvement in the large transdisciplinary project AVATARS, the group also made significant contributions to the MOG research programme 'Seed Biology'.

The systems biological investigations on temporal and spatial dynamics of growth processes conducted by the group, are embedded in the IPK research themes 5 (Enhancing Plant Shoot

Selected publications

Heuermann MC et al. (2024) Strong prevalence of light regime-specific QTL in Arabidopsis detected using automated high-throughput phenotyping in fluctuating or constant light. ***Physiol. Plant.*** 176: e14255.

Knoch D et al. (2024) Integrated multi-omics analyses and genome-wide association studies reveal prime candidate genes of metabolic and vegetative growth variation in canola. ***Plant J.*** 117: 713-728.

Hobby* D, Tong* H, Heuermann* M et al. (2025) Predicting plant trait dynamics from genetic markers. ***Nat. Plants*** 11: 1018-1027.

Knoch D et al. (2025) A spatio-temporal transcriptomic and proteomic dataset of developing *Brassica napus* seeds. ***Sci. Data*** 12: 759.

Shi* R, López-Malvarv* A et al. (2025) Integrating high-throughput phenotyping and genome-wide association analyses to unravel Mediterranean maize resilience to combined drought and high temperatures. ***Plant Stress*** 17: 100954.

** Joint first authorship*

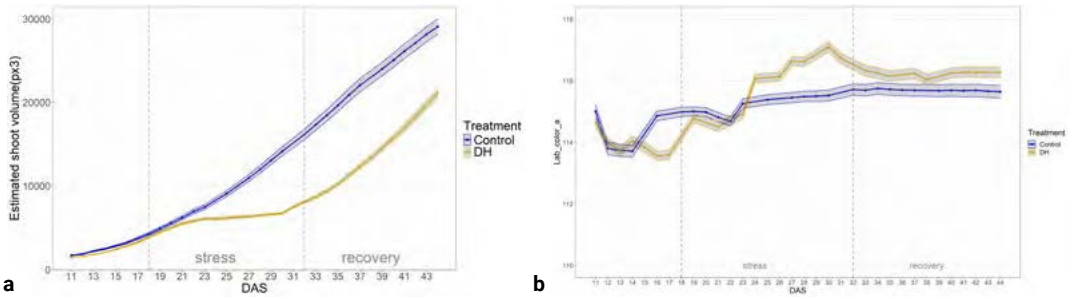


Figure 1: *Dynamic trait values (BLUP means) measured under control and combined drought and heat stress conditions: (a) estimated shoot volume, (b) Lab_color_a. DAS: days after sowing (Shi et al. 2025).*

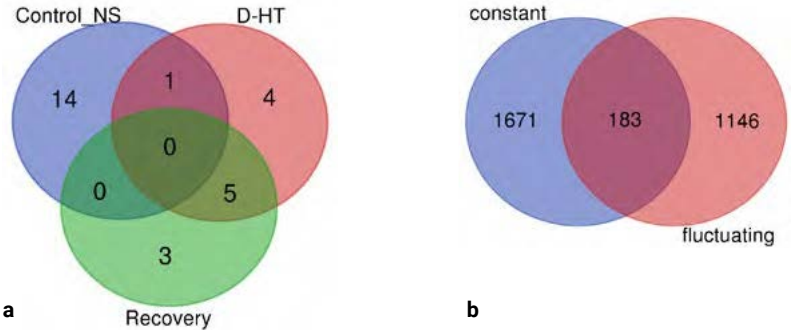


Figure 2: *a) VENN diagramm of marker-trait associations found under control/non-stress, combined drought and heat (D-HT), and during the D-HT recovery treatments in Mediterranean maize lines (Shi et al., 2025). b) Distinct sets of marker-trait associations detected in constant vs. fluctuating light regimes in Arabidopsis thaliana (Heuermann et al., 2024).*

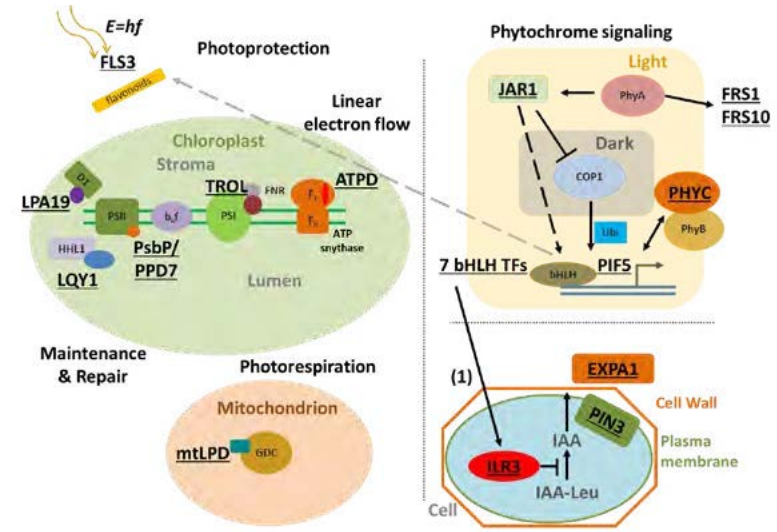


Figure 3: *Potential functions of 15 selected Arabidopsis thaliana candidate genes (bold & underlined) with their biological contexts that are associated with phenotypic trait expression in fluctuating light. (Heuermann et al. 2024)*

Performance), 4 (Roots for Resource-Efficient Crops), and 2 (Exploiting Bio-Digital Plant Data). This integration enables the identification and validation of gene functions within complex biological process networks.

Additionally, the group co-ordinated jointly with APP the IPK-wide plant phenotyping efforts and the corresponding research infrastructure enhancement, maintenance and use.

Outlook

By investigating model and crop species including Arabidopsis, rapeseed, barley, and wheat, the group aims to identify and characterise genetic loci that govern biomass production and seed yield under agriculturally relevant dynamic environmental conditions. To this end, time-resolved systems-level analyses will be further conducted to explore genetic factors influencing plant growth regulation, biomass heterosis, and stress resilience, also integrating spatial dynamics at the organ level, particularly the interplay between shoot and root systems. Genetic, physiological, and morphological predictors of yield and hybrid performance will be evaluated, with the goal of identifying robust biomarkers and predictive models.

Through the identification and characterisation of relationships between genetic factors, endo-phenotypes (molecular and physiological characteristics), and performance-related exophenotypes influenced by dynamic external cues, the group will further contribute to IPK's central research mission by generating fundamental knowledge on the molecular mechanisms that determine plant performance in changing environments.



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

Head: Dr. Jędrzej Jakub Szymański

Mission

The Network Analysis and Modelling (NAM) group develops computational and systems biology approaches to link genetic variation with complex plant traits. Its core objective is to identify regulatory mechanisms and molecular networks connecting genome structure, gene regulation, metabolism, and phenotype, with a focus on agriculturally relevant traits and plant performance under changing environmental conditions. NAM integrates multi-omics and multi-modal data using machine learning, deep learning, and network-based modelling to build predictive and interpretable genotype–phenotype models. In doing so, the group provides advanced bioinformatics and data-integration expertise that supports experimental research and crop improvement strategies across the department.

Results

During the reporting period 2024–2025, the NAM group delivered major advances in AI-driven regulatory genomics, integrative multi-omics analysis, and systems genetics of complex plant traits.

A key achievement was the development of deep learning approaches to decode cis-regulatory DNA. In Peleke *et al.* (2024), convolutional neural networks trained on regulatory sequences accurately predicted gene expression across model plant species and revealed sequence features underlying tissue- and condition-specific transcription. Importantly, interpretable model components enabled the identification of regulatory elements mediating the effects of non-coding genetic variation. This work was extended in Peleke *et al.* (2025), where transferable and accessible deep learning frameworks (deepCRE & deepCIS) were introduced. By applying transfer learning across species and transcription factor binding datasets, these models enable robust prediction of gene expression and regulatory variant effects even with limited training data, directly supporting predictive genomics and breeding applications.

In parallel, the NAM group advanced integrative systems biology approaches for trait dissection. The PanomiX framework (Sahu *et al.*, 2025) enables the joint analysis of genomic, transcriptomic, metabolomic, phenomic, and environmental data to identify coordinated molecular modules underlying complex traits. This scalable framework provides interpretable links between molecular variation and phenotypic outcomes and is now used across collaborative projects on growth, metabolism, and stress adaptation.

The group also made major contributions to stress biology through large-scale transcriptomic integration. In Psaroudakis *et al.* (2024), hundreds of tomato RNA-seq datasets were integrated to dissect heat, drought, and salt stress responses. While most transcriptional changes were found to be context-dependent, a small, robust core heat stress response was identified, comprising evolutionarily conserved genes involved in protein folding, redox homeostasis, regulation, and transport. Several of these genes colocalise with known heat tolerance loci, demonstrating the value of FAIR data integration for identifying biologically meaningful stress-response mechanisms.

In the area of complex trait genetics, NAM contributed integrative analyses combining high-throughput phenotyping, multi-omics data, and genome-wide association studies. In Knoch *et al.* (2024), thousands of robust QTL for early vegetative growth in canola were identified and prioritised across phenotypic, transcriptomic, and metabolomic layers. QTL colocalisation, correlation analyses, and network approaches revealed prime candidate genes, regulatory modules, and subgenome-specific contributions to biomass accumulation, providing mechanistic insight into early growth performance and biomass accumulation.

Together, these results establish NAM as a central driver of computational innovation at IPK, delivering methods and insights that link regulatory variation to complex traits and enable predictive modelling from genome to phenotype.

Selected publications

Knoch D et al. (2024) Integrated multi-omics analyses and genome-wide association studies reveal prime candidate genes of metabolic and vegetative growth variation in canola. ***Plant J.*** 117: 713-728.

Peleke FF et al. (2024) Deep learning the *cis*-regulatory code for gene expression in selected model plants. ***Nat. Commun.*** 15: 3488.

Rolletschek H et al. (2024) Mechanical forces orchestrate the metabolism of the developing oilseed rape embryo. ***New Phytol.*** 244: 1328-1344.

Sahu A et al. (2025) panomiX: Investigating mechanisms of trait emergence through multi-omics data integration. ***Plant Phenomics*** 7: 100131.

Washburn JD et al. (2025) Global genotype by environment prediction competition reveals that diverse modeling strategies can deliver satisfactory maize yield estimates. ***Genetics*** 229: iyae195.

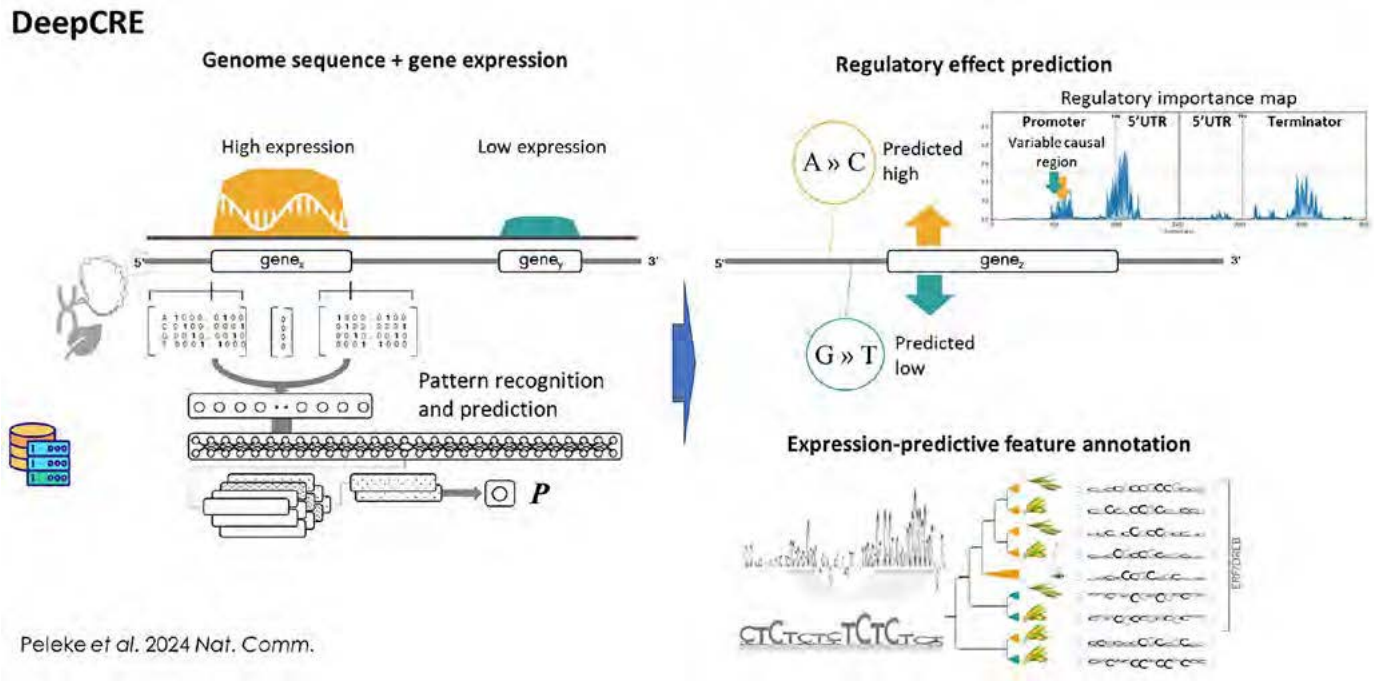


Figure 1: *DeepCRE, convolutional neural networks trained on regulatory sequences accurately predict gene expression (Peleke et al., Nat. Commun. 2024). Interpretable model components reveal sequence features (cis-regulatory elements) that drive transcription of genes.*

Embedding in IPK Research Themes

The work of the NAM group is embedded across multiple IPK research themes, with strongest contributions to theme 2 (Exploiting Bio-Digital Plant Data) and theme 1 (Activating Genetic Diversity). Through the development of machine learning methods for regulatory annotation and genotype–phenotype modelling, NAM supports predictive breeding and the functional interpretation of genetic variation. By applying systems genetics and dynamic modelling approaches, the group also contributes to research themes 4 (Roots for Resource-Efficient Crops) and 5 (Enhancing Plant Shoot Performance), linking genetic variation to physiological traits above- and below-ground. In addition, NAM plays a cross-cutting role in coordinating bioinformatics, systems modelling, and FAIR data management activities across departments, thereby enabling efficient integration of experimental and computational research within IPK.

Outlook

In the coming years, the NAM group will play a central enabling role in large-scale, integrative research initiatives, most prominently INTEGRA, PREBreed, and Twin, where computational modelling and AI-driven inference are essential for translating genomic diversity into actionable breeding knowledge. Within these projects, NAM provides the analytical and conceptual backbone for integrating pangenomic, regulatory, phenotypic, and environmental data, and for developing predictive models that connect genetic variation with trait performance. A core strategic focus is the use of artificial intelligence to identify functionally trait-associated alleles, with particular emphasis on regulatory variants and gene-network effects that are inaccessible to classical genetics. By combining deep learning–based regulatory annotation, variant-effect prediction, and systems-level modelling, NAM aims to enable smart breeding and targeted trait engineering strategies that move beyond single-gene targets towards network-informed allele selection. Through its contributions to digital-twin concepts and biodigital plant data infrastructures, NAM seeks to establish scalable, FAIR, and interpretable AI frameworks that support allele discovery, prioritisation, and deployment across crops and environments. In doing so, the group will help position IPK at the forefront of predictive, data-driven crop improvement, linking genome-scale knowledge directly to breeding decisions and future-ready trait design.



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

Head: Dr. Kerstin Neumann

Mission

The general objective of Automated Plant Phenotyping group is to improve crop performance and resilience to secure future yields under the dual challenges of a growing global population and climate change. The group manages and develops key plant phenotyping infrastructures at IPK, including state of the art whole-plant phenotyping platforms and the innovative IPK-PhenoSphere. Our research employs advanced plant phenomics to understand plant growth, physiology, and performance under optimal and abiotic stress conditions such as drought and heat or its combination or in response to nutrient deficiency. By integrating high-throughput phenotypic data with diverse genetic mapping panels and genome-wide information, we dissect the genetic architecture and temporal dynamics of complex traits related with biomass formation and stress tolerance, primarily in cereals and legumes. In addition, we promote FAIR phenotypic data management, the effective use of plant genetic resources, and the application of advanced digital approaches such as deep learning to support data-driven crop improvement.

Results

Within the framework of the INCREASE project, we implemented and evaluated theoretical non-photochemical quenching (NPQ(T)) as a high-throughput proxy for conventional NPQ to assess photosynthetic performance of chickpea under drought stress (Lauterberg *et al.* 2024). As conventional NPQ measurements require dark adaptation and are poorly suited for automated phenotyping, we tested whether NPQ(T), derived from light-adapted plants, provides a robust and scalable alternative for high-throughput phenotyping (HTP). A diverse panel of 60 chickpea genotypes (30 desi and 30 kabuli types) was phenotyped under well-watered and drought + recovery conditions using our medium-sized HTP system. NPQ(T) showed a strong correlation with conventional NPQ ($r \approx 0.9$) and was subsequently evaluated together with other HTP traits and with yield components. NPQ(T) increased under drought and decreased upon re-watering (Figure 1), reflecting enhanced energy dissipation in stress. Drought stress caused strong reductions in biomass and clear changes in plant architecture and colour traits (Figure 2). NPQ(T) showed significant correlations with biomass and yield-related traits such as hundred-seed weight, demonstrating its physiological relevance for drought performance. *Desi* genotypes generally maintained higher biomass and showed smaller relative changes in NPQ(T) than *kabuli* types, consistent with their greater drought tolerance. Overall, our results establish NPQ(T) as a rapid and informative trait that can be readily integrated into phenomics pipelines to support the identification of drought-tolerant germplasm. In a follow-up study, we analysed responses to combined heat and drought stress followed by recovery in the same panel. NPQ(T) during the severe stress phase emerged as the strongest predictor of grain yield ($R^2 = 0.73$). Genome-wide association analyses for yield and NPQ(T) based on whole-genome sequencing data are currently underway to identify underlying loci and candidate genes.

Additionally, APP has explored coffee root system architecture (RSA) under low and high nitrogen input in the frame of the EU project BOLERO. Based on cultivated and wild coffee species, we identified a species-specific response to nitrogen and together with the project partners generated root transcriptomic and microbiome data along with root anatomy studies. Based on root and shoot HTP data, Allocation Plasticity (AP) was determined identifying two species with higher AP and candidate genes in these two species under low N are involved in electron transport, sucrose synthesis and nitrate assimilation.

APP supported the conduction of 3 container- and 8 rhizotron- system experiments and 20 experiments across the 3 state-of the art HTP systems. In the DPPN Access 2.0 project, 4 collaborative experiments have been conducted in 2024-25.

Selected publications

Lauterberg M et al. (2024) Implementation of theoretical non-photochemical quenching ($NPQ_{(T)}$) to investigate NPQ of chickpea under drought stress with High-throughput Phenotyping. ***Sci. Rep.*** 14: 13970.

Gladilin E et al. (2025) End-to-end deep learning approach to automated phenotyping of greenhouse-grown plant shoots. ***Agronomy*** 15: 1117.

Sharma R et al. (2025) On the origin of the late-flowering *ppd-H1* allele in barley. ***Theor. Appl. Genet.*** 138: 246.

Soleimani S et al. (2025) Tillering plasticity of drought-stressed barley genotypes under different re-watering regimes. ***BMC Plant Biol.*** 25: 1368.

Wonneberger R et al. (2025) Integrating metabolomics and high-throughput phenotyping to elucidate metabolic and phenotypic responses to early-season drought stress in Nordic spring wheat. ***BMC Plant Biol.*** 25: 987.

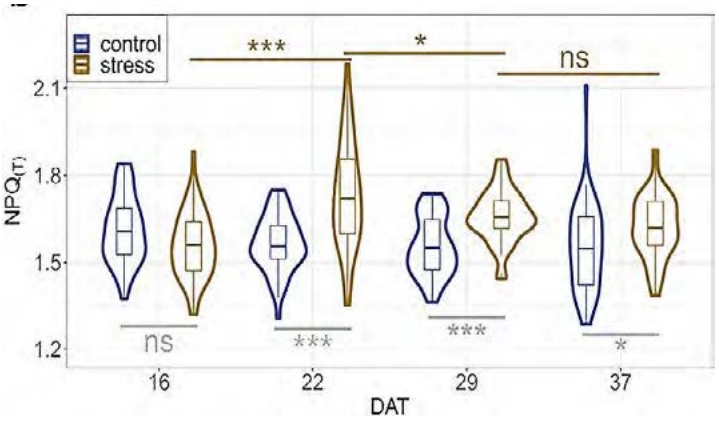


Figure 1: *NPQ(T) in time-course before (DAT 16), during (DAT 22, 29) and after (DAT 37) drought stress for 60 chickpea genotypes in well-watered and in drought treatment. DAT = days after transplanting*

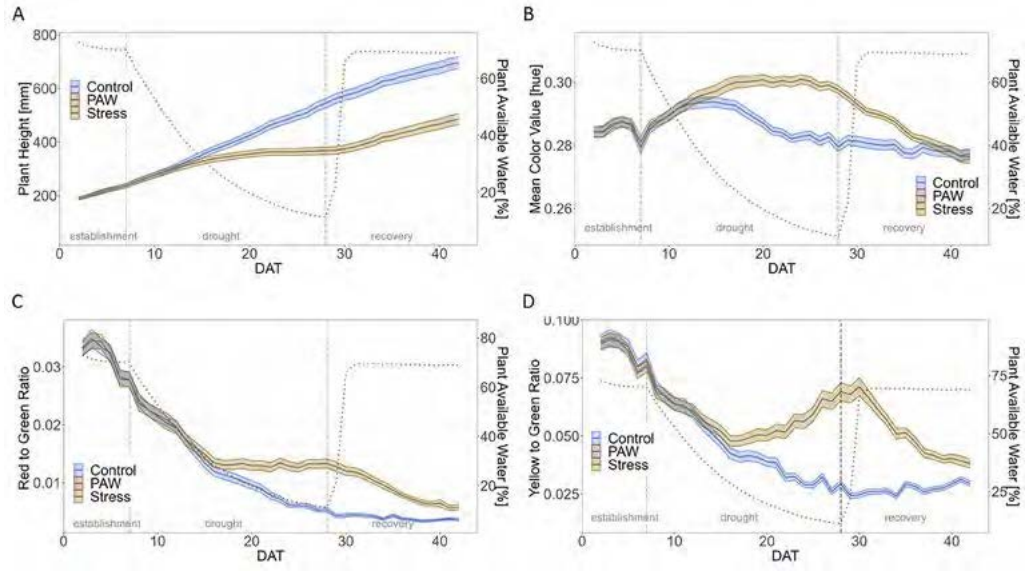


Figure 2: *Further HTP traits in time-course: biomass, yellow to green ratio, height and red to green ratio for 60 chickpea genotypes in well-watered and in drought treatment. DAT = days after transplanting*

Embedding in IPK Research Themes

As the group responsible for the IPK plant phenotyping infrastructure, we play a central role in research addressing plant performance under present and future climate scenarios and are an integral part of the research programme Growth Dynamics. Through our research activities, the group primarily contributes to Research Theme 4 (Improving Resilience of Root Systems) and Research Theme 5 (Enhancing Plant Shoot Performance).

Outlook

We continue the chickpea work by analysing GWAS for relevant traits in combined heat and drought stress. Currently, we address in more detail the challenge of phenology with groups BA and NAM in the DFG HetCrop project. In the Drive-project led by the QG group, we will test combined heat and drought on the medium-sized HTP system and test contrasting wheat genotypes under projected future conditions in the IPK-PhenoSphere to support and validate crop modelling approaches. Our work further investigates root plasticity and function to enhance nutrient acquisition and to explore interactions with beneficial microbiomes in cereals in the frame of the GreenEra-Hub project CerealBio. The network of collaborators is strengthened, by the DPPN Access 2.0 and TNA project Microbes4Climate and by the role of K. Neumann as the new chair of the GPZ Plant Phenotyping working group. Future research aims at exploring multistress (biotic and different abiotic stresses) responses in barley and durum wheat together with the BIM group (HORIZON-CL6-2025-01-BIODIV-12: Breeding for resilience: enhancing multi-stress tolerance in crops). The citizen science experiment of INCREASE continues to have a huge outreach to the public and we seek funding beyond the project time in the recently opened call HORIZON-CL6-2026-02-FARM2FORK-03: Boosting the competitiveness of protein crops in Europe (IA).



RESEARCH GROUP
METABOLIC DIVERSITY (MD)

Head: Dr. John C. D'Auria

Mission

The Metabolic Diversity (MD) group investigates the production, modification, and deployment of primary and specialised metabolites in crops and the influence of these compounds on growth, health, seed quality, and yield. We combine biochemistry, analytical chemistry, genetics, and synthetic biology to map biosynthetic pathways, identify regulatory genes, and develop experimental platforms for testing metabolite functions across species. Our goal is to obtain mechanistic insight and practical tools that link molecular metabolism to agronomic traits and enable translation into resilient, high-value crop improvements.

Results

During 2024–2025, the MD group produced verifiable advances in pathway discovery, functional validation, and methods for rapid testing, anchored by five key publications.

Pathway discovery and biochemical validation. We resolved the complete biosynthetic route of the allelopathic alkaloid gramine in barley, demonstrating a cryptic oxidative rearrangement and providing enzyme-level evidence for each step (Leite Dias *et al.*, Science 2024). Heterologous reconstruction in yeast and Nicotiana has enabled quantitative production assays that supply material for ecological tests and substrate specificity analyses.

Comparative genomics to guide candidate selection. Phylogenomic and synteny analyses of BAHD and SCP/SCPL gene families clarified their expansion and diversification in specialised metabolism (Naake *et al.*, Phil. Trans. R. Soc. B 2024). We applied these evolutionary filters to reduce false positives from co-expression screens and prioritise acyltransferase and serine carboxypeptidase candidates for biochemical assays.

Alkaloid evolution and synthetic biology. A synthesis review of tropane alkaloid evolution highlighted lineage-specific biosynthetic strategies and motivated our modular yeast approach (Chavez *et al.*, Curr. Opin. Plant Biol. 2024). Using modular expression in yeast, we identified and biochemically validated previously unknown enzymes in tropane pathways and deposited expression constructs for community use.

Crop-scale metabolomics and phenotyping. Integrating untargeted metabolomics with high-throughput phenotyping in Nordic Spring wheat produced a metabolic atlas of early season drought responses (Wonneberger *et al.*, BMC Plant Biol. 2025). Targeted GC-TOF/MS validation across independent experiments confirmed several metabolites as candidate markers for drought resilience and informed selection for future collaborative projects. Several other similar studies were published in this period focusing on barley and coffee biotic and abiotic stress responses.

Transformation methods for non-model crops. We optimised Agrobacterium-mediated transient and stable transformation protocols for common and Tartary buckwheat, shortening the validation cycle for candidate genes and enabling in planta complementation tests (Leite Dias *et al.*, Int. J. Mol. Sci. 2025).

Impact. The combined outputs moved multiple discoveries from candidate lists to validated biochemical pathways, produced crop-relevant metabolite markers, and delivered practical tools that accelerate functional testing and translation into breeding and management strategies.

Selected publications

Chavez BG, Leite Dias S, D'Auria JC (2024) The evolution of tropane alkaloids: Coca does it differently. ***Curr. Opin. Plant Biol.*** 81: 102606.

Leite Dias* S, Chuang* L, Liu* S et al. (2024) Biosynthesis of the allelopathic alkaloid gramine in barley by a cryptic oxidative rearrangement. ***Science*** 383: 1448-1454.

Naake T et al. (2024) Phylogenomic and synteny analysis of BAHD and SCP/SCPL gene families reveal their evolutionary histories in plant specialized metabolism. ***Philos. Trans. R. Soc. Lond. B Biol. Sci.*** 379: 20230349.

Leite Dias S et al. (2025) Efficient *Agrobacterium*-mediated methods for transient and stable transformation in common and Tartary buckwheat. ***Int. J. Mol. Sci.*** 26: 4425.

Wonneberger R et al. (2025) Integrating metabolomics and high-throughput phenotyping to elucidate metabolic and phenotypic responses to early-season drought stress in Nordic spring wheat. ***BMC Plant Biol.*** 25: 987.

** Joint first authorship*



Figure 1: *Flowers of Hypericum perforatum, specifically genotype HyPR01, which is known to produce copious amounts of hypericin, a natural product with medicinal properties such as anticancer and a potential treatment for Alzheimer's disease.*

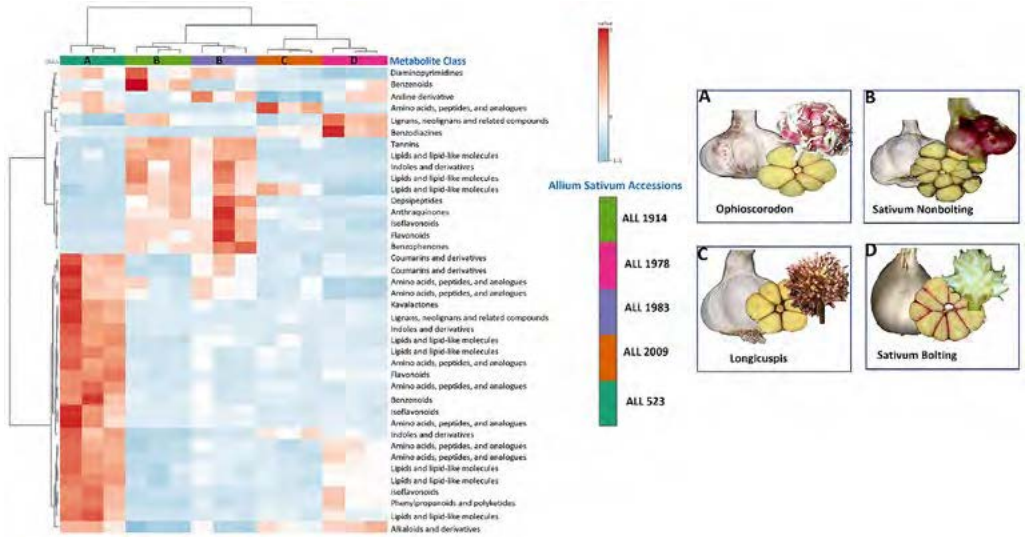


Figure 2: *HCA of 40 ANOVA-significant metabolites grouped by chemical ontology classes, revealing metabolic markers of genetic variation among five Allium sativum accessions representing four subspecies (Ophioscorodon, Sativum non-bolting, Longicuspis, and Sativum bolting).*

Embedding in IPK Research Themes

The MD group advances five IPK themes: Activating Genetic Diversity, by metabolite-guided genebank screening to reveal useful alleles and chemotypes; Generating and Exploiting Biodigital Plant Data, by integrating metabolomics with genomics and phenomics and delivering annotated datasets and APIs; Engineering Genomes and Chromosomes, by providing candidate genes, CRISPR constructs, and transformation workflows; Improving Resilience of Root Systems, by identifying root-relevant metabolites and testing effects on root physiology and microbe interactions; and Enhancing Plant Shoot Performance, by linking specialised metabolism to yield and stress traits and producing metabolic markers for selection.

Outlook

Over the next reporting period, the MD group will scale multisite longitudinal sampling across target crops, such as garlic and barley. This will include the publication of curated and annotated metabolomic datasets with standardised metadata and APIs. We will complete prioritised enzyme validations using phylogenomic filters and modular yeast reconstructions, develop targeted LC MS/MS assays for low abundance metabolites, and validate metabolic markers in multi-environment trials. We will also expand and optimise our ongoing spatial transcriptomics platform development to integrate the platform into several key IPK relevant research themes.



RESEARCH GROUP **IMAGE ANALYSIS** (BA)

Head: Dr. Evgeny Gladilin

Mission

The research group Image Analysis (BA) focuses on development of advanced algorithms and integrative software tools for quantitative analysis of multimodal and multidimensional image data from diverse imaging systems including major IPK high-throughput phenotyping facilities (IPK-PhenoSphere, conveyor-based whole plant systems, LTA, LTB, LTC). The research activities of the group include development of novel methods for a wide spectrum of image analysis tasks from image segmentation, co-registration, classification to quantitative phenotyping and computational modelling of relevant plant structures, e.g., shoots, roots, leaves, awns, seeds, tissues, and cells.

Results

Within the reported period, research activities of the Image Analysis group were dedicated to further development of algorithmic solutions for efficient analysis of shoot and root images from automated phenotyping facilities in glasshouses, phytochambers, and the IPK-PhenoSphere. A number of novel phenotyping tasks originating from several third-party funded projects in cooperation with other IPK groups and external parties were in focus of the group research. Within the scope of the BMFTR funded SmartRoot, NeatWheat, DPPN Access 2.0 projects, a novel CNN-based approach to multi-class segmentation of Rhizotron root images was developed for a differential analysis of primary and second root architecture in context of nitrogen treatment studies. The results of this study carried out in cooperation with AG MPE and APP demonstrate the capability of the developed AI multi-classed root image segmentation to accurately differentiate and quantify dynamics of growth of primary and secondary root system in barley plants, (Narisetti *et al.*, Comput. Electron. Agric. 2026) see Figure 1.

Systematic investigations of different AI approaches to spike/awns detection and segmentation in green-house images of wheat and barley cultivars were performed to enable a robust software tools quantitative phenotyping of grain development in course of plant shoot growth (Ullah *et al.* Plant Meth. 2024 and Ullah et al Plant Phen. 2025). In addition to major two tasks of plant image segmentation and pattern detection, novel AI frameworks for automated image generation and end-to-end (i.e. image-to-trait) computation were in focus of group investigations in this period (Gladilin *et al.* Agronomy 2025). Furthermore, the group continued the line of research within the scope of the BMFTR AVATARS (Gladilin *et al.* Agronomy 2025) project by developing software pipeline for hyperspectral image analysis and physics-based modelling of seed growth using 2D and 3D image data (Maria-Antony *et al.* iScience 2024). In 2025, the PhD student in the Image Analysis group, Narendra Narisetti, successfully defended his PhD thesis on "Development of automated approaches to high-throughput plant image analysis" at the Harz University of Applied Sciences.

Selected publications

Maria Antony AN, Narisetti N, Gladilin E (2024) Linel2D-Net: A deep learning approach to solving 2D linear elastic boundary value problems on image domains. ***iScience*** 27: 109519.

Ullah S et al. (2024) High-throughput spike detection in greenhouse cultivated grain crops with attention mechanisms-based deep learning models. ***Plant Phenomics*** 6: 0155.

Gladilin E et al. (2025) End-to-end deep learning approach to automated phenotyping of green-house-grown plant shoots. ***Agronomy*** 15: 1117.

Narisetti N (2025) Development of automated approaches to high-throughput plant image analysis. (PhD Thesis) Hochschule Harz, Promotionszentrum Ingenieurwissenschaften und Informationstechnologien (IWIT), Wernigerode. 199 pp.

Ullah S et al. (2025) Automated generation of ground truth images of greenhouse-grown plant shoots using a GAN approach. ***Plant Methods*** 21: 126.

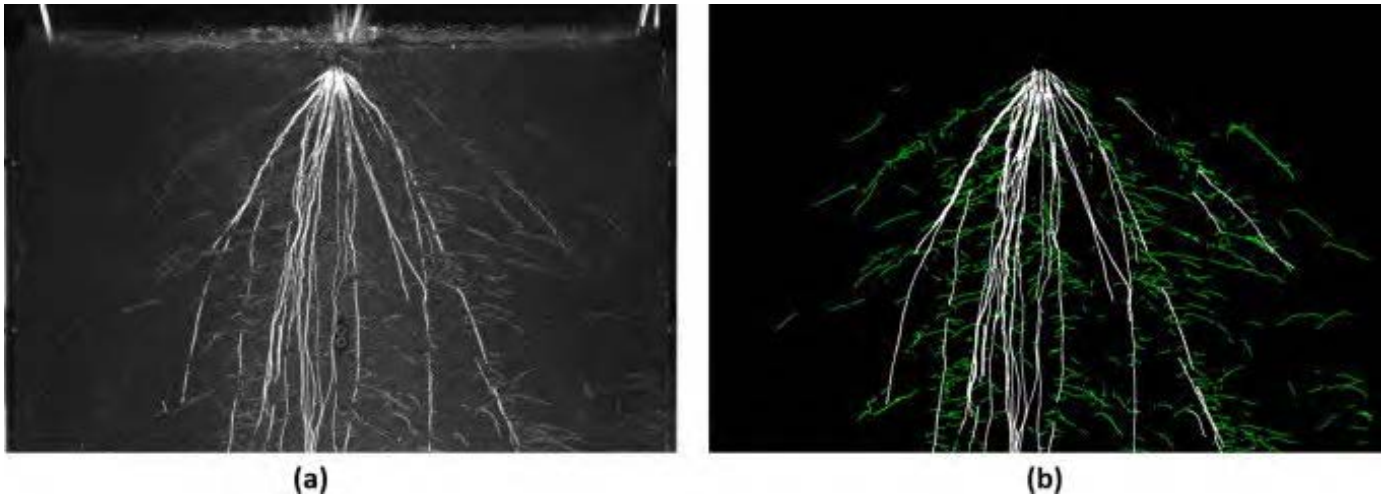


Figure 1: *: Example of multi-class segmentation of barley root image: (a) original, (b) segmented lateral roots.*

Embedding in IPK Research Themes

Efficient analysis of a continuously growing amount of heterogeneous multimodal image data poses a challenging task even to state-of-the-art machine and deep learning methods. With development of image analysis solutions, in particular, advanced AI approaches to segmentation, classification, quantification as well as predictive modelling of plant structures, the group essentially contributes to the Research Theme 2. “Exploiting Biodigital Plant Data” with further links to Research Themes 3 “Roots for resource efficient crops” and 4. “Enhancing shoot performance”.

Outlook

The Image Analysis group is tightly involved in a number of phenotyping projects (EU Bolero, DFG Hetcrop, BMFTR DPPN Access 2.0) requiring further development of algorithmic solutions and software pipelines for whole shoot/root image analysis but also phenotyping of small plant parts and organs, such as spike, awn, seeds, nodules segmentation and classification. The group will continue the development of methods and applications to further data modalities including hyperspectral and 3D imaging from the IPK-PhenoSphere facility. On methodological side, investigation and application of efficient AI methods for conventional analytic but also novel generative, predictive and e2e tasks will remain in the focus of future.



RESEARCH GROUP **SEED DEVELOPMENT** (SE)

Head: Dr. Jozefus Schippers

Mission

The research focus of the group Seed Development is on the molecular and genetic regulation of plant development and stress adaptation, with special emphasis on transcriptional and signalling networks that guide grain development. This includes the identification of transcriptional networks that control cell proliferation, cell differentiation, organ size and nutrient storage. In addition, we focus on unravelling the impact of abiotic stress on plant development and survival, during heat, drought and flooding in crops and model systems. Ultimately, we perform molecular functional genomics studies in cereals to reveal relevant processes and in the long-term provide means to tailor crops for future needs.

Results

The research of the SE group can be divided into several topics that are in line with its objective to obtain a molecular understanding of plant development and stress adaptation. These topics are: (i) Molecular and genetic regulation of endosperm and endosperm transfer cell (ETC) development in barley (ii) Implications and regulation of reactive oxygen species (ROS) homeostasis for plant development and stress signaling (iii) Sink-source relationships during plant senescence and grain filling. Next to that, the group has developed two main methodology platforms: laser capture microdissection (LCM) coupled to RNA-seq and DNA-affinity Purification Sequencing (DAP-SEQ), to enable the elucidation of molecular and genetic pathways.

The study of endosperm development focusses on the elucidation of gene-regulatory-networks (GRNs) to obtain a molecular understanding of seed formation in a spatial and temporal resolution. An important reached goal was the implementation of DAP-seq in barley, wheat, sugar beet and maize. This has resulted in the elucidation of the GRNs of transcription factors regulating barley endosperm development, sugar beet size, maize drought tolerance and spike development in barley and wheat. Our current goals are to validate the GRNs through genetic models and use the obtained knowledge for targeted approaches to modify gene expression to achieve beneficial effects on plant performance.

In addition, the SE group continues its molecular research on two-component signaling (TCS) pathways, stress signaling pathways (hypoxia, heat and drought) and ROS signaling. In mosses, we have uncovered an essential role of superoxide dismutase for male gametogenesis and will test this knowledge in the future in cereals, as especially heat waves have a detrimental effect on plant fertility and their reproductive success.

The SE group is well-embedded within the MOG department through the AVATARS project. In addition, we have active collaborations within the IPK on the elucidation of GRNs using DAP-seq, and transcript analysis using the LCM platform. We now are part of the PREBreed consortium led by Prof Stein. Furthermore, we have active collaborations with researchers in Germany, but also outside on research themes that align with the main aims of the group. In recent years we have hosted multiple BSc and MSc students, and the group has been represented numerous times at national and international conferences.

Selected publications

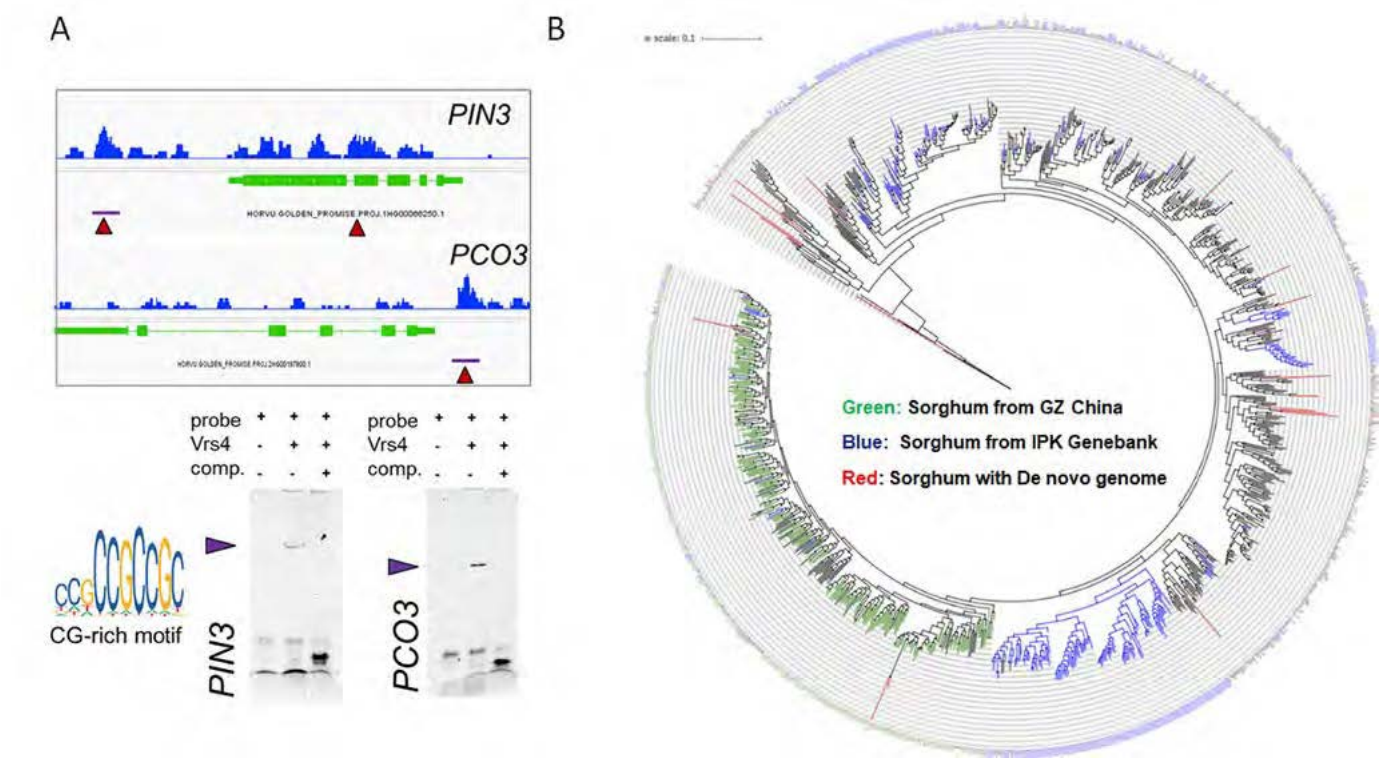
Brunner S et al. (2024) Field trials reveal trade-offs between grain size and grain number in wheat ectopically expressing a barley sucrose transporter. ***Field Crops Res.*** 316: 109506.

Schippers JHM et al. (2024) ERFVII-controlled hypoxia responses are in part facilitated by MEDIATOR SUBUNIT 25 in *Arabidopsis thaliana*. ***Plant J.*** 120: 748-768.

Hertig CW et al. (2025) Genome-wide characterization of two-component system elements in barley enables the identification of grain-specific phosphorelay genes. ***BMC Plant Biol.*** 25: 209.

Renziehausen T et al. (2025) Oxygen sensing and plant adaptation to flooding in a changing climate. ***Philos. Trans. R. Soc. Lond. B Biol. Sci.*** 380: 20240238.

Wang H, van Dongen JT, Schippers JH (2025) Differential regulation of 26S proteasome activity, abundance and transcription during leaf development and senescence. ***J. Exp. Bot.*** 76: 4374-4387.



Embedding in IPK Research Themes

The group strongly contributes to all three MOG research programmes (Growth Dynamics, Seed Biology, Systems Genetics) by uncovering fundamental knowledge on the molecular processes that determine plant performance and yield under changing environments. We combine state-of-the art molecular techniques with genome-wide omics-approaches and physiological assessments to identify and characterise genes, mechanisms and networks that regulate and control grain formation and plant survival. Within the department we actively pursue common projects, like for instance AVATARS (HET, AAN, IMM), and integrate metabolomics expertise (MD group), and plant phenotyping approaches (HET, APP). Next to that, we collaborate with groups from all other departments, particularly with the CSF group to resolve the process of tissue-specific elimination of B chromosomes in embryos of monocots.

Outlook

The SE group has developed several tools (i.e. DAP-seq, protoplast assays) that enabled us to uncover trancriptional networks underlying grain development. We currently focus on validating the biological impact of the networks by generating trangenic barley lines (PRB) and using the allelic variation in IPK's genebank (RGR, GGR). Our main aim is to enhance functional genomics in barley through several collaborative projects with other research groups and commercial partners. In addition, we have initiated working on Sorghum bicolor, which represents an attractive future crop for Europe. The main challenge for the group is to maintain the excellent research level.

Figure 1: *A snapshot from two projects of the research group SE. (A) Genome browser representation of binding events by the transcription factor VRS4, reveals that the promoters of the auxin transporter gene PIN3 and the hypoxia core gene PCO3 are bound by VRS4. Subsequent EMSA assay confirms binding of VRS4 in vitro to the identified sequence motifs present in both promoters. (B) We sequenced the IPK sorghum collection in collaboration with Prof. Dr. Hai-Chun Jing and revealed that it is a highly diverse and interesting collection. We currently use this information for a GWAS study on grain properties.*





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

Head: Dr. Ljudmilla Borisjuk (until 31. August 2025) and
Dr. habil. Hardy Rolletschek (from 1. September 2025)

Mission

Our research team advances the understanding of assimilate supply, metabolism, and internal architecture in living plants and seeds, with a strong focus on plant MRI and NMR–based approaches. Using non-invasive, *in vivo* and spatially resolved approaches, we trace the uptake, transport, and conversion of assimilates into storage products. MRI is tightly integrated with near-infrared microspectroscopy, mass spectrometry, and molecular tools to achieve a comprehensive, multimodal view on plant function. This unique *in vivo* imaging platform enables us to address long-standing questions in plant growth and development and serves as a hub for data integration and international collaboration.

Results

Understanding seed development and metabolism *in vivo* is central to plant biology and crop improvement yet remains technically challenging due to the structural complexity and heterogeneity of tissues. Our research establishes advanced MRI–based approaches as a non-invasive platform to resolve structural, metabolic, and developmental processes in intact, living seeds and other sink organs.

Our MRI platform has contributed to a range of studies aimed at the non-invasive visualisation of the internal structure of crop plants, providing access to aspects of plant interiors that are not accessible with conventional methods. This is exemplified by investigations in maize, where MRI enabled detailed insights into internal organisation beyond the reach of standard analytical tools (Yu *et al.*, 2024, Nat. Genetics).

We developed and implemented chemical exchange saturation transfer (CEST-) MRI for plant systems, enabling sensitive *in vivo* detection of sugars and amino acids in metabolically active sink organs, including seeds, fruits, tubers, and taproots of major crops (Figure 1A). Unlike conventional magnetic resonance spectroscopy, CEST MRI is robust against magnetic susceptibility artefacts and therefore allows metabolic imaging in heterogeneous botanical samples. The method provides unprecedented spatial and temporal insight into assimilate distribution and dynamics and was rigorously validated using complementary techniques such as chemical shift imaging, infrared microscopy, chromatography, and mass spectrometry (Mayer *et al.*, 2024, Sci. Adv).

We demonstrated that beyond biochemical and molecular regulation, mechanical constraints play a decisive role in triggering seed maturation. By experimentally manipulating spatial constraints on embryo growth *in vivo* and *in vitro*, and combining MRI-based 3D reconstruction with molecular, cellular, and metabolic analyses, we show that mechanical restriction accelerates the transition from cell proliferation to storage accumulation in the developing seed of oilseed rape. This process is associated with cell cycle arrest, altered redox metabolism, transcriptional reprogramming, and metabolic flux control, establishing mechanical signaling as an important driver of embryo maturation (Rolletschek *et al.*, 2024, New Phytol).

To advance current seed phenotyping approaches, we developed the MRI-Seed-Wizard, a deep learning–based tool for automated analysis of plant MRI data (Figure 1B). This platform enables non-destructive, three-dimensional quantification of seed morphometry, internal architecture, and composition, including traits inaccessible to conventional imaging methods. Advanced MRI protocols allow simultaneous analysis of multiple seeds, substantially increasing throughput. The applicability of this approach is demonstrated in cereal grains and is readily transferable to a wide range of crop species (Plutenko *et al.*, 2025, Jour. Exp. Bot).

Selected publications

Mayer S et al. (2024) Metabolic imaging in living plants: A promising field for chemical exchange saturation transfer (CEST) MRI. ***Sci. Adv.*** 10: eadq4424.

Rolletschek H et al. (2024) Mechanical forces orchestrate the metabolism of the developing oilseed rape embryo. ***New Phytol.*** 244: 1328-1344.

Yu P et al. (2024) Seedling root system adaptation to water availability during maize domestication and global expansion. ***Nat. Genet.*** 56: 1245-1256.

Plutenko I et al. (2025) MRI-Seed-Wizard: combining deep learning algorithms with magnetic resonance imaging enables advanced seed phenotyping. ***J. Exp. Bot.*** 76: 393-410.

Sahu A et al. (2025) panomiX: Investigating mechanisms of trait emergence through multi-omics data integration. ***Plant Phenomics*** 7: 100131.

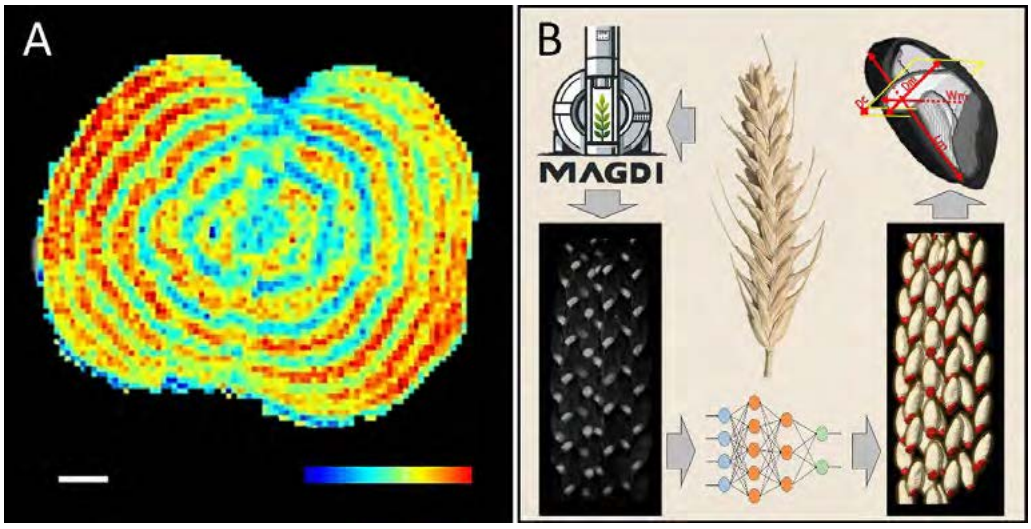


Figure 1: *Pioneering work at AAN shows how MRI can provide non-invasive access to the internal structure and composition of plants, paving the way for the digitalisation of living plants. (A) shows spatial sugar distribution in sugar beet taproots, as revealed by CEST MRI (Mayer et al., 2024). (B) The integration of MRI and artificial intelligence within the BMFTR project MAGDI (MAGnetic Resonance for the DIgitalisation of Plants) resulted in the development of the MRI-Seed-Wizard, which opens up new possibilities for the automated phenotyping of seeds (Plutenko et al., 2025).*

Integrating complex multi-omics and phenotyping data remains a challenge in plant science. We were further involved in development of panomiX, a user-friendly toolbox that automates multi-omics integration and machine-learning–based interaction analysis. Applied to a plant heat-stress dataset combining phenotyping, transcriptomics, and infrared spectroscopy, the new toolbox revealed condition-specific links between photosynthetic traits and stress-responsive kinases. The platform simplifies data interpretation and accelerates the identification of candidate genes underlying plant traits (Sahu *et al.*, 2025, Plant Phenomics).

Our results not only establish plant MRI as a powerful *in vivo* platform for studying plant life but also demonstrate its central role in integrating diverse omics approaches to link metabolism, mechanics, and development across biological scales. By combining advanced MRI methodologies with artificial intelligence and multi-omics analyses, our research enables a systems-level understanding of seed biology and delivers practical tools for seed phenotyping and crop improvement.

Embedding in IPK Research Themes

Our work is integrated into the IPK Research Themes *Enhancing Plant Shoot Performance* and *Generating and Exploiting Bio-Digital Plant Data*. To provide services on an Institute-wide level, our research group is developing technological platforms such as MRI and high-resolution mass spectrometry.

Outlook

Future work will push the boundaries of plant MRI, establishing it as a central tool to unravel how assimilates move, accumulate, and shape seed and plant performance. Major priority will be given to the spatially resolved analysis of sink organs, the study of dynamic processes and their modelling, use of AI-driven image analysis and tracer-based visualisations (BMFTR project MAGDI and other research proposals). Of further relevance will be the study of plant-microbiome interactions (DFG project). By reconstructing vascular networks in 3D, and capturing dynamic allocation processes, we aim to generate knowledge that directly informs breeding for yield and resilience.



YOUNG INVESTIGATOR GROUP **INTEGRATIVE MECHANISTIC MODELS** (IMM)

Head: Dr. Mary-Ann Ebeling (01.01.2021 – 30.09.2025)

Mission

The primary mission of the working group was the development and application of integrative metabolic modelling approaches to elucidate complex plant traits. Specifically, within the AVATARS project, our objective was to reconstruct organ- and time-specific metabolic networks for Brassica napus during seed development. These models integrated multi-omics data (transcriptomics, proteomics, metabolomics) along with genotypic and environmental information. Leveraging flux balance analysis (FBA), we sought to predict metabolic phenotypes and adjust metabolic fluxes throughout seed development. This work establishes a functional context for data analysis, ultimately enhancing the understanding of seed metabolism across diverse conditions.

Results

The reporting period was characterised by the resumption and finalisation of work following a 20-month interruption due to parental leave (Oct 2021 – May 2023). Work focused on the integration of heterogeneous datasets obtained from the AVATARS project partners to construct high-fidelity metabolic models of B. napus seed development, see Figure 1.

The workflow illustrates the process of generating high-fidelity, time-resolved metabolic network models for *B. napus* seeds. It begins with the collection of multi-omics data (transcriptomics, proteomics, metabolomics) along with genotypic and environmental information (A). These heterogeneous datasets are harmonised, pre-processed, and systematically integrated (B) to refine the automatically reconstructed B. napus metabolic network (C). The integration step applies constraints, derived from omics data and environmental conditions to enzyme capacities and objective functions within the model. The final integrative mechanistic model (D) allows for the application of Flux Balance Analysis (FBA) to simulate time- and organ-specific flux distributions and predict metabolic phenotypes, providing functional context to the observed omics data.

A major component of this phase was the systematic integration of collected genotypic, multi-omic, and environmental data as flux constraints on enzyme capacities and objective functions. The goal was to generate linked, time-resolved metabolic networks capable of simulating flux distributions during different developmental stages. We specifically aimed to compare flux-balance-derived metabolic phenotypes with measured metabolic seed traits to assess the consequences of genetic and environmental perturbations.

Furthermore, to facilitate the exploration of these complex multi-omics datasets, we developed a custom Streamlit web application, see Figure 2. Following the pre-processing and harmonisation of all transcriptomic, proteomic, and metabolomic data for compatibility with Python-based modelling workflows, this tool was deployed to allow for interactive visualisation across five developmental stages and seed organs. The application features specific modules for exploring regulatory miRNA-mRNA subnetworks and comparing gene regulatory patterns. Ultimately, this interface supports the functional interpretation of metabolic shifts by allowing researchers to view empirical omics data alongside simulated flux distributions.

Initial automated reconstruction of *B. napus* lipid metabolism pathways proved insufficient, yielding topologically incomplete models that failed to match experimental flux data due to the pathway's complexity and compartmentalization. This "negative" finding necessitated extensive manual curation, demonstrating that standard automated pipelines require substantial expert refinement for highly specialised plant metabolic networks to achieve biological accuracy.

As a dedicated subproject within the AVATARS initiative, we conducted a comprehensive analysis on the regulatory microRNA (miRNA) landscape during *Brassica napus* seed development. Using Principal Component Analysis (PCA) and Uniform Manifold Approximation and Projection (UMAP), we demonstrated that miRNA expression patterns are predominantly driven by developmental stage and organ identity, rather than by genotype or environmental conditions (benign vs. detrimental). We identified *bna-miR159* as the most abundantly expressed miRNA, suggesting it

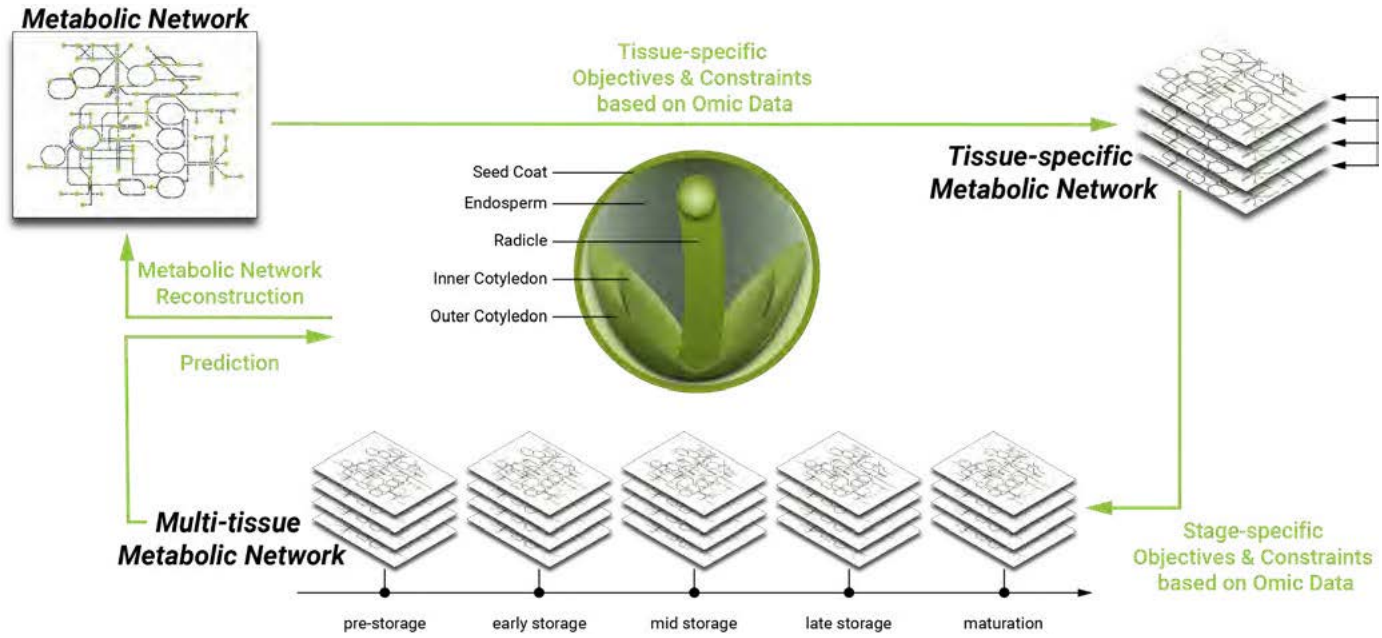


Figure 1: *Workflow to create an integrative metabolic whole seed model for B. napus seed development as part of the AVATARS project.*



a **b** **c**

Figure 2: *Streamlit Application for Multi-Omics Integration in B. napus Seed Development*

(A) Landing page of the custom Streamlit web application developed to facilitate interactive exploration of transcriptomic, proteomic, and metabolomic datasets. (B) Visualisation of integrated omics data, exemplified by expression profiles of selected miRNAs and their predicted mRNA targets across developmental stages and seed organs. (C) Entry point for targeted exploration of regulatory relationships via an interactive graph of miRNA–mRNA subnetworks. This tool enables dynamic comparison of gene regulatory patterns and is designed to interface with computed flux distributions for functional interpretation.

plays a central regulatory role in the seed. Furthermore, we successfully reconstructed functional miRNA-mRNA subnetworks, see Figure 2(C), linking key families—such as *miR156* (flowering/SPL targets) and *miR172* (lipid metabolism/AP2 targets)—to specific biological processes. Notably, the analysis revealed that the core developmental miRNA programme is highly robust, showing limited global variation in response to environmental stress markers.

Embedding in IPK Research Themes

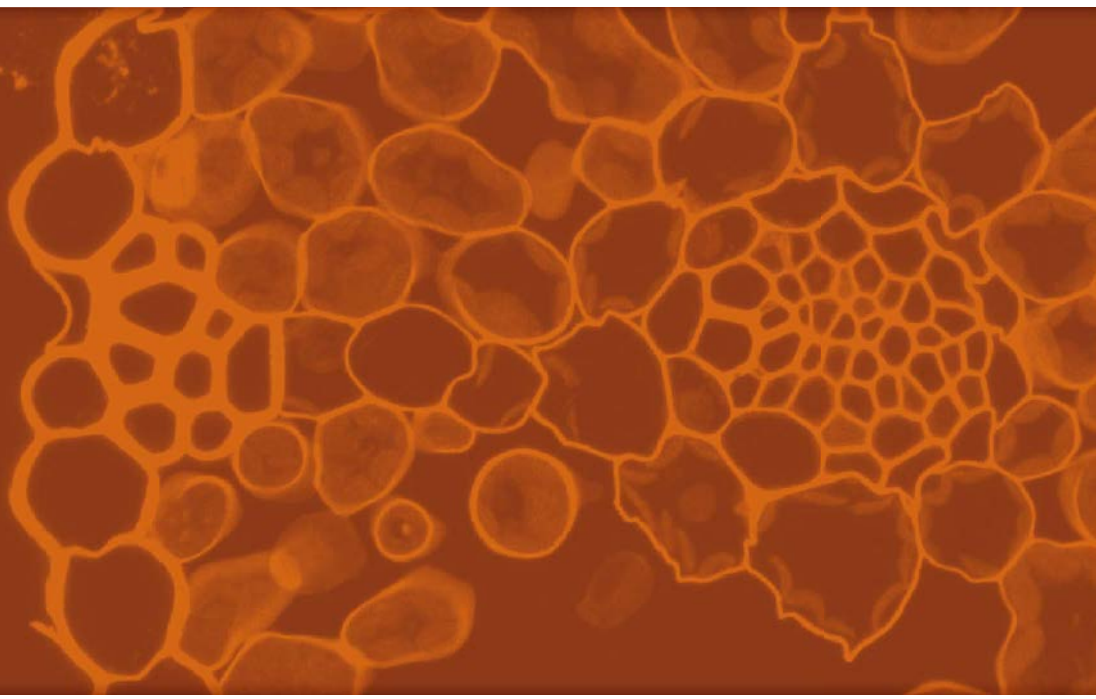
The group's work aligns with the IPK Research Strategy 2025–2030, specifically contributing to Theme 2: Exploiting biodigital plant data. By integrating multi-omics datasets into functional metabolic models, we directly addressed the challenge of transforming raw data into mechanistic knowledge. Additionally, the focus on *B. napus* seed development supports Theme 4: Enhancing shoot performance, as our models aimed to optimise seed quality and yield through a better understanding of metabolic flux distribution during reproductive development.

Following the completion of the AVATARS project, existing research questions will continue to be addressed with RG HET, SE, AAN and BA.

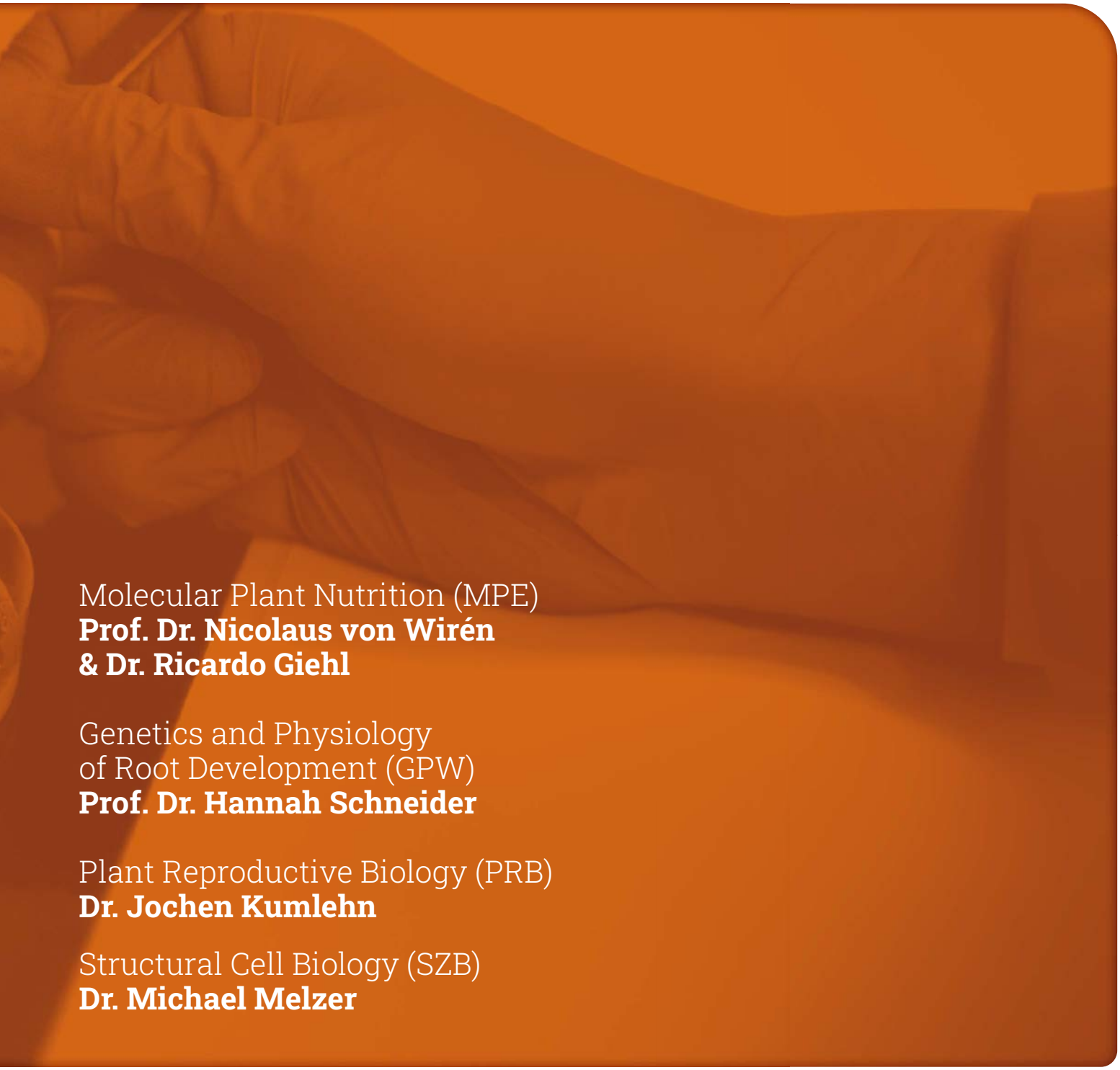
Outlook

The AVATARS project officially concluded in September 2025. With the end of the project funding and no follow-up financing acquired, the young investigator's group IMM was closed effective September 2025. Consequently, there are no future research priorities to report. The former group leader, Dr. Mary-Ann Ebeling, has transitioned to a new role within the institute, focusing on Research Data Management (RDM) to support the long-term preservation and accessibility of the generated data in plant sciences, ensuring their continued utility for the scientific community in line with FAIR principles and IPK's commitment in the NFDI's DataPLANT, FAIRagro, NFDI4Biodiversity and the LeibnizData research network.





PHYSIOLOGY
AND
CELL BIOLOGY



Molecular Plant Nutrition (MPE)
Prof. Dr. Nicolaus von Wirén
& Dr. Ricardo Giehl

Genetics and Physiology
of Root Development (GPW)
Prof. Dr. Hannah Schneider

Plant Reproductive Biology (PRB)
Dr. Jochen Kumlehn

Structural Cell Biology (SZB)
Dr. Michael Melzer

DEPARTMENT PHYSIOLOGY AND CELL BIOLOGY



DEPARTMENT PHYSIOLOGY AND CELL BIOLOGY

Head: Prof. Dr. Nicolaus von Wirén

Mission

The mission of the department is primarily the characterisation and manipulation of performance and stress resilience traits in crops. Research focuses on transport, metabolic and developmental processes in different plant organs, which are relevant for the agronomic performance and stress tolerance of crops or their adaptation to agricultural and biotechnological production conditions. These fundamental and application-oriented 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. With a strong focus on resource efficiency and root-related traits, departmental research addresses core topics of the German National Sustainability Strategy and the Federal High-Tech Strategy as well as the UN sustainability goals.

Research

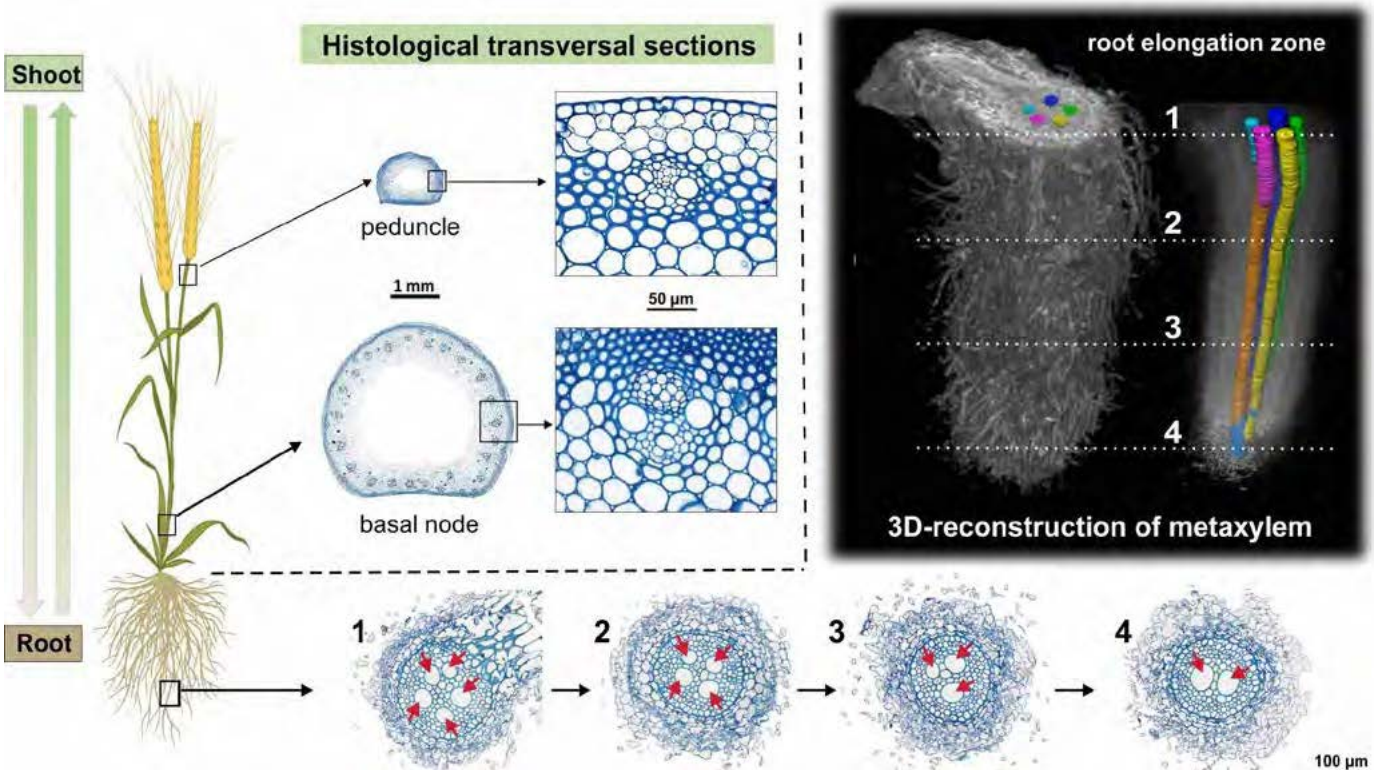
The scientific programme of the department is devoted to the characterisation and manipulation of plant performance and stress resilience traits in crops. With a strong focus on root- and nutrient-related traits, the department constitutes a major driving force for the IPK Research Theme 'Roots for resource-efficient crops'. Combining diverse phenotyping approaches with physiological, biochemical and anatomical analyses, the MPE and GPW groups quantify and characterise new root traits for subsequent discovery of underlying physiological processes or molecular mechanisms. Anatomical traits and specialised cellular structures undergo more detailed analysis in the SZB group that employs different microscopy techniques to elucidate cell biological features, not only in roots but also in other plant organs. Subsequent trait modification is enabled by the PRB group through genome editing and crop transformation. By designing new protocols and molecular components for gene and genome editing approaches, the PRB group makes a major contribution to the Research Theme 'Engineering genomes and chromosomes'.

Proper vascular development is essential for efficient water, nutrient and assimilate exchange between roots and shoots. In a common approach, the GPW and SZB groups investigate variation in vasculature anatomy along the root axis. The internal anatomy of roots is non-uniform, characterised by specialised zones with a reduction in vasculature that shifts along the developmental gradient of the root (Figure 1). Research focuses on the regulation and functional significance of these developmental transitions, investigating why such patterns vary across species and root types. By building on established characterisations in temperate grasses, this work aims to identify the genetic and hormonal mechanisms governing these anatomical shifts. Exploring how physiological features coordinate with these changes will determine their prevalence across plant diversity and their potential for providing advantages under environmental stress.

The Rapid Anatomics Tool was developed as a low-cost and accessible solution for high-throughput root imaging by combining 3D-printed components with readily available commercial equipment. It streamlines the phenotyping process through a blockface-like imaging technique that utilises near-ultraviolet autofluorescence to capture high-quality images without the need for traditional chemical staining. We will leverage this tool to explore inter- and intraspecific variation in root anatomical traits (Jones *et al.* 2025). This allows for the quantification of anatomical features across various root types and tissues, including the development of aerenchyma for metabolic

Jones DH, Baca Cabrera JC, Behrend D, Wells DM, Swift JF, Atkinson JA, Schön M, Lobet G, Hanlon MT, Schneider HM (2025). The Rapid Anatomics Tool (RAT): A low-cost root anatomical phenotyping platform reveals changes in root anatomy along the root axis. Plant Phenomics 8, 100150.

Rezaeva BR, I Otto, G Hensel, P Pouramini, A Peterson, J Kumlehn (2025) Genetic transformation of the oilseed crop camelina using immature zygotic embryos. Plant Methods 21, 35.



efficiency and sclerenchyma for structural integrity (Figure 2). To provide a comprehensive view of plant adaptation, these traits are evaluated across different root zones, ranging from the young, elongating tips to the more mature, lignified sections.

Figure 1: *Histological characterisation of the vascular continuum in cereal crops. In barley adventitious roots, the number of basal metaxylem vessels typically increases in later-formed roots, yet often reduces to a single distal vessel within 20 cm. Conversely, seminal roots maintain a single vessel of consistent size along their entire length. These contrasting patterns suggest that vascular programming and its temporal regulation during root ageing differ fundamentally between root types.*

Highlights

Barley (*Hordeum vulgare* L.) is a cereal commodity and one of the most important staple food crops worldwide. Profiting from high-quality genome sequencing of the germplasm in IPK's genebank, we explored the natural variation in the nutrient composition of grains in a spring barley mapping panel representing worldwide genomic variation. Using genome-wide association mapping and haplotype analysis for grain Zn concentrations led to the identification of HvMTP1.2, a member of the Metal Tolerance Protein 1 family. Heterologous expression in yeast confirmed Zn transport activity of HvMTP1.2 across the tonoplast for vacuolar Zn loading (Figure 3). Promoter-reporter analyses

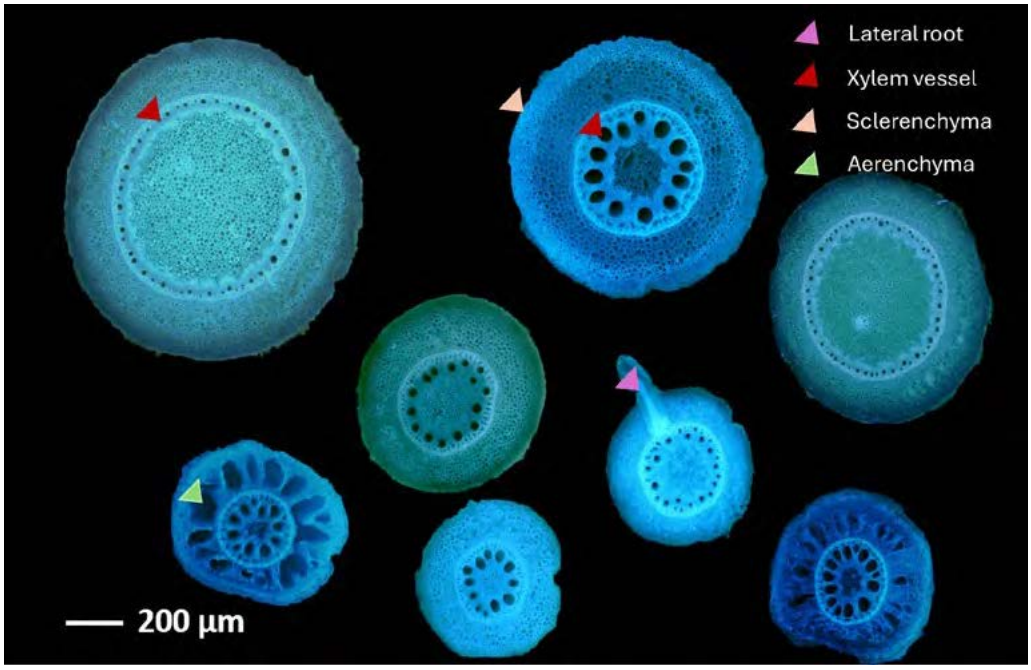


Figure 2: *Anatomy of root tissues from different cereal crop species. Transverse cross-sections show diversity in tissue organisation within different roots from maize, wheat, and barley, including the development of aerenchyma and sclerenchyma and variation in vascular size and number and lateral branching.*

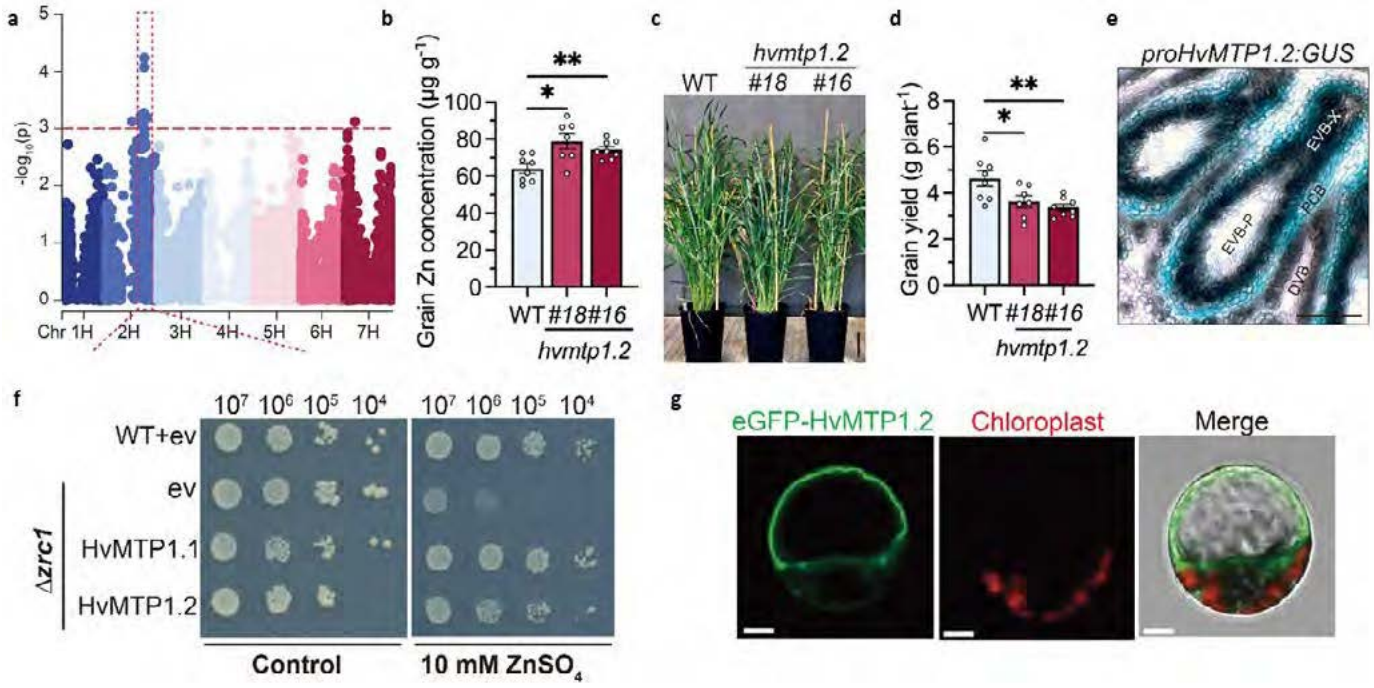


Figure 3: *Characterisation of the Zn transport protein MTP1.2 in barley. a, Manhattan plot associating grain Zn concentrations to SNPs in a field-grown spring barley panel. Chromosomes are depicted in different colours. b-d, Grain Zn concentrations (b), appearance of plants (c), and grain yield (d) of wild-type and hvmtp1.2 knock-out lines grown in soil. g, β-glucuronidase staining in a node cross section of a proHvMTP1.2::eGFP-GUS reporter line. f, Yeast growth complementation of HvMTP1.1 and HvMTP1.2. Empty vector, HvMTP1.1 or HvMTP1.2 were introduced into yeast strain Δzrc1, defective in vacuolar Zn transport, and yeast cells were grown on medium containing 0 (control) or 10 mM Zn. g, Subcellular localisation of HvMTP1.2 in barley mesophyll protoplasts expressing 35S::eGFP-HvMTP1.2.*

localised its expression primarily in seeds and in developing nodes, where HvMTP1.2 expression resides in the parenchyma cell bridge and directs Zn translocation from the root towards the spike and grains. CRISPR/Cas9-mediated disruption of HvMTP1.2 caused excess Zn accumulation in nodes, going along with inhibited node and shoot development and lower grain yield, whereas grain Zn concentrations increased. Resequencing of the HvMPT1.2 gene in more than 100 accessions identified allelic variation in the promoter and in the coding sequence that associate with altered grain Zn levels. Ongoing research explores regulatory mechanisms caused by the underlying genetic variation of HvMTP1.2.

In future, our research on the role of nodes in nutrient translocation and storage will be expanded. We are currently analysing the ionome of nodes of the IPK pangenome panel consisting of 76 field-grown wild barley species, cultivated lines and landraces. Together with microscopic analyses of node structures, we aim at identifying genetic factors causing node-dependent nutrient accumulation processes in plants.

Regarding the elucidation of plant reproductive mechanisms and regenerative processes in cell cultures, the PRB and SZB groups have a long-standing and particularly intensive collaboration. Aiming to develop biotechnological methods for the oilseed crop camelina (*Camelina sativa*), the PRB group succeeded in establishing efficient adventitious shoot formation based on the novel principle of cultivating immature embryos that feature pluripotent cells in their hypocotyl. Through detailed microscopic analysis of cellular development, the SZB group showed that cells in the outer layers of the hypocotyl act as the origin of adventitious shoots (Figure 4). This regeneration system then proved suitable for establishing robust methods of transgenesis and genome editing in camelina (Rezaeva *et al.* 2024).

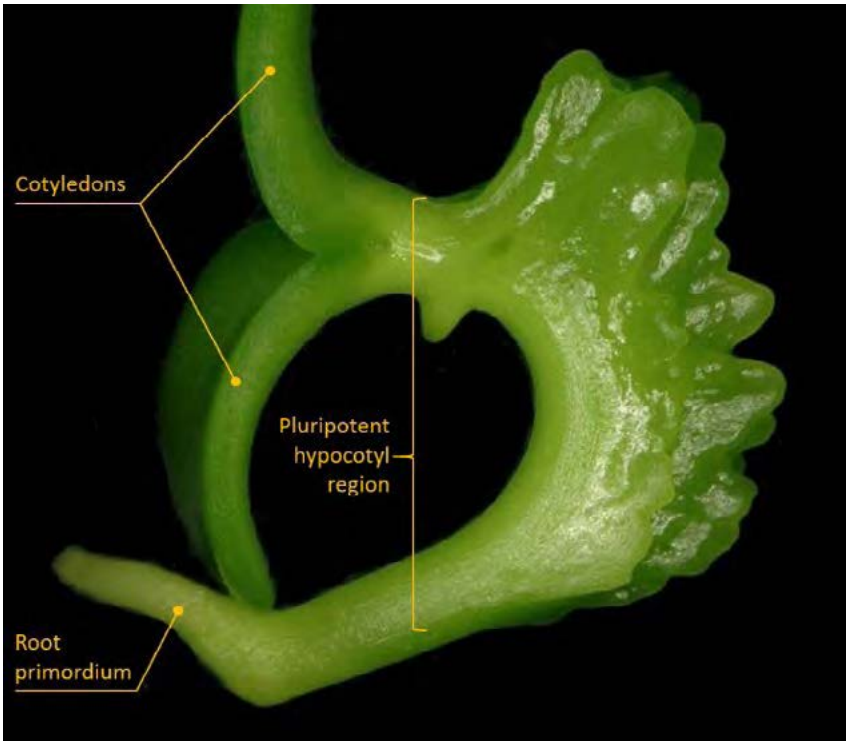


Figure 4: *Adventitious shoot formation in Camelina tissue culture. Massive formation of regenerable structures at the hypocotyl of cultivated immature embryos of Camelina (Rezaeva et al. 2025).*

Outlook

Of major priority in departmental research is the advancement and application of novel methods for site-directed genome engineering, which facilitate the generation of precisely intended modifications of the genomic DNA sequence and go beyond current targeted mutagenesis approaches. These approaches are going to be employed 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 are currently used in translational approaches for precise genome editing in barley.

Building on these foundations, the upcoming period will emphasise the genetic dissection of root anatomical and architectural traits to directly drive crop improvement. Through the implementation of the Rapid Anatomics Tool (RAT), extensive germplasm collections will be screened to establish direct links between specific gene functions and physiological outcomes.

With the successful application in the DFG call for excellence clusters, IPK became member of the CEPLAS 'Cluster of Excellence on Plant Sciences'. Apart from a number of cooperative projects between PZB and CEPLAS members on the generation of 'smart' plants, CEPLAS provides the opportunity to establish a new research group under lead of a W2 professorship on 'Root-microbiome interactions'. This will further strengthen the department's research profile in root-related rese¬arch topics. The new professorship will build a direct link with IPK and CEPLAS, be located at the IPK and affiliated with both, the IPK and the University of Düsseldorf.





RESEARCH GROUP **MOLECULAR PLANT NUTRITION** (MPE)

Heads: Prof. Dr. Nicolaus von Wirén
and Dr. Ricardo Giehl

Mission

The Molecular Plant Nutrition group investigates the transport and metabolism of mineral nutrients and their influence on phytohormone regulation, plant development and stress tolerance. Our research focuses on deciphering nutrient sensing mechanisms adapting root developmental processes to local nutrient availabilities or systemic nutritional signals. Additionally, we study rhizosphere processes like the role of root exudates in mobilising poorly soluble nutrients, as well as mechanisms underlying nutrient uptake efficiency and nutrient accumulation in grains. The generated knowledge provides routes to develop stress-resilient and nutrient-efficient crops.

Results

Dynamic regulation of coumarin biosynthesis mediates pH-dependent iron mobilisation

Iron (Fe) bioavailability to plants is severely limited in slightly acidic to alkaline soils, significantly impairing growth and crop yields. In many non-graminaceous species, Fe acquisition is supported by the secretion of diverse coumarins, but the specific physiological contributions of these phenylpropanoid-derived metabolites have remained elusive. We found that, under acidic conditions, root-secreted sideretin can directly reduce Fe(III) in the rhizosphere. At alkaline pH, the transcription factor MYB72 shifts biosynthesis from sideretin towards fraxetin, the latter acting primarily as an Fe(III) chelator to provide soluble Fe(III) for FRO2-mediated reduction at the root surface. These findings reveal how plants dynamically adjust their coumarin secretion profiles to optimise Fe acquisition across varying soil pH (Paffrath *et al.*, 2024).

A new type of plant metalloreductases protects root growth under low phosphorus

Phosphorus (P) is essential for undisturbed plant growth. However, its availability in soils is often limited due to sorption of phosphate onto iron (Fe) or aluminium (Al) (hydr)oxides. To mobilise sorbed P, plants secrete organic acids like malate. While effective, this process inadvertently increases Fe solubilization and subsequent accumulation in root tips, increasing the risk of Fe-triggered root meristem damage. Combining transcriptomics, electrophysiology, AlphaFold-supported modelling and reverse genetics approaches, we identified and characterised a member of the CYBDOM protein family – named HYP1 – as a central component in a mechanism that protects root meristem integrity when P is limited (Figure 1A). We demonstrated that HYP1 mediates ascorbate-dependent electron transport across the plasma membrane to reduce Fe(III)-chelates in the root apoplast. This activity prevents malate-induced Fe overaccumulation in the root apical meristem and thus relieves the root from Fe-dependent growth suppression. Our findings shed light on the physiological roles of the poorly characterised CYBDOM proteins and identified a promising target for improving root growth under P-limiting conditions (Maniero *et al.*, 2024).

Enhancing nitrogen-uptake efficiency in barley via HvBSK3;1 allele editing

Root plasticity is key to efficient nitrogen (N) capture, responding to both external N availability and internal demand. We previously demonstrated in *Arabidopsis thaliana* that the brassinosteroid signaling gene AtBSK3 is critical for stimulating root growth in response to mild N deficiency. CRISPR/Cas9-mediated disruption of the barley ortholog *HvBSK3;1* strongly attenuated low N-induced root foraging. Given that a proline (P) to leucine (L) substitution within the predicted kinase domain of AtBSK3 increases root elongation under low N, we analysed exome capture data of 750 barley accessions and found that HvBSK3;1 always carries the "weak" P allele. Introduction of the synthetic HvBSK3;1-L variant into the *A. thaliana bsk3,4,7,8* quadruple mutant resulted in more efficient complementation of the foraging response compared to the wild-type HvBSK3;1-P variant

Selected publications

Cid GA et al. (2024) Transcriptomic and metabolomic approaches elucidate the systemic response of wheat plants under waterlogging. ***J. Exp. Bot.*** 75: 1510-1529.

Maniero RA et al. (2024) Ferric reduction by a CYBDOM protein counteracts increased iron availability in root meristems induced by phosphorus deficiency. ***Nat. Commun.*** 15: 422.

Paffrath V et al. (2024) A major role of coumarin-dependent ferric iron reduction in strategy I-type iron acquisition in Arabidopsis. ***Plant Cell*** 36: 642-664.

Yu P et al. (2024) Seedling root system adaptation to water availability during maize domestication and global expansion. ***Nat. Genet.*** 56: 1245-1256.

Tunc CE, von Wirén N (2025) Hidden aging: the secret role of root senescence. ***Trends Plant Sci.*** 30: 553-564.

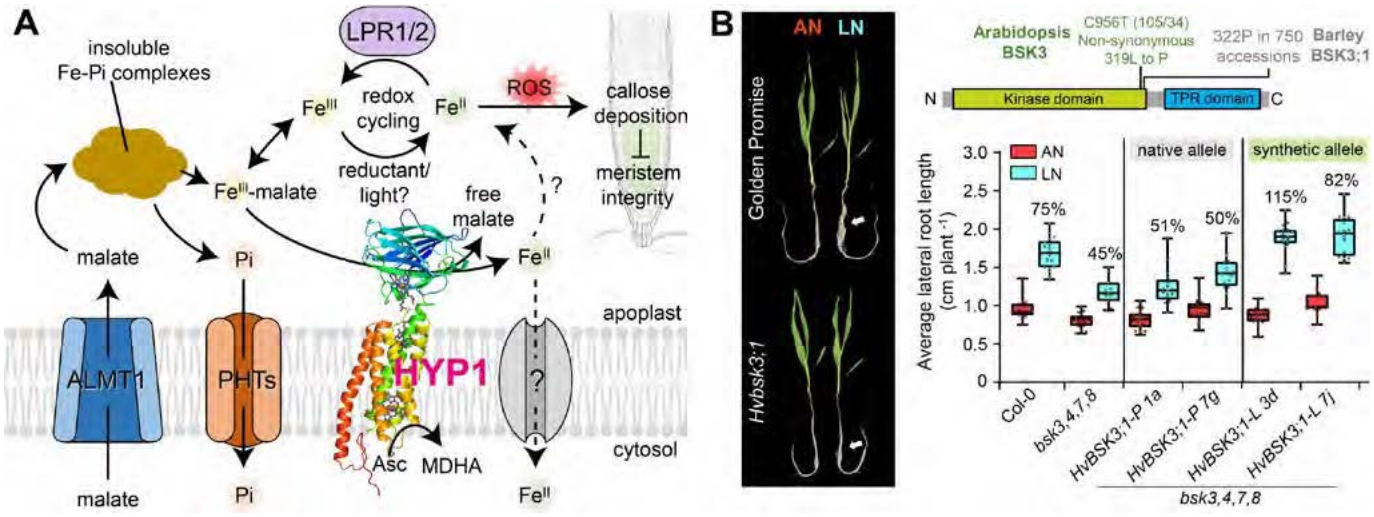


Figure 1: *: Discovery of a mechanism that protects root meristem integrity under limited P availability. (A) In response to P deficiency, plant roots secrete malate to solubilize phosphate (Pi) sorbed onto Fe (hydr)oxides for subsequent uptake. Buildup of soluble Fe(III)-malate complexes and Fe precipitation in the root apoplast can generate oxidative stress via redox cycling reactions, leading to loss of root meristem integrity. Our findings demonstrate that HYP1 uses electrons from cytosolic ascorbate (Asc) to reduce apoplastic Fe(III)-chelates, thereby preventing Fe overaccumulation and maintaining root growth (Maniero et al., 2024). (B) Function of HvBSK3;1 in low N-induced root growth stimulation in barley. Left, phenotypic characterisation of cv. Golden Promise and one generated Hvbsk3;1 mutant grown under adequate N (AN) or low N (LN). The arrows indicate differences in root growth under low N. Right, quantitative results showing that the synthetic HvBSK3;1-L allele generated by site-directed mutagenesis confers increased lateral root elongation in response to low N when expressed in the A. thaliana bsk3,4,7,8 quadruple mutant.*

(Figure 1B). Building on these promising results, we are collaborating with RG PRB and the Tissier lab (IPB-Halle) to explore base-editing approaches to directly introduce this allelic substitution in barley. While base editors have so far failed to generate the desired single-nucleotide substitution, we obtained initial promising results with template-driven homology-directed repair. Completing this work will help to showcase the power of precise gene editing for improving nutrient-efficiency traits in crops.

Embedding in IPK Research Themes

With discoveries on root responses and adaptations to nutrient deficiencies, the group's research is central to Research Theme 4. By performing mapping approaches on seed traits in inter-departmental collaborations, the group also contributes to Research Theme 5.
Within IPK and beyond, the group offers access to its technical platforms consisting of UPLC-MS/MS (phytohormones), HR-ICP-MS and ICP-OES (mineral elements), IR-MS (stable isotopes) and IC/LC-MS (primary metabolites and specific metabolite groups).

Outlook

Improving nutrient use efficiency is key for sustainable and resource-efficient crop production. Thus, we will continue our research on the discovery of molecular players underlying nutrient acquisition, allocation and nutrient-responsive root development and physiology. In model species, we are exploiting a multi-targeted genome editing approach for transcriptome-scale gene function identification. In frame of the CRC 'SNP2Prot' we characterise natural allelic variants of YUCCA proteins for proteoform changes and auxin-related functions together with protein scientists from MLU Halle. In barley, we will functionally validate candidate genes potentially associated with root-N contact and N use efficiency, which were mapped from a root phenotyping screen performed in the rhizotron platform of the IPK-PhenoSphere. By combining root phenotyping with placed natural isotopes, we will also determine the utility of different root traits for N capture efficiency. This work will be complemented by the characterisation of novel regulators of N uptake, mapped from 15N influx experiments carried out with a historical panel of cultivated European barley. Within the frame of the Cluster of Excellence on Plant Sciences (CEPLAS), our group will generate and test the first generation of SMART plant prototypes, in which engineered or synthetic promoters will drive predefined and condition-dependent modifications in root system architecture and exudate composition. These prototypes will serve as proof-of-concept to evaluate the effectiveness and trade-offs of single and multiple root trait modifications for efficient P capture.



RESEARCH GROUP
GENETICS AND PHYSIOLOGY OF ROOT DEVELOPMENT (GPW)

Head: Prof. Dr. Hannah Schneider

Mission

Our mission is to understand how root architectural and anatomical traits function and are genetically controlled across environments, and how their plasticity shapes water and nutrient capture, energetic costs, and plant performance. By linking root physiology, development, and genetics, we aim to provide a mechanistic foundation for breeding climate-resilient, resource-efficient crops that support sustainable food production.

Results

During the reporting period, we achieved breakthroughs in defining the functional utility, genetic control, and evolutionary history of root phenotypes. By integrating physiology, advanced phenotyping, and modelling, we dissected how specific root traits drive stress adaptation.

Regarding phenotypic plasticity, we identified the most effective metrics for detecting genotype-by-environment interactions in maize under water stress. We demonstrated that indices based on environmental ratios or the Finlay-Wilkinson slope are superior for mapping genetic architecture, providing a robust framework for breeding climate-adaptive crops (Arenas *et al.*, 2025).

Investigating anatomical plasticity, we overturned the assumption of uniform root response to drought, proving that adaptations are strictly node-specific (Koehler *et al.*, 2025). We further established the Poaceae root cortex as a primary driver of adaptation. In a comprehensive review, we synthesized the roles of cortical tissues (Jones *et al.*, 2025a) and specifically identified that the width of cortical parenchyma walls regulate metabolic costs under suboptimal water availability (Sidhu *et al.*, 2024). We also reviewed how these cortex modifications are strictly coordinated in time and space (Kawa *et al.*, 2025), emphasising their potential as precise breeding targets.

We reconstructed the evolutionary trajectory of maize roots over the last 18,000 years. Our *in silico* analysis revealed that rising Early Holocene CO2 favoured reduced nodal root numbers and multiseriate cortical sclerenchyma for deeper rooting, whereas increased seminal root number evolved later (c. 3,500 BP) in response to agricultural soil degradation (Lopez-Valdivia *et al.*, 2025a). We validated the relevance of anatomical traits in modern germplasm, providing evidence that variation in root anatomy contributes to local adaptation in Mexican native maize (McLaughlin *et al.*, 2024) and confirmed, through functional-structural plant-soil modelling, that specific anatomical phenotypes are associated with broad environmental adaptation (Lopez-Valdivia *et al.*, 2025b).

Moving beyond abiotic stress, we explored biotic and systemic interactions. In a review article, we revealed how root developmental cues interplay with rhizosphere signals from mycorrhizal fungi to shape root anatomy (Grondin *et al.*, 2024). At the cropping system level, we demonstrated that far-red light perception by the shoot, common in cereal-legume mixtures, influences root growth, establishing a critical shoot-root signaling axis (Wang *et al.*, 2025). Expanding this perspective to physical constraints, we characterised the detrimental effects of a compacted subsoil layer on root development (Heinen *et al.*, 2025), providing a clearer picture of root responses to soil physical limitations.

Finally, we addressed the technological bottleneck in anatomical phenotyping. We developed the Rapid Anatomics Tool (RAT) for high-throughput, stain-free imaging (Jones *et al.*, 2025b). Validated in wheat, these tools revealed unquantifiable gradients in vascular complexity, unlocking large-scale genetic screens (Figure 1). To ensure community adoption, we also published standardised protocols for preparing, imaging, and analysing maize root cross-sections (Sidhu and Schneider 2025a,b) and advocated for leveraging these datasets to design future roots through database integration (Phalempin *et al.*, 2025).

Selected publications

Arenas S et al. (2025) Modeling plant phenotypic plasticity and its underlying genetic architecture: a comparative study. ***J. Exp. Bot.*** 76: 2239-2251.

Jones DH et al. (2025) The root cortex of the Poaceae: a diverse, dynamic, and dispensable tissue. ***Plant Soil*** 514: 1627-1662.

Koehler T et al. (2025) Node of origin matters: comparative analysis of soil water limitation effects on nodal root anatomy in maize (*Zea mays* L.). ***Ann. Bot.*** 136: 1031-1046.

Lopez-Valdivia I et al. (2025) *In silico* analysis of the evolution of root phenotypes during maize domestication in Neolithic soils of Tehuacán. ***New Phytol.*** 248: 339-353.

Wang JL et al. (2025) Far-red light perception by the shoot influences root growth and development in cereal-legume crop mixtures. ***Plant Soil*** 509: 969-986.

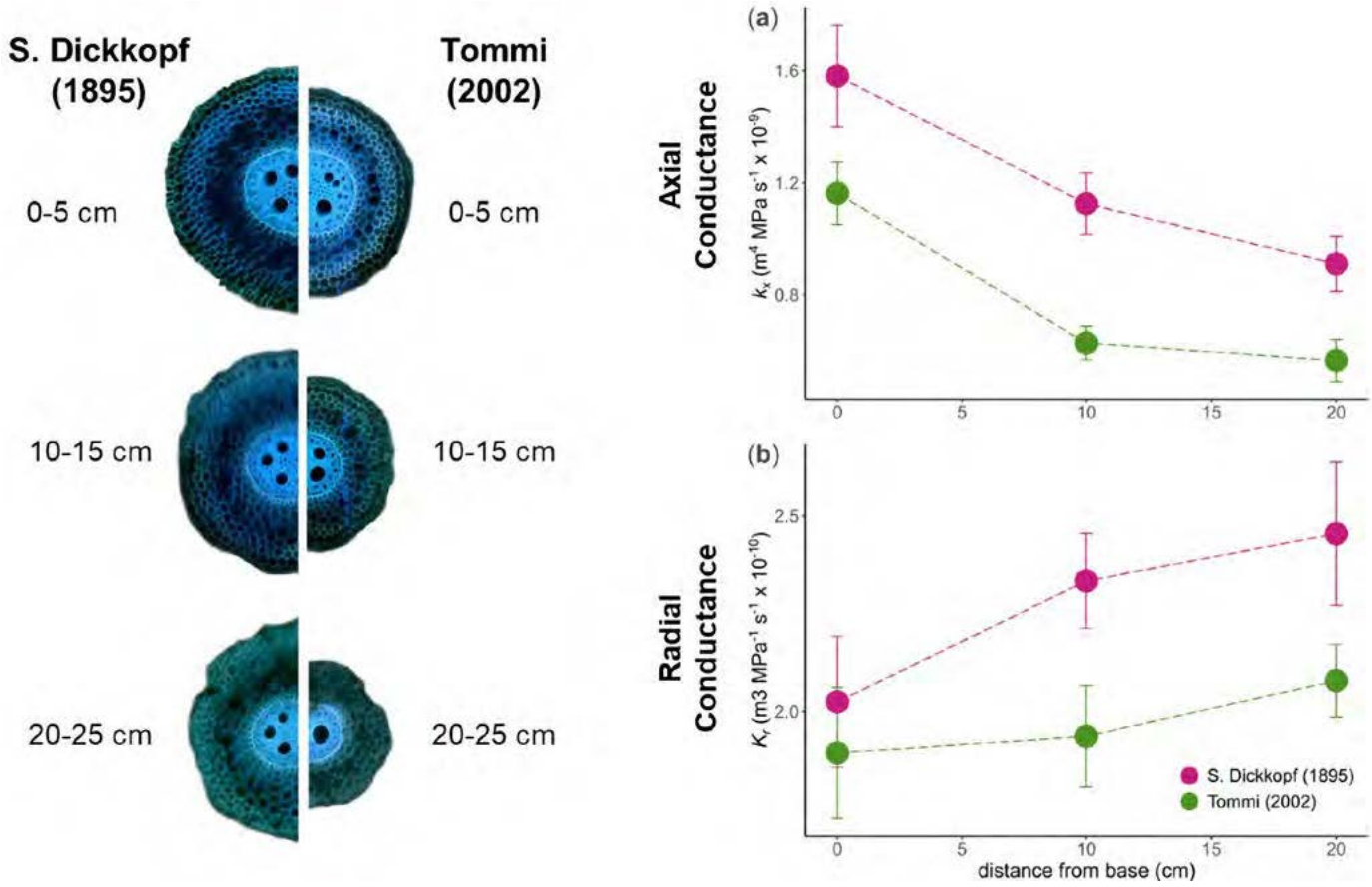


Figure 1: *Root anatomy differs between two German winter wheat cultivars along the root axis as investigated with the Rapid Anatomics Tool. Panels (a) and (b) show how differences in vascular architecture along the root axis influence axial and radial conductance. The older cultivar, S. Dickkopf (released 1895), shows less vascular change along the root axis compared to the modern cultivar Tommi (released in 2002). Error bars indicate standard error. Adapted from Jones et al. (2025b) and Baca-Cabrera et al. (2025).*

Embedding in IPK Research Themes

This working group serves as the foundation for Research Theme 4 'Roots for resource-efficient crops'. We identify specific genes that modulate root traits vital for resource efficiency, including multiseriate cortical sclerenchyma and root cortical aerenchyma. We phenotype diverse germplasm to uncover adaptive alleles, which aligns with 'Activating Genetic Diversity'. Our findings advance bio-digital data through sophisticated modelling and image analysis in support of 'Exploiting Bio-Digital Plant Data'. These targets undergo validation through genetic engineering under 'Engineering Genomes and Chromosomes', and are ultimately integrated with shoot analysis in 'Enhancing Shoot Performance', to accelerate the development of climate-smart crops.

Outlook

In the coming period, the working group will prioritise elucidating the genetic control of root anatomical and architectural traits to support breeding. Leveraging the high-throughput Rapid Anatomics Tool (RAT), we will screen large germplasm collections to link gene function with physiology. A central objective is to identify and validate genes controlling anatomy across distinct root classes, particularly those governing cortical cell fate. We will employ quantitative genetics to discover functional markers for stress tolerance, validating targets via mutant and transgenic lines. Furthermore, we aim to resolve the adaptive value of plasticity by identifying key regulatory signals, integrating these insights into a maize multi-scale model to predict adaptive responses for crop improvement.



RESEARCH GROUP **PLANT REPRODUCTIVE BIOLOGY** (PRB)

Head: Dr. Jochen Kumlehn

Mission

The Plant Reproductive Biology group has a strong focus on the establishment of enabling technologies, in particular plant genetic engineering and the generation of true-breeding plants originating from haploid cells. Thereby, we aim to facilitate both basic research and translational approaches. Special attention is devoted to biological mechanisms relevant to plant reproduction, domestication, plant-pathogen interaction, as well as to yield- and quality-related traits.

Results

Site-directed genome modification triggered by CRISPR-associated (Cas) endonucleases has been firmly established as a technological platform. In this context, we have devised the modular and versatile CasCADE vector system that allows for complex cloning procedures in a single reaction and facilitates the integration of newly emerging functional components. This system has been used in a variety of approaches to address multiple genomic target motifs simultaneously (e.g. Jiang *et al.* 2024, Leite Dias *et al.* 2024, Jayakodi *et al.* 2024).

To meet the need to expand our genetic engineering platform beyond cereal crops, we have begun to work on oilseed rape and camelina. A genetic transformation method was developed that, for the first time, achieved high efficiencies in the current winter rapeseed variety Express 617 (Figure 1). Thus, we have made a significant contribution to the usability of this experimental model, whose complete genome sequence is also available.

Based upon a novel principle of adventitious shoot formation from immature embryos of the emerging oilseed crop camelina, we have established robust methods of genetic transformation and genome editing (Rezaeva *et al.* 2024, *Plants*; Rezaeva *et al.* 2025, *Plant Methods*). Employing this technology, we managed to knock out all three homeoalleles of the *FATTY ACID ELONGASE 1* gene in camelina. The plants produced have an increased content of the particularly valuable triple unsaturated α-linolenic acid, while the nutritionally problematic erucic acid has been reduced to undetectable levels (Figure 2, Rezaeva *et al.* 2025). Given the deficiency of omega-3 fatty acids in the diets of most Europeans, the unparalleled oil quality of our genome-edited camelina plants is of remarkable relevance.

A project concept developed for establishing novel principles of precise and flexible genome editing was chosen by the BMFTR for funding. This allowed for the spin-off of the independent research group Genome Editing and Biotechnology in June 2025.

The PRB group is particularly committed to science communication. Within the reporting period, members of the group have informed the public in over 20 contributions in various formats about our work and the as yet untapped potential of genetic engineering in agriculture.

Embedding in IPK Research Themes

By creating new allelic variants through genome editing, producing populations of doubled haploids, and maintaining valuable genotypes via reproductive biology approaches, we contribute to increasing genetic diversity and provide particularly suitable genotypes for crop plant research and breeding. The bio-digital resources available at the IPK have been forming an essential basis for identifying candidate genes in various of our scientific approaches (Research Theme 2). We have been improving performance-determining traits of crops using our expertise in genome editing and reproductive biology (Research Theme 3). In this context, we have been investigating and modulating plant performance-related biological mechanisms in both, root systems (Research Theme 4) and aboveground organs (Research Theme 5).

Selected publications

Jayakodi M et al. (2024) Structural variation in the pangenome of wild and domesticated barley. ***Nature*** 636: 654-662.

Jiang G et al. (2024) Non-cell-autonomous signaling associated with barley ALOG1 specifies spikelet meristem determinacy. ***Curr. Biol.*** 34: 2344-2358.

Leite Dias* S, Chuang* L, Liu* S et al. (2024) Biosynthesis of the allelopathic alkaloid gramine in barley by a cryptic oxidative rearrangement. ***Science*** 383: 1448-1454.

Feng J-W et al. (2025) A haplotype-resolved pangenome of the barley wild relative *Hordeum bulbosum*. ***Nature*** 645: 429-438.

Rezaeva BR et al. (2025) Targeted mutagenesis of *FATTY ACID ELONGASE 1* entails near complete elimination of very long chain fatty acids in the seeds of camelina cultivar Ligena. ***aBIOTECH*** 6: 816-830.

** Joint first authorship*

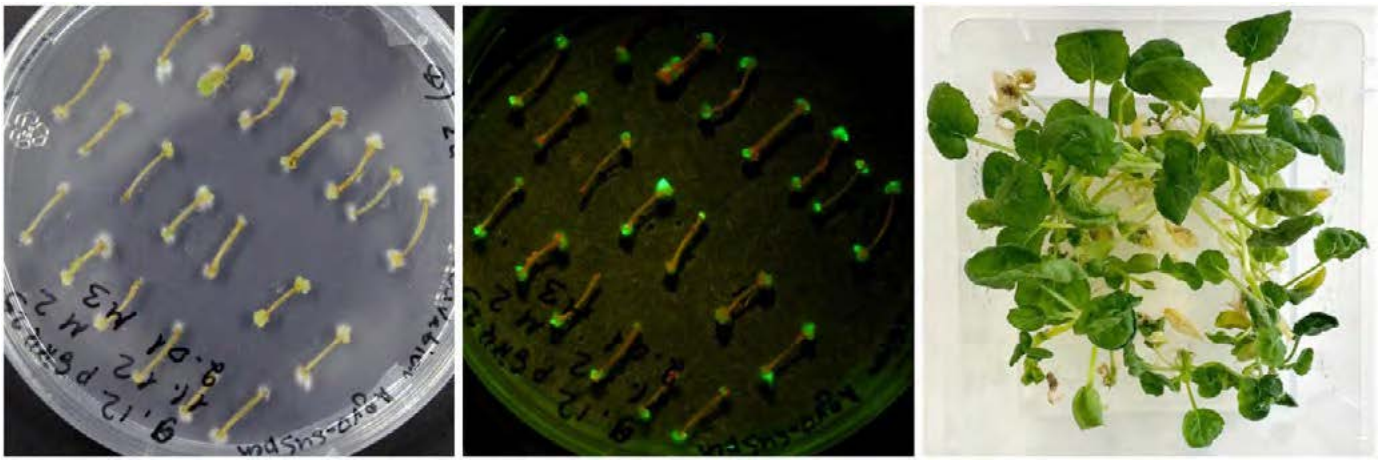


Figure 1: *Agrobacterium-mediated genetic transformation of winter oilseed rape. Left: hypocotyl segments of seedlings; centre: evidence of efficient DNA-transfer indicated by the emission of green light upon expression of the GREEN FLUORESCENT PROTEIN gene at the explants' ends; right: regeneration of transgenic plantlets via callus and adventitious shoot formation (Photos: Dr. Barno Rezaeva).*

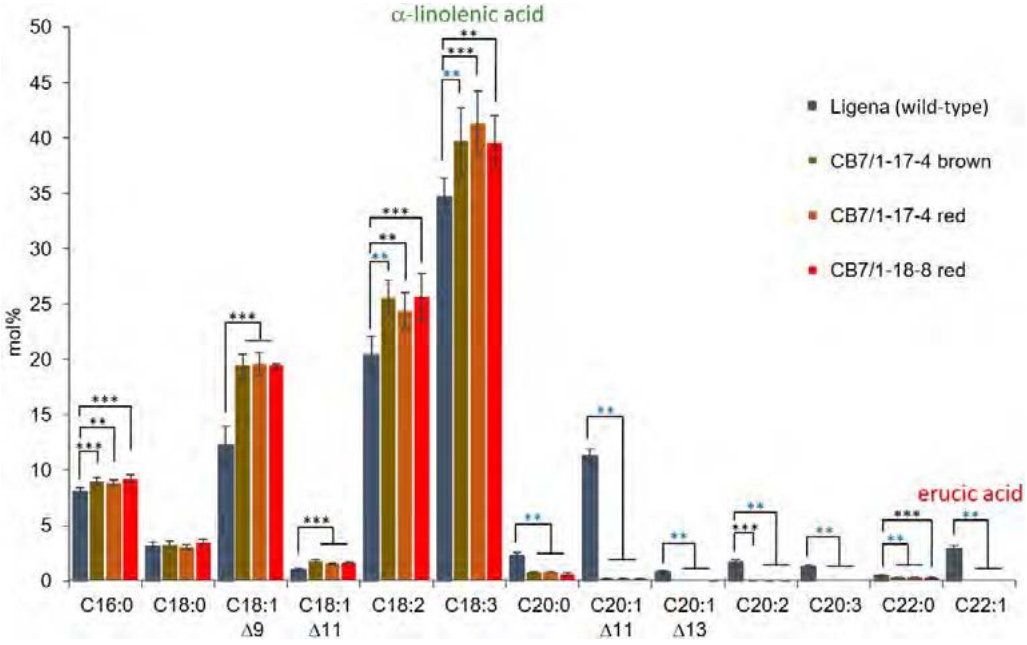


Figure 2: *Fatty acid profiles of wild-type (cv. Ligena, blue columns) and genome-edited camelina lines (brown, orange, and red columns). The knockout of the FATTYACID ELONGASE 1 gene entails a significant increase in the content of nutritionally valuable unsaturated fatty acids (C18:1, C18:2, C18:3) and a near-complete removal of the problematic erucic acid (C22:1). Asterisks indicate the levels of statistically significant differences (cooperation with Prof. Ivo Feussner's group, University of Göttingen).*

Outlook

With regard to genetic engineering technologies for important crops, we strive to keep pace with the rapid developments in this field and, in particular, to pursue novel approaches for the development of more precise genome editing methods. These cutting-edge tools will be used for the functional validation of genes and to improve plant performance, i.e., yield potential, resilience, and increasingly also quality features of harvested products. In addition, we will seamlessly continue our activities to increase plant diversity in agriculture by establishing biotechnologies for species such as buckwheat and quinoa that are lagging behind in terms of progress in plant breeding.



RESEARCH GROUP **STRUCTURAL CELL BIOLOGY** (SZB)

Head: Dr. Michael Melzer

Mission

As research group and core facility for light and electron microscopy of the IPK, we focus on morphology, cellular ultrastructure and the spatial distribution of proteins and molecules in plant tissues. The overarching research goal of the group is to identify and characterise agronomically important structural traits and their modulation in response to biotic and abiotic factors. Our data provide insights into 2D and 3D ultra-/structural adaptations of plant tissues, cells or cellular components as prerequisite to characterise gene and protein functions involved in crop performance or to optimise plant biotechnological processes.

As central facility for microscopy, we provide access to all IPK employees to use the light and electron microscopy equipment with support and training by our group's staff.

Results

The plant vasculature plays and important role in plant growth and performance. In close collaboration with the research groups GPW, AAN, PBP and FPS, we investigate the initiation of vascular development in different organs of the crop species barley and wheat (Figure1).

A main focus is the development of the spike vasculature in the timeframe between initiation and the stage when the spike reaches maximum yield potential. In barley, first vascular traces become visible at double ridge stage (WA 2.0) in the form of two lateral vein initials oriented perpendicular to the main veins of the culm underneath. Rachis vasculature rapidly expands by multiple orders of central veins initiated in between the lateral veins. All early rachis veins do not connect to other vein initials, suggesting that they constitute an independent entity within the rachis. By the time of maximum yield potential (WA 5.0), the complete complement of rachis veins has been laid out with vein number along the still immature rachis reflecting the values seen in mature spikes. Spikelet development lags behind that of the rachis with first undisputed vein initials in glume and lemma not appearing until after lemma primordium (WA 3.0). With the exception of the lodicles, small organs whose sole role is to open the flower at anthesis, all major spike organs are present by WA 5.0 and the accompanying vasculature initiated. It is by this stage that extending vein initials of glumes and lemma enter the central part of the rachis to merge with the veins existing there thus generating a functional continuum (Rutten *et al.* 2024).

In collaboration with the research group MPE and the University of Rosario (CONICET, Argentina) ultrastructural analysis of chloroplasts showed that cells expressing plastid-specific flavodoxin display reduced endoreduplication, accompanied by decreased organ size, providing new insights into how chloroplast-generated redox signals regulate leaf growth.

In frame of the Cluster of Excellence on Plant Sciences (CEPLAS), single-nuclei sequencing at the Institute of Plant Biochemistry of the Heinrich-Heine University (HHU) of Düsseldorf in combination with our immunogold localisation of selected photorespiratory proteins by transmission electron microscopy (Figure 2), elucidated how cellular specialisation determines interconnected structural pathways. Our analysis revealed a *Moricandia arvensis*-specific shift in expression of genes directly associated with photorespiratory reactions (glycine decarboxylase complex, glutamate:glyoxylate aminotransferase, and glycolate oxidase), suggesting a shuttle of several C2 metabolites to the bundles sheath. In addition, associated pathways, such as ammonium assimilation, synthesis of specific amino acids, redox regulation, and transport, also showed enhanced abundance in the *M. arvensis* bundle sheath (Triesch *et al.* 2025). Further studies will focus on anatomic modifications underlying C2 photosynthesis in *Moricandia* to identify the genetic regulators governing their development.

In 2024/2025, our group has contributed to 26 publications based on external and internal collaborations.

Selected publications

Jayakodi M et al. (2024) Structural variation in the pangenome of wild and domesticated barley. ***Nature*** 636: 654-662.

Kavka M et al. (2024) Phenotypic screening of seed retention and histological analysis of the abscission zone in *Festuca pratensis* and *Lolium perenne*. ***BMC Plant Biol.*** 24: 577.

Rutten T et al. (2024) Anatomical insights into the vascular lay-out of the barley rachis: implications for transport and spikelet connection. ***Ann. Bot.*** 133: 983-996.

Kuo Y-T et al. (2025) Kinetochore mutations and histone phosphorylation pattern changes accompany holo- and macro-monocentromere evolution. ***Nat. Commun.*** 16: 11332.

Triesch S et al. (2025) Single-nuclei sequencing of *Moricandia arvensis* reveals bundle sheath cell function in the photorespiratory shuttle of C_3-C_4 intermediate Brassicaceae. ***J. Exp. Bot.*** 76: 5129-5144.

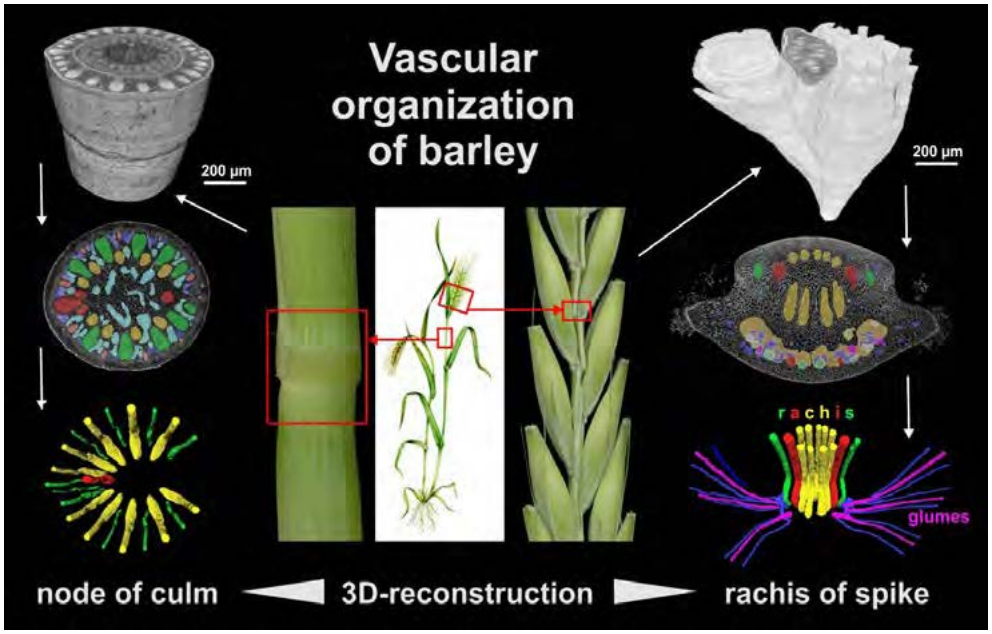


Figure 1: *Differences in the vascular organisation of nodes and rachis in barley. The veins from the outer sphere of a culm node betray their leaf origin with a single large mid-rib like vein (red), flanked by somewhat smaller lateral veins (maroon), alternated with small intermediate veins (green). The rachis vasculature consists of two main midrib veins (red), separated by two rows of lateral veins (yellow) and with the intermediate veins reduced to two single strands (green) on the outside of the main veins (T. Rutten).*

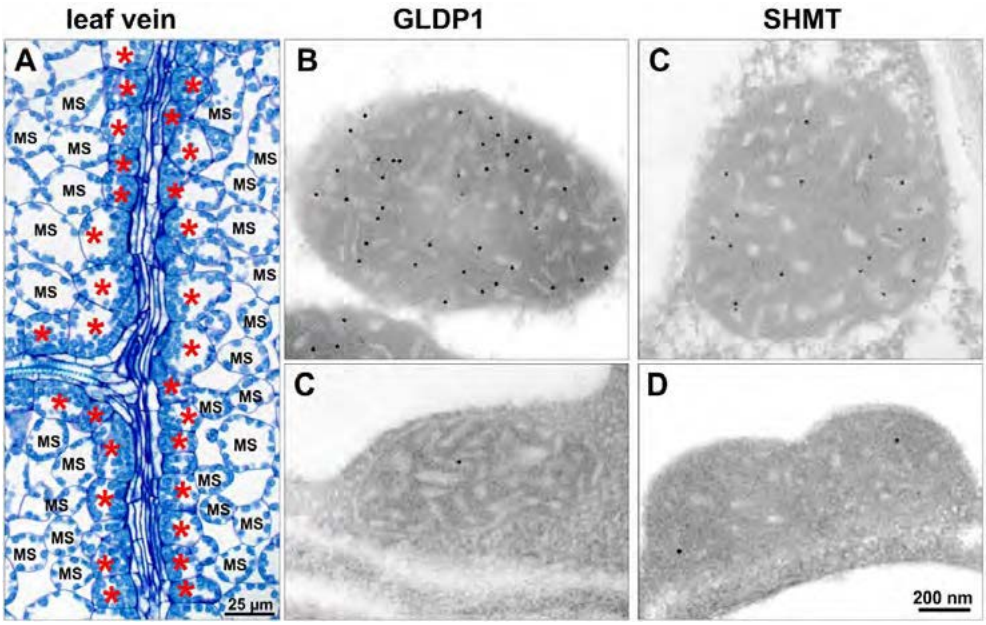


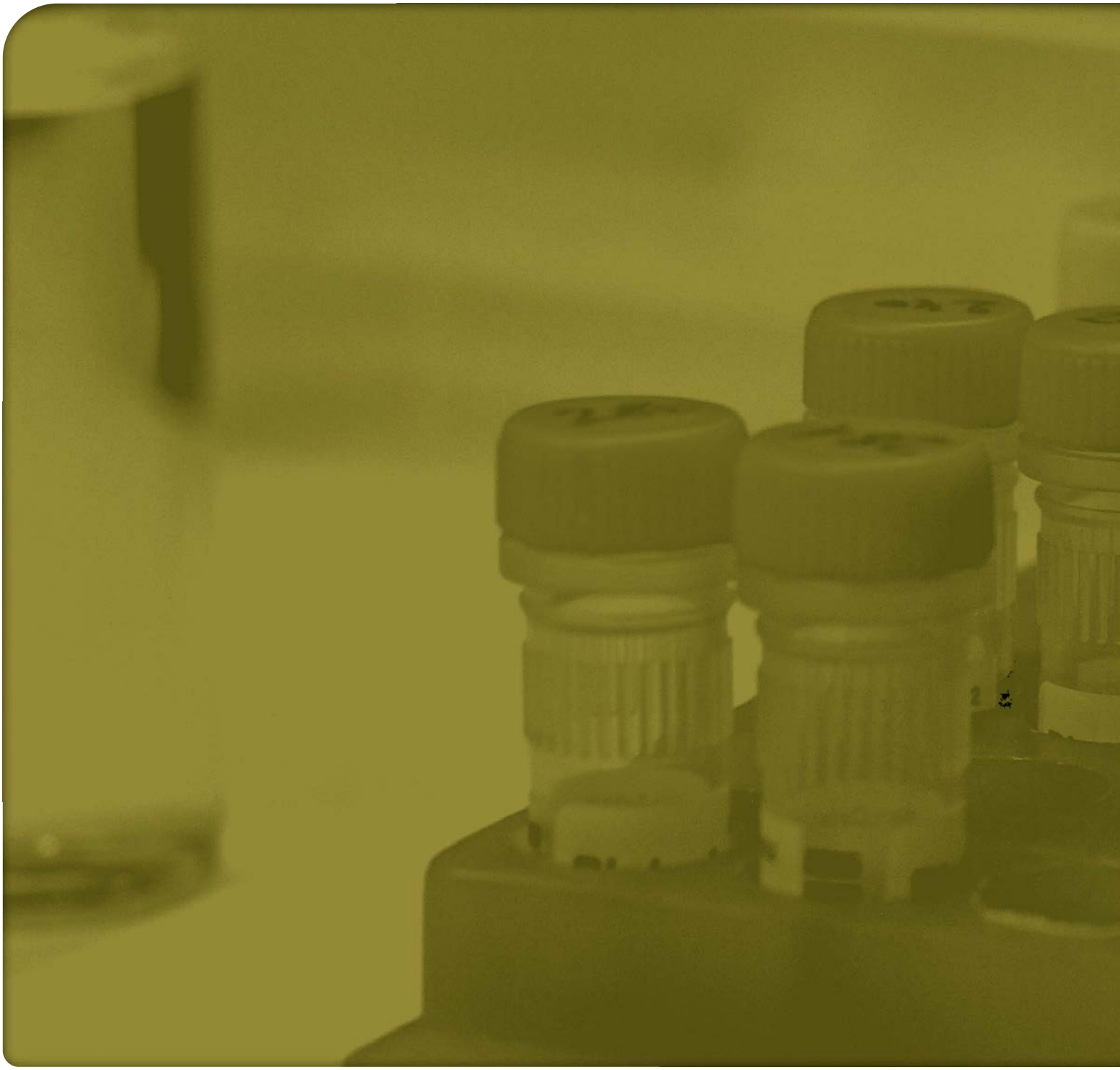
Figure 2: *Immunogold localisation in mesophyll and bundle sheath cell of the C3-C4 intermediate Brasicaceae Moricandia arvensis. (A) Light microscopy of leaf vasculature, bundle sheath (red star) and mesophyll cells (MS). Localisation of the photorespiratory enzymes P-protein of glycine decarboylase complex (GLDP1) and serine hydroxymethyltransferase in mitochondria of bundle sheath (B-C) and mesophyll cells (D-E) using 10 nm protein A-gold and transmission electron microscopy. MS, mesophyll cells (M. Melzer).*

Embedding in IPK Research Themes

Thanks to multiple internal collaborations across all departments of the IPK, the group is firmly integrated in all five research themes of the IPK.
The ongoing intense collaboration with the Heinrich Heine University in Düsseldorf with a focus on the investigation of developmental and structural aspects of C3-C4 intermediate forms of Brassicaceae will be continued as part of the new Cluster of Excellence for Plant Sciences (CEPLAS III).

Outlook

In collaboration with GPW, the three-dimensional representation of the vascular system of wheat along the root axis will lead to the identification of new morphological and structural features and complement ongoing intense studies on the vascular organisation, connectivity and functionality of the entire plant.
The new Jeol JEM-F200 transmission electron microscope is equipped with STEM tomography. The method enables us to record a series of images from sections with a thickness of up to 1 µm at different tilt angles. Generating three-dimensional images at maximum structural resolution will further expand the range of methods available and thus opens up new research opportunities at the IPK.



INDEPENDENT



Meiosis (ME)
Dr. Stefan Heckmann

Plant Reproductive Genetics (PRG)
Dr. Steven Dreissig

Functional Plant Structures (FPS)
Dr. Yongyu Huang

Biotechnology and Genome Editing (BGE)
Dr. Robert Hoffie

INDEPENDENT RESEARCH GROUPS



INDEPENDENT RESEARCH GROUP: **MEIOSIS** (ME)

Head: Dr. Stefan Heckmann

Research Mission

The Meiosis team, an independent research group funded initially by the BMFTR and currently by the ERC, aims to unlock hidden genetic diversity in crops to accelerate breeding. In many plants, including barley, much of the genome remains untapped in breeding, due to rare and uneven meiotic recombination events (the natural reshuffling of parental DNA). To address this bottleneck, we use barley and Arabidopsis to unravel the molecular mechanisms governing recombination and to develop tools for analysing and directing meiotic outcomes. Our ultimate goal is to translate these discoveries into innovative breeding strategies for rapid, targeted development of resilient, high-performing crops.

Results

To develop novel strategies for accelerating breeding, the independent research group Meiosis applies molecular cytogenetic approaches focused on three main areas: (a) understanding meiotic homologous recombination control; (b) developing tools to assess and modify locally and globally meiotic homologous recombination outcomes; and (c) applying this knowledge in barley to alter its recombination landscape.

a) Using TurboID-based meiotic proteomics, we identified new candidate proteins with meiotic phenotypes, including SCEP3, a novel, conserved central element protein of the synaptonemal complex (tripartite, meiosis-specific structure physically linking homologous chromosomes). Depletion of SCEP3 in *Arabidopsis thaliana* disrupts synaptonemal complex formation but results in increased and near randomly distributed crossovers (COs) compared to wild type. We further dissected synaptonemal complex composition with TurboID proteomics. While sex-specific differences in CO patterning (heterochiasmy) are well known, female meiosis remains cytologically challenging to access. To address this, we developed Female Meiotic Cell Identification (FeM-ID) in *A. thaliana*, enabling rapid identification and analysis of female meiotic cells across ecotypes, tetraploids, and mutants. Using FeM-ID, we can demonstrate both similarities and notable differences between male and female meiosis, filling an important knowledge gap.

b) To study homologous recombination frequency and outcome at defined loci in the genome, we established marker systems in plants that also enabled us to identify factors influencing local repair events. Additionally, we developed a polyprotein-based system utilising so-called ribosome-skipping peptides for meiosis-specific, coordinated co-expression of proteins. These advances enabled us to further explore tools for targeted meiotic DNA double-strand break induction and to analyse resulting local repair outcomes, showing that targeted homologous recombination can be triggered.

c) To manipulate the barley meiotic recombination landscape, we functionally dissected key meiotic genes embarking on barley stripe mosaic virus-induced genome editing (BSMVIGE). For instance, depletion of the anti-CO factors RECQ4 and FIGL1 reduces class I COs but increases class II COs; complete loss of RECQ4 results in a hyperrecombination phenotype. HEI10, a pro-CO ZMM factor, is crucial for class I CO formation and shows haploinsufficiency, suggesting its dosage-dependent regulation of CO numbers in barley. Together, our data show that recombination in barley can be manipulated.

In summary, we have identified novel meiotic candidate genes, established advanced tools for dissecting and editing meiotic processes, and demonstrated that the recombination landscape in barley is plastic and can be altered.

Selected publications

Cuacos M, Heckmann S (2025) Diversity favoured: heterozygosity attracts crossovers. ***Nat. Plants*** 11: 1706-1707.

Feng C et al. (2025) The synaptonemal complex central element SCEP3 interlinks synapsis initiation and crossover formation in *Arabidopsis thaliana*. ***Nat. Plants*** 11: 1353-1366.

Feng J-W et al. (2025) A haplotype-resolved pangenome of the barley wild relative *Hordeum bulbosum*. ***Nature*** 645: 429-438.

Schüler* D, Lange* M et al. (2025) Data management in balance – a decade of balancing pragmatism, sustainability and innovation at plant research center IPK Gatersleben. ***J. Integr. Bioinform.*** 22: 20250012.

** Joint first authorship*

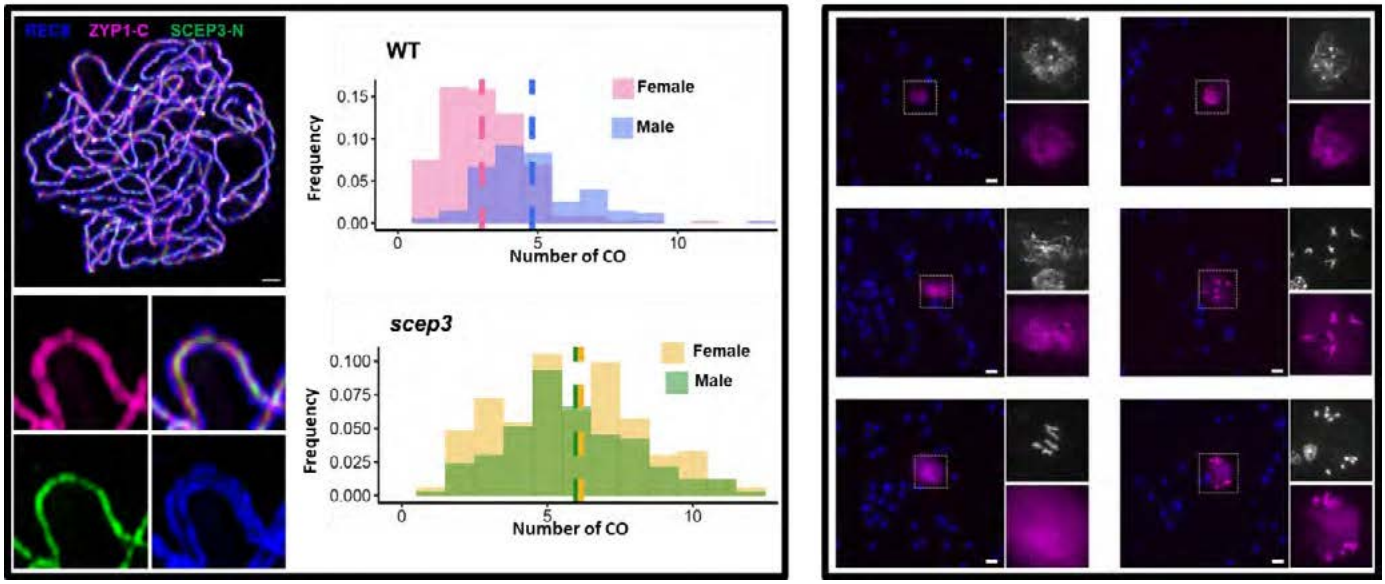


Figure 1: *Left section: The novel central element protein of the Arabidopsis thaliana synaptonemal complex, SCEP3, localises between homologous chromosomes during meiotic pachytene (immunolocalization visualised using 3D structured illumination microscopy; scale bar: 2 µm). In the absence of SCEP3, crossover (CO) frequency in offspring is significantly increased, primarily due to elevated female COs, thereby erasing sex-specific differences in recombination (heterochiasmy). This figure part is modied from the original publication PMID: 40579437; DOI: 10.1038/s41477-025-02030-9, licensed under a Creative Commons Attribution 4.0 International License. Right section: Female Meiotic Cell Identification (FeM-ID) in A. thaliana: Proximity-based labelling allows the identification and characterisation of female meiotic cells. DNA is stained with DAPI (blue), and female meiotic cells are marked by biotin (purple). Scale bar: 10 µm. Figure adapted from the original publication (PMID: 41662370 DOI: 10.1093/plcell/koag024), licensed under a Creative Commons Attribution 4.0 International License.*

Embedding in IPK Research Themes

Our research contributes directly to the overarching goal of exploiting genetic diversity for crop improvement and is part of Research Theme 3: Engineering Genomes and Chromosomes, as well as Research Theme 1: Activating Genetic Diversity. We work closely with the Breeding Research Department on new breeding strategies to edit recombination, thereby unlocking genetic diversity and supporting its mission.

Outlook

Our overarching aim is to redistribute and to increase meiotic recombination events in a targeted manner to accelerate plant breeding, in close aligment with the mission of the Breeding Research Department. The future main topics of our team will be: the synaptonemal complex and its role in recombination; dissecting female meiosis in comparison to males (heterochiasmy); manipulating local recombination outcomes; activating the secondary gene pool; and altering the barley recombination landscape. Our research into the control of meiotic recombination to unlock hidden genetic diversity contributes to Research Themes #3 Engineering Genomes and Chromosomes and #1 Activating Genetic Diversity.



INDEPENDENT RESEARCH GROUP: **PLANT REPRODUCTIVE GENETICS** (PRG)

Head: Dr. Steven Dreissig

Mission

Reproductive processes, such as gamete formation, pollen development, and reshuffling of genetic information through recombination, play an essential role in evolution, plant breeding, and crop fertility. We aim to improve our understanding of how genetic diversity and environmental factors shape quantitative variations in reproductive processes within and between populations, and to use this knowledge to improve plant breeding methods. We combine population genetics and molecular genetics, and use both computational and experimental approaches. Our research focuses on rye (*Secale cereale*) and barley (*Hordeum vulgare*).

Results

Identifying the genetic basis and environmental plasticity of male reproductive traits in rye (Waesch et al. 2025, BMC Plant Biol; Waesch et al. 2025, JXB)

Understanding how environmental factors shape male reproductive traits is crucial in plant breeding and evolutionary biology. We investigated the impact of soil nutrient availability and genetic divergence on male reproductive traits in the wind-pollinating grass *Secale cereale*, leveraging the long-term 'Eternal Rye' monoculture field trial established in 1878. We used high-throughput multispectral imaging flow cytometry (MIFC), impedance flow cytometry, microscopy, deep learning-based object detection models, and population genomics, to characterise phenotypic diversity and genetic architecture of pollen and anther morphology across 1600 diverse rye individuals. Our work showed that selection for larger pollen grains and longer anthers occurred throughout the domestication of rye (Waesch *et al.* 2025, BMC Plant Biol). Furthermore, we showed that nutrient deficiency, compared to nutrient enrichment, significantly reduced anther length and pollen number per anther, whereas pollen size and viability remained stable or increased in certain populations (Waesch *et al.* 2025, JXB). Under nutrient-rich conditions, we observed a trade-off between pollen size and number, which was absent under nutrient-deficient conditions, suggesting shifts in resource allocation strategies. These findings highlight the substantial influence of environmental plasticity on male reproductive traits and their genetic control in rye.

Using population-wide single-pollen nuclei genotyping in rye to shed light on the genetic basis and environmental plasticity of meiotic recombination (Waesch et al. 2025, New Phytol)

The core molecular machinery of meiosis is conserved deep across eukaryotic lineages. Nevertheless, recombination landscapes vary at multiple scales, from chromosomes to populations, caused by an interaction of genetic and environmental factors. To improve our understanding of the causes

Selected publications

*Waesch C, Pfeifer M, Dreissig, S (2024) Characterising the genomic landscape of differentiation between annual and perennial rye. ***Evol. Appl.*** 17: e70018.

Feng C et al. (2025) The synaptonemal complex central element SCEP3 interlinks synapsis initiation and crossover formation in *Arabidopsis thaliana*. ***Nat. Plants*** 11: 1353-1366.

Waesch C et al. (2025) Pollen and anther morphological variation in rye was shaped by domestication. ***BMC Plant Biol.*** 25: 389.

** This publication is based on work that has been carried out at the Institute of Agricultural and Nutritional Sciences, Martin-Luther-University Halle-Wittenberg.*

and consequences of this variation, we need to identify the underlying genetic architecture. We explored the genetic basis and environmental plasticity of meiotic recombination in a large rye population grown under control and nutrient-deficient conditions. We used single-pollen nuclei (SPN) genotyping to directly measure male meiotic crossovers in 3,136 pollen nuclei from 584 individuals. We detected a significant reduction of crossovers in response to nutrient deficiency. Using genome-wide association scans, we uncovered the genetic basis of crossover count, crossover interference, and intra-chromosomal shuffling. The presence of multiple additive loci with small to intermediate explained phenotypic variance suggested a polygenic architecture of crossover traits. Loci associated with crossover traits were unique to control or nutrient deficient conditions, suggesting that alleles regulating crossover traits are dependent on genotype-by-environment interactions, which strongly emphasises the environmental plasticity of meiotic recombination. Finally, we revealed differences in recombination landscapes measured in gametophytes and sporophytes, which may be explained by a post-meiotic survivorship bias.

Embedding in IPK Research Themes

We contribute to IPK's research mission by leveraging genebank and genomic resources to enhance plant performance and resilience to abiotic stress. We use population genomics (collab. Genebank), microscopy and single-cell genotyping (collab. Breeding Research), and high-throughput single-cell phenotyping (collab. iDiv Leipzig), to characterise the genetic basis and environmental plasticity of recombination, pollination traits, and fertility. By combining expertise in population genomics and molecular biology, we act as a collaborative bridge between research groups in multiple departments and provide complementary skills to address shared goals in Research Themes 'Activating Genetic Diversity' and 'Engineering Genomes and Chromosomes'.

Outlook

In contemporary and future research projects, we will focus our efforts on characterising the genetic basis and environmental plasticity of fertility and male reproductive traits in rye, barley, and triticale. A key aim will be to improve temperature resilience of meiosis and pollen development to ensure fertility, and therefore seed yield, under increasingly challenging environmental conditions. Furthermore, we aim to identify alleles modulating cross-pollination traits in rye and triticale, with the potential of improving hybrid breeding in self-pollinating crops, such as wheat.



INDEPENDENT RESEARCH GROUP: **FUNCTIONAL PLANT STRUCTURES** (FPS)

Head: Dr. Yongyu Huang

Mission

The independent research group Functional Plant Structures studies how plants build their physical structures as a basis to better understand plant survival and productivity. We exploit the natural and induced genetic diversity in barley to identify genes, pathways, and mechanisms that control stem and spike development. Our goal is to uncover how plant form relates to performance and to provide structural and biological insights that support the development of resilient, high-yielding crops for a changing world.

Results

Developmental and evolutionary control of barley spike shape

Spikes of the Triticeae display a mesotonic shape, in which spikelet size declines bidirectionally from a central maximum. We developed protocols to dissect the phenotypic variation of developing spikes of barley (*Hordeum vulgare* L.; Di *et al.*, under review). We identified two major loci, including one termed *SIF (SPIKELET INITIATION AND FERTILITY)*, that specifies the rate of spikelet meristem initiation. This 'fast-slow' strategy in spikelet initiation orchestrates the proximal-distal patterning of the spikelet to shape barley spikes size (Huang *et al.*, under review). Another locus, termed SHAPE, coordinates leaf-derived signals and growth duration to drive heterochronic spikelet growth, thereby establishing the mesotonic spike form (Yang, *et al.*, in preparation). Variation at both loci contributes to spike architectural diversity across barley subpopulations. Ongoing work will test how variation in spike shape influences grain yield performance under mini-greenhouse conditions that mimic field-like environments.

Decoupled regulation of growth rate and duration determines stem form

Along the barley stem, internodes vary dramatically in size, shape, and anatomy, forming a characteristic proximal–distal gradient (Figure 1). Our results show that this variation arises from differences in the rate and duration of internode initiation and elongation along the proximal–distal axis, driven by an autoregulatory feedback mechanism that coordinates these processes during stem morphogenesis (Di *et al.*, in preparation). We further demonstrated that mutations affecting cell wall properties constrain this proximal–distal patterning, leading to dwarfism and reduced environmental plasticity under high nitrogen availability and dense planting conditions (Di *et al.*, unpublished). Ongoing work includes the functional elucidation of the underlying molecular pathways using transcriptomic analyses.

A developmental repertoire of height-related mutants

To systematically dissect the developmental bases of plant height variation, we assembled a collection of approximately 140 barley mutants from the NordGen barley Genebank that displays a broad range of height phenotypes. Guided by our findings on the decoupled regulation of growth rate and growth duration in stem and spike form, we conducted a detailed phenotypic screening of this set of mutants. We quantified internode number and length, elongation dynamics, and associated spike traits to distinguish alterations in growth rate from changes in growth duration. The collection captures diverse developmental trajectories underlying reduced or increased plant height, including defects in internode initiation, impaired elongation, and altered proximal–distal patterning. Several mutants exhibit phenotypes analogous to those associated with our stem and spike regulatory pathways, providing a foundation for gene identification and mechanistic dissection in the future.

Selected publications

Huang Y, Schnurbusch T (2024) The birth and death of floral organs in cereal crops. ***Annu. Rev. Plant Biol.*** 75: 427-458.

Huang Y et al. (2024) Dynamic phytomeric growth contributes to local adaptation in barley. ***Mol. Biol. Evol.*** 41: msae011.

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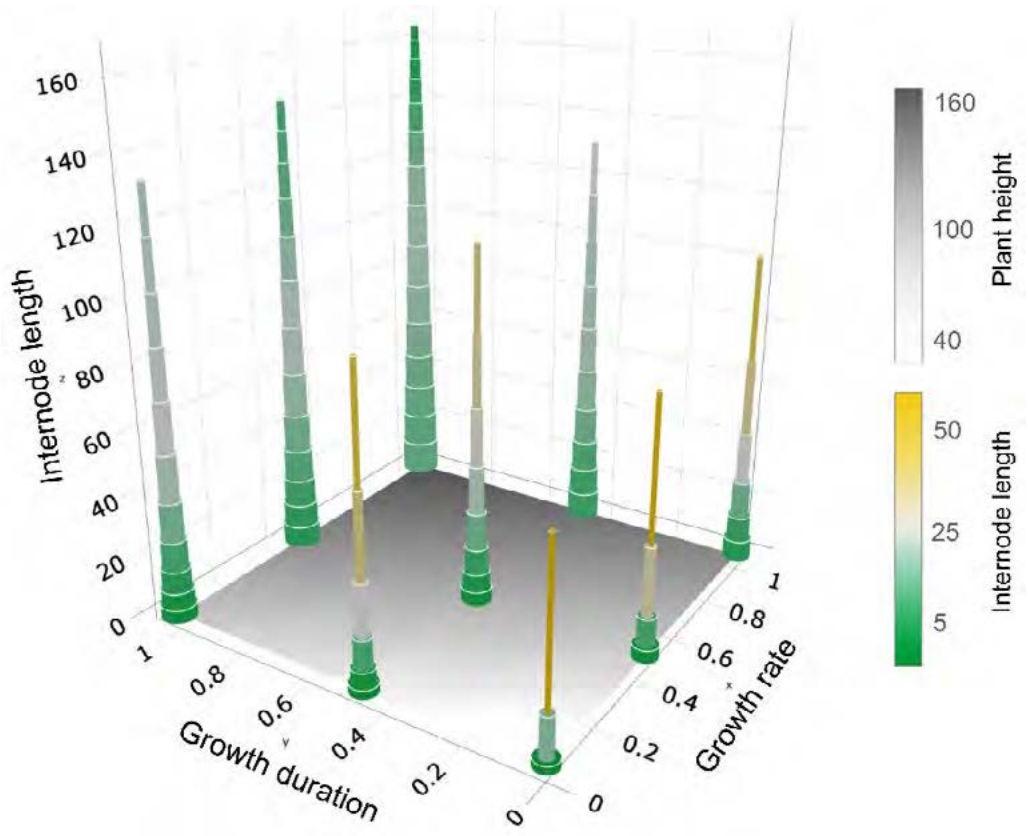


Figure 1: *Internode length as a result of growth rate and growth duration. Different combinations of growth rate and growth duration generate distinct architectural outcomes. This exemplifies the research goal of the Functional Plant Structures group: to understand how genetic and developmental mechanisms control growth dynamics to shape plant architecture and performance.*

Embedding in IPK Research Themes

With the increasing number of sequenced plant genomes, a major challenge is linking genetic information to phenotypic outcomes. Our research addresses this gap and aligns with IPK's Research Themes, including (1) Activating genetic diversity; (2) Exploiting biodigital plant data; (3) Engineering genomes and chromosomes and (5) Enhancing plant shoot performance. Recently, we successfully repaired a single base-pair mutation that contributed to the domestication of barley spike architecture.

Outlook

Building on our mechanistic insights into the genetic and developmental control of barley stem and spike architecture, future priorities will address the full functional spectrum of genes controlling shoot development by integrating trait modelling, genome evolution, and genome engineering. This approach will enable the dissection of complex trait variation and improve the prediction of plant performance across diverse growth conditions. Building on IPK infrastructures and strategic priorities, the research group is developing competitive third-party funding proposals to advance architecture-based crop improvement strategies for resilient and productive cereals.



INDEPENDENT RESEARCH GROUP: **BIOTECHNOLOGY AND GENOME EDITING** (BGE)

Head: Dr. Robert Hoffie

Mission

Established in June 2025 based on funding from the BMFTR, the independent research group 'Biotechnology and Genome Editing' (BGE) develops and establishes novel methodological approaches in plant biotechnology, both for basic and application-oriented research. Biotechnology plays a key role in the functional analysis of genes and their allelic variants. Well-established genome editing approaches, such as targeted mutagenesis with Cas endonucleases from the bacterial CRISPR system, make an important contribution here, but are still limited by a certain randomness of the resulting gene sequences. Our group is therefore developing more precise and efficient methods of genome editing that allow gene variants to be reproduced accurately. The underlying aim is to make the natural genetic diversity in crops easier accessible to research and for subsequent breeding approaches.

Results

The first six months of the group's work were invested into setting up the laboratory, hiring qualified personnel and establishment of basic methods. The barley protoplast assay was of extraordinary importance here and we were successful to establish and optimise the routine isolation and transformation of barley mesophyll protoplasts within the first months (Figure 1).

Our current research is conducted in frame to the BMFTR-funded project PROGRESS and aims (i) to develop a new method for precise genome editing based on microhomology-mediated end joining (MMEJ) and (ii) to increase editing efficiency by improving the gRNA scaffold as crucial component of the Cas endonuclease genome editing system. For both work packages, comprehensive literature studies were obtained first.

To repair DNA double strand breaks, non-homologous end joining (NEHJ) is the predominant repair mechanism, that fuses together the blunt ends of the breakage. In contrast, MMEJ is characterised by single strand end resection that prevents NHEJ and enables short (2-20 bp) homologous sequences at both sides of the break to mitigate annealing of the single stranded ends. To activate MMEJ for precise genome editing, exonucleases as fusion partners for Cas9 were selected, to combine the targeted DNA double strand induction by Cas9 and the single strand end resection to avoid NHEJ to become active. The *Arabidopsis* Exo1 and the viral UL12 have been previously described to be capable of single strand end resection of Cas9 induced DNA double strand breaks but were mainly used to enhance homology-directed repair (HDR) that requires long end resection. Therefore, MRE11 was selected as a crucial component of the endogenous enzymatic complex that is responsible for short DNA end resection to initiate MMEJ. In total, six endonuclease-exonuclease fusion modules have been cloned for the CasCADE vector system and are currently under investigation.

The gRNA is the under-engineered component of the Cas endonuclease genome editing system, although it is crucial for efficient targeting and editing of the genomic sequence of choice. Its scaffold forms a secondary structure with characteristic stem-loops that interact with Cas9 and make the 20 bases target-specific part of the gRNA accessible to the DNA strand. However, base pairing between the target-specific part and the gRNA scaffold can disturb the proper formation of these

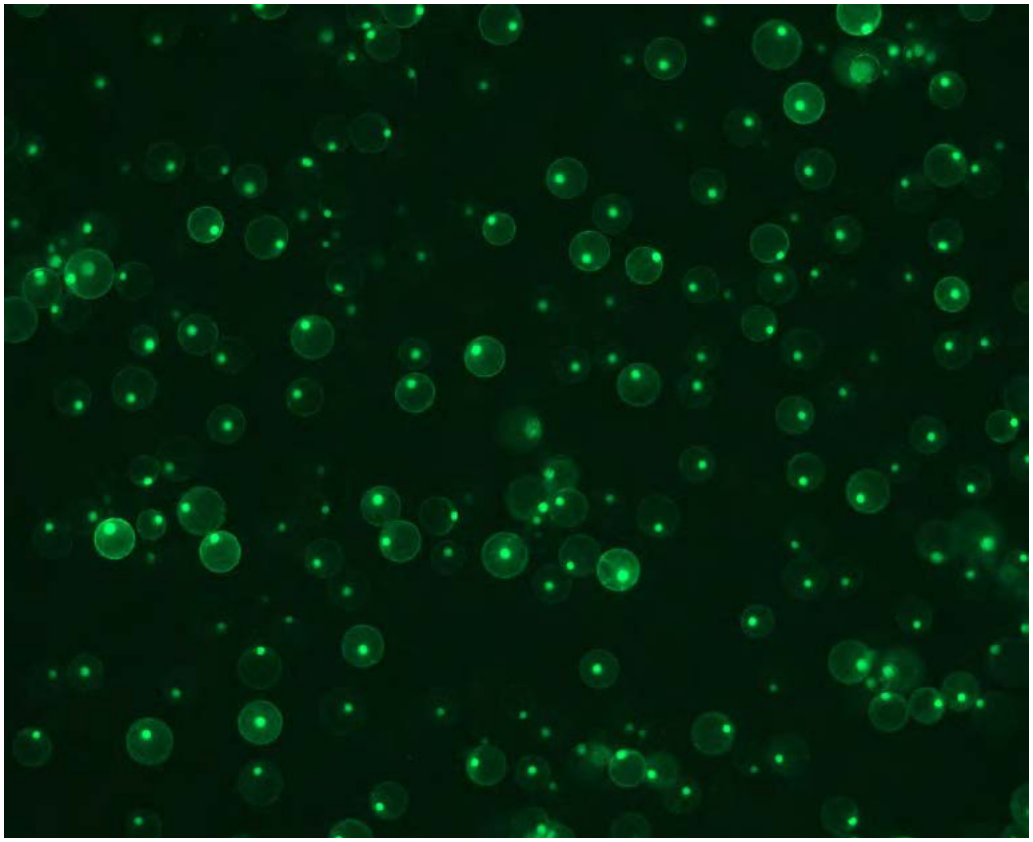


Figure 1: *GFP fluorescence of barley mesophyll protoplasts proof high transformation efficiency. Protoplasts are used in the BGE group as cell-based system for rapid optimisation cycles in method development.*

crucial stem loops, thereby reducing the loading of Cas9 with the gRNA or preventing the target recognition. Both results in reduction of editing efficiency. To improve the gRNA scaffold, in total five new variants with different modifications regarding length and sequence composition were selected from recent publications from microbes and animal cell systems and will first be established in a plant system. The respective gRNA module vectors for the CasCADE system were generated and are currently under investigation.

Embedding in IPK Research Themes

With the development of novel genome editing technologies, the group contributes directly to Research Theme 3, Engineering Genomes and Chromosomes. Furthermore, the aim is to employ those new methods to investigate and utilise allelic variants of candidate genes to enhance crop performance, contributing to the Research Themes 1 - Activating Genetic Diversity, 4 - Roots for Resource-Efficient Crops and 5 - Enhancing Plant Shoot Performance.

Outlook

The group's future plans comprise the implementation of the BMFTR-funded PROGRESS project: Based on the newly established Cas9-exonuclease fusions, approaches will be developed to integrate or replace DNA fragments with precise sequence alterations in our candidate genes as proof of concept of our novel method.

Once the characteristics of the new gRNA scaffolds proved to be beneficial for targeting efficacy, they will also guide us for our future aim: The tailoring of individual gRNA scaffold for individual gene targets to ensure the proper formation of the correct secondary gRNA structure even for sequences that cannot be targeted today. Beyond that, the BGE groups aims for the acquisition of further funding.

Publications

List of publications 01.01.2024 – 31.12.2025

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Meyer zu Vilsendorf M (2024) Ermittlung der Temperaturänderung während des Handlings von Kryoproben und potentieller Überschreitungen kritischer Temperaturen. (Master Thesis) Gottfried Wilhelm Leibniz Universität Hannover, Naturwissenschaftliche Fakultät, Hannover. 53 pp.

Morad M (2024) Characterization of root traits of novel semi-dwarf rye genotypes. (Master Thesis) Christian-Albrechts-Universität zu Kiel, Fakultät für Agrar- und Ernährungswissenschaften, Institut für Pflanzenbau und Pflanzenzüchtung, Kiel. 56 pp.

Pinninti K (2024) Transcriptomic analysis of thermomorphogenesis in tomato seedlings. (Master Thesis) Christian-Albrechts-Universität zu Kiel, Kiel.

Potlapalli BP (2024) Extending the CRISPR-Cas9-based imaging toolbox to improve the detection of chromosomal DNA. (PhD Thesis) Martin-Luther-Universität Halle-Wittenberg, Naturwissenschaftliche Fakultät III Agrar- und Ernährungswissenschaften, Geowissenschaften und Informatik, Halle/S. 131 pp.

Rakhi AA (2024) Role of protein complexes containing CuZnSOD proteins during transcription and abiotic stress signalling in land plants. (Master Thesis) Hochschule Anhalt (FH), Köthen. 54 pp.

Ramm N (2024) Analyse von Strigolacton-Mutanten in Gerste. (Bachelor Thesis) Otto-von-Guericke Universität Magdeburg, Fakultät für Verfahrens- und Systemtechnik, Magdeburg. 54 pp.

Ramzan H (2024) Nitrogen use efficiency in contrasting elite winter wheat lines (EL) and plant genetic resources (PGR). (Master Thesis) Università degli Studi di Milano Statale, Mailand/Italien.

Rembe M (2024) The use of genome-wide prediction to increase efficiency in plant breeding programs. (PhD Thesis) Martin-Luther-Universität Halle-Wittenberg, Naturwissenschaftliche Fakultät III Agrar- und Ernährungswissenschaften, Geowissenschaften und Informatik, Halle/S.

Sangien S (2024) Transcriptomic analysis for the identification of genes involved in B chromosome elimination. (Master Thesis) Technische Hochschule, Deggendorf.

Sarala GP (2024) Elucidation and functional characterization of the phenylpropanoid pathway in Hortensia species. (PhD Thesis) Martin-Luther-Universität Halle-Wittenberg, Naturwissenschaftliche Fakultät I Biowissenschaften, Halle/S. 156 pp.

Schmidt M (2024) The potential of wheat variety mixtures to enhance grain yield and yield stability. (Master Thesis) Universität für Bodenkultur (BOKU), Wien/Österreich.

Sorourmofrad M (2024) Understanding the contribution of plant genetic resources (PGRs) to disease resistance traits in wheat. (Master Thesis) Gottfried Wilhelm Leibniz Universität Hannover, Naturwissenschaftliche Fakultät, Hannover.

Spieß JM (2024) Die Cas9-Endonuklease von *Staphylococcus aureus* als alternatives Werkzeug für die Genom-Editierung von Gerste. (Bachelor Thesis) Hochschule Anhalt, Fachbereich Angewandte Biowissenschaften und Prozesstechnik, Köthen. 100 pp.

Suraweera IU (2024) Subtilisin-like protease as a potential modulator of barley's defense response. (Master Thesis) Christian-Albrechts-Universität zu Kiel, Fakultät für Agrar- und Ernährungswissenschaften, Kiel. 57 pp.

Tawale AB (2024) Phenotype and transcriptome analysis of an ancestral allele's effect on the durum wheat spike. (Master Thesis) Indian Institute of Science Education and Research (IISER), Tirupati, India. 69 pp.

Thomsen LE (2024) Integrating genomic predictions into an applied wheat breeding program. (Master Thesis) Universität Hohenheim, Stuttgart.

Tunc CE (2024) Physiological processes and molecular determinants of root senescence in barley. (PhD Thesis) Martin-Luther-Universität Halle-Wittenberg, Naturwissenschaftliche Fakultät I Biowissenschaften, Halle/S. 173 pp.

Vogelsang N (2024) Complementation of the yeast Δtps2 deletion mutant by expression of TPPs involved in wheat floret abortion. (Master Thesis) Hochschule Anhalt, Fachbereich Angewandte Biowissenschaften und Prozesstechnik, Köthen. 78 pp.

Wülpern M (2024) Vergleich von GBS-, WGS, und SNP-Chip-Datensätzen zur Eignung für die phylogenetische Bauminferenz mit der Neighbor-Joining-Methode am Beispiel von Gerste. (Bachelor Thesis) Hochschule Emden-Leer (FH), Fachbereich Technik - Naturwissenschaftliche Technik, Emden. 41 pp.

Yalagapati S (2024) Centromere targeting mechanism of KNL2 protein variants through analysis of their interaction with centromeric DNA. (Master Thesis) Biotechnology at Vignan's Foundation for Science, Technology & Research, Guntur, India. 58 pp.

Theses 2025

Agacka-Moldoch M (2025) Tobacco seed viability in relation to storage conditions and mapping of QTL controlling this trait (in Polish language). (PhD Thesis) Institute of Soil Science and Plant Cultivation, Pulawy, Poland. 110 pp.

Agsten L (2025) Funktionelle Validierung eines Nonhost-Resistenzgens der Gerste gegen nicht adaptierten Weizenmehltau. (Bachelor Thesis) Hochschule Mittweida, Mittweida. 88 pp.

Bauernfeind E (2025) Molekulare Analyse von transgenen HvD27-Überexpressionslinien in *Hordeum vulgare*. (Bachelor Thesis) Martin-Luther-Universität Halle-Wittenberg, Halle/S. 47 pp.

Binder H (2025) Recurrent reciprocal genomic selection in wheat. (Master Thesis) Martin-Luther-Universität Halle-Wittenberg, Halle/S.

Bolesta L (2025) Einfluss von CROSSOVER JUNCTION ENDONUCLEASE MUS81 auf die meiotische Temperaturresilienz von *Arabidopsis thaliana*. (Bachelor Thesis) Martin-Luther-Universität Halle-Wittenberg, Naturwissenschaftliche Fakultät III Agrar- und Ernährungswissenschaften, Geowissenschaften und Informatik, Halle/S. 30 pp.

Brendel FL (2025) Characterization and isolation of genes and enzymes involved in gramine biosynthesis in Lupinus species. (Master Thesis) Martin-Luther-Universität Halle-Wittenberg, Halle/S. 27 pp.

Chavez BG (2025) Unraveling topane alkaloid biosynthesis in *Erythroxylum coca*. (PhD Thesis) Martin-Luther-Universität Halle-Wittenberg, Naturwissenschaftliche Fakultät I Biowissenschaften, Halle/S. 127 pp.

Chen J (2025) Identification of trans-acting factors that control the non-Mendelian drive of the rye B chromosome. (PhD Thesis) Martin-Luther-Universität Halle-Wittenberg, Naturwissenschaftliche Fakultät III Agrar- und Ernährungswissenschaften, Geowissenschaften und Informatik, Halle/S. 104 pp.

Damodaran D (2025) Genetic and physiological insights into immature inflorescence greening: exploring key genes in barley and wheat. (Master Thesis) Indian Institute of Science Education and Research (IISER), Tirupati, India, 56 pp.

Datta S (2025) Establishment of apomictic processes in barley. (Bachelor and Master Thesis, dual degree) Kalinga Institute of Industrial Technology, India.

Friedenberger L (2025) Der Einfluss von Strigolactonen auf die Pflanzenarchitektur der Gerste (*Hordeum vulgare*). (Bachelor Thesis) Martin-Luther-Universität Halle-Wittenberg, Halle/S. 47 pp.

Friedrich L (2025) Molekularbiologische Charakterisierung des Wachstums-Kandidatengens IQD15 aus der pflanzenspezifischen Calmodulin-bindenden IQ67-Domäne-Familie in *Arabidopsis thaliana*. (Bachelor Thesis) Hochschule Osnabrück, Osnabrück. 47 pp.

Frohn S (2025) Appearance and role of CuZnSOD proteins on early land plant evolution. (PhD Thesis) Universität Bielefeld, Bielefeld. 124 pp.

Guo Y (2025) A haplotype-based evolutionary history of barley domestication. (PhD Thesis) Martin-Luther-Universität Halle-Wittenberg, Naturwissenschaftliche Fakultät III Agrar- und Ernährungswissenschaften, Geowissenschaften und Informatik, Halle/S. 122 pp.

Kalide P (2025) Konzeption und Entwicklung einer Softwarelösung zur Erfassung von Beschreibungen und Annotationen auf Digitalisaten von Herbarbelegen. (Bachelor Thesis) Otto-von-Guericke Universität Magdeburg, Fakultät für Informatik, Magdeburg. 65 pp.

Klösgen VJ (2025) Expanding the breeder's toolbox with artificial intelligence enabled workflow for genomic predictions. (Master Thesis) Martin-Luther-Universität Halle-Wittenberg, Halle/S. 45 pp.

Koulli S (2025) Influence of candidate gene IQD15 on root growth in *Arabidopsis thaliana*: growth on agar and soil. (Bachelor Thesis) Martin-Luther-Universität Halle-Wittenberg, Halle/S. 47 pp.

Langkutsch C (2025) Selektion homozygoter Linien von umamit-Mutanten und deren phänotypische Charakterisierung. (Bachelor Thesis) Hochschule Anhalt, Fachbereich Angewandte Biowissenschaften und Prozesstechnik, Köthen. 40 pp.

Lauterberg MM (2025) Utilizing high-throughput phenotyping to dissect plant genetic resources of wheat and chickpea under drought stress. (PhD Thesis) Martin-Luther-Universität Halle-Wittenberg, Naturwissenschaftliche Fakultät III Agrar- und Ernährungswissenschaften, Geowissenschaften und Informatik, Halle/S. 101 pp.

Leite Dias S (2025) Exploring plant allelopathy: from alkaloid pathway evolution to enzyme discovery and crop engineering. (PhD Thesis, kumulativ) Friedrich-Schiller-Universität Jena, Fakultät für Biowissenschaften, Jena. 266 pp.

Lell M (2025) Data integration strategies for genomic prediction and association studies in wheat breeding. (PhD Thesis, kumulativ) Martin-Luther-Universität Halle-Wittenberg, Naturwissenschaftliche Fakultät III Agrar- und Ernährungswissenschaften, Geowissenschaften und Informatik, Halle/S. 73 pp.

Lindecke F (2025) Exploration of the HvBT-HvMYB1-HvMTP1s module in regulating Zn-dependent shoot development in barley. (Master Thesis) Hochschule Anhalt, Molekulare Biotechnologie, Köthen. 92 pp.

Lubenau P (2025) Anlysis of the IQD15 – 18 gene family subclade in *Arabidopsis thaliana*. (Bachelor Thesis) Martin-Luther-Universität Halle-Wittenberg, Halle/S.

Ma Y (2025) Dissecting the mechanism of nuclear restitution in *Arabidopsis* male meiosis. (PhD Thesis) Martin-Luther-Universität Halle-Wittenberg, Naturwissenschaftliche Fakultät III Agrar- und Ernährungswissenschaften, Geowissenschaften und Informatik, Halle/S. 131 pp.

Majolo Willers H (2025) Functional characterization of RNA polymerases IV and V in the transcriptional regulation of centromeric repeats in *Arabidopsis thaliana*. (Bachelor Thesis) Berliner Hochschule für Technik, Studiengang Biotechnologie, Berlin. 61 pp.

Maniero RA (2025) Identification and characterization of genes involved with iron-dependent root growth under limiting phosphorus. (PhD Thesis) Martin-Luther-Universität Halle-Wittenberg, Naturwissenschaftliche Fakultät I Biowissenschaften, Halle/S. 138 pp.

Muqaddasi RK (2025) Insights into the genetics of pre-anthesis tip degeneration in barley (*Hordeum vulgare* L.). (PhD Thesis, kumulativ) Martin-Luther-Universität Halle-Wittenberg, Naturwissenschaftliche Fakultät III Agrar- und Ernährungswissenschaften, Geowissenschaften und Informatik, Halle/S.

Narisetti N (2025) Development of automated approaches to high-throughput plant image analysis. (PhD Thesis) Hochschule Harz, Promotionszentrum Ingenieurwissenschaften und Informationstechnologien (IWIT), Wernigerode. 199 pp.

Nimmalagottu SK (2025) Endophytic microorganisms and their influence on *in vitro* performance of potato plantlets. (Master Thesis) Göttingen, Georg-August Universität Göttingen, Fakultät für Agrarwissenschaften, Abteilung Nutzpflanzengenetik, Göttingen. 27 pp.

Rajendran M (2025) Establishment of protoplast transformation and enhancement of genome editing in rapeseed by generation and testing of *cas9* vector modules with different nuclear localization signals and promoter/terminator systems. (Master Thesis) Martin-Luther-Universität Halle-Wittenberg, Halle/S. 75 pp.

Reincke A (2025) The role of N-methyltransferases in the biosynthesis of gramine in plants. (Bachelor Thesis) Hochschule Anhalt, Studiengang Biotechnologie, Köthen. 71 pp.

Rezayeva BR (2025) Genetic engineering in the oilseed crop camelina: establishment and application. (PhD Thesis, kumulativ) Gottfried Wilhelm Leibniz Universität Hannover, Naturwissenschaftliche Fakultät, Hannover. 158 pp.

Shresta S (2025) Cas9-mediated neutralization of a small upstream ORF in the 5' UTR of *CELLULOSE SYNTHASE-LIKE F6* in barley protoplasts. (Master Thesis) University of Milan, Mailand. 86 pp.

Somasundaram S (2025) Gametophyte-specific degradation of Centromeric Histone3 (CENH3) to investigate the mechanism of uniparental genome elimination in *Arabidopsis thaliana*. (PhD Thesis) Martin-Luther-Universität Halle-Wittenberg, Naturwissenschaftliche Fakultät III Agrar- und Ernährungswissenschaften, Geowissenschaften und Informatik, Halle/S. 100 pp.

Ulagappan K (2025) Biochemical, ultrastructural and transcriptional aspects of cryopreservation in meristematic tissue of garlic shoot tips. (PhD Thesis) Martin-Luther-Universität Halle-Wittenberg, Naturwissenschaftliche Fakultät I Biowissenschaften, Halle/S. 85 pp.

van Nahl BU (2025) Analyse des durch den Transkriptionsfaktor HvNAC6 kontrollierten genregulatorischen Netzwerks bei Gerste während der Kornentwicklung und Stress. (Bachelor Thesis) Martin-Luther-Universität Halle-Wittenberg, Halle/S. 25 pp.

Westendorf AE (2025) Validierung von Zielgenen der Typ-B Response Regulatoren (HvRR11/-14) in Gerste (*Hordeum vulgare*). (Bachelor Thesis) Martin-Luther-Universität Halle-Wittenberg, Halle/S. 27 pp.

Yadala R (2025) Identification and characterization of EMB1674, as a novel KNL2 variant: revealing its centromere targeting mechanism and critical role in plant-specific kinetochore assembly. (PhD Thesis) Martin-Luther-Universität Halle-Wittenberg, Naturwissenschaftliche Fakultät III Agrar- und Ernährungswissenschaften, Geowissenschaften und Informatik, Halle/S. 124 pp.

Zhang H (2025) Improved genome and population genomics unveil the winter hardiness and breeding signatures in faba bean. (PhD Thesis, kumulativ) Georg-August-Universität Göttingen, Fakultät für Agrarwissenschaften, Göttingen. 145 pp.

Third party projects

Third-party funded projects acquired and ongoing in the 2024/2025 reporting period.

Acronym: Project Name	Principle Investigator (Pi) Project Participants at IPK	Funding Agency	Duration (Start)	Duration (End)	Overall budget (Euro)
EpiC-p-epBAR: Das Pan-Epigenom der Gerste	Stein, N.	BMFTR	01.07.22	30.06.25	657.135
DIP: DiPisum - Digitalisierungsgetriebene Entwicklung Sachsen-Anhalts zu einem Innovationszentrum für Erbsenzucht, -anbau und –verwertung, TP A	Stein, N.	BMFTR	01.04.24	31.12.28	86.912
MZF: RYE-HUB - Nutzung der unerforschten Vielfalt des Roggens durch genombasierte Züchtung für eine klimaresiliente Getreideproduktion - Teilvorhaben C	Stein, N.	BMFTR	01.11.24	31.10.28	1.115.071
Genebank2.0-P3: Pflanzenzüchtungsforschung-P3-Verbundvorhaben: Genomik-basierte Nutzbarmachung genetischer Ressourcen im Weizen für die Pflanzenzüchtung, TP A	Stein, N.	BMFTR	01.11.22	31.10.25	375.820
SHAPE-P3: Pflanzenzüchtungsvorhaben-P3-Verbundvorhaben:"Strukturelle Genomvariation, Haplotypendiversität und das Gerste Pan-Genom - Erforschung der strukturellen Genomdiversität für die Gerstenzüchtung (SHAPE3) - Teilprojekt A""	Stein, N.	BMFTR	01.02.23	31.01.26	1.383.347
ALBATROS: Mikrobielle, genetische und metabolische Anpassung verschiedener Weizensorten an Trockenheit	Börner, A.	BMFTR	01.01.24	31.12.26	142.478
Fortress-Wheat: Bioökonomie International 2021: Untersuchung und Aufklärung neuer genetischer Variation in der Interaktion zwischen Weizen und Rostkrankheiten für einen pestizidreduzierten Weizenanbau-TP2	Mascher, M.	BMFTR	01.10.22	30.09.25	40.462
Genebank2.0-P3: Pflanzenzüchtungsforschung-P3-Verbundvorhaben: Genomik-basierte Nutzbarmachung genetischer Ressourcen im Weizen für die Pflanzenzüchtung, TP A	Mascher, M.	BMFTR	01.11.22	31.10.25	242.772
SHAPE-P3: Pflanzenzüchtungsvorhaben-P3-Verbundvorhaben:"Strukturelle Genomvariation, Haplotypendiversität und das Gerste Pan-Genom - Erforschung der strukturellen Genomdiversität für die Gerstenzüchtung (SHAPE3) - Teilprojekt A""	Mascher, M.	BMFTR	01.02.23	31.01.26	245.972
DIP: DiPisum - Digitalisierungsgetriebene Entwicklung Sachsen-Anhalts zu einem Innovationszentrum für Erbsenzucht, -anbau und –verwertung, TP A	Jayakodi	BMFTR	01.04.24	31.12.28	261.134
P4ST:WIR! Physics for Food	Dehmer, K.	BMFTR	01.01.23	31.12.24	238.422
Fortress-Wheat: Bioökonomie International 2021: Untersuchung und Aufklärung neuer genetischer Variation in der Interaktion zwischen Weizen und Rostkrankheiten für einen pestizidreduzierten Weizenanbau-TP1	Reif, J.	BMFTR	01.10.22	30.09.25	232.092
DIP: DiPisum - Digitalisierungsgetriebene Entwicklung Sachsen-Anhalts zu einem Innovationszentrum für Erbsenzucht, -anbau und –verwertung, TP A	Reif, J.	BMFTR	01.04.24	31.12.28	803.250

Acronym: Project Name	Principle Investigator (Pi) Project Participants at IPK	Funding Agency	Duration (Start)	Duration (End)	Overall budget (Euro)
"MZF: DRIVE - Datengetriebene und genom-editierte Züchtung lokal angepasster Weizensorten zur Steigerung der Agrarbiodiversität, der nachhaltigen Klimaresistenz und der Ressourceneffizienz-TP A"	Reif, J.	BMFTR	01.11.24	31.12.28	623.449
Genebank2.0-P3: Pflanzenzüchtungsforschung-P3-Verbundvorhaben: Genomik-basierte Nutzbarmachung genetischer Ressourcen im Weizen für die Pflanzenzüchtung, TP A	Reif, J.	BMFTR	01.11.22	31.10.25	603.564
SHAPE-P3: Pflanzenzüchtungsvorhaben-P3-Verbundvorhaben:"Strukturelle Genomvariation, Haplotypendiversität und das Gerste Pan-Genom - Erforschung der strukturellen Genomdiversität für die Gerstenzüchtung (SHAPE3) - Teilprojekt A""	Reif, J.	BMFTR	01.02.23	31.01.26	206.914
EpiChrom: EpiC-Epigenetik, Epigenetische Konsequenzen von Chromosomrestrukturierungen - TP B	Houben	BMFTR	01.07.22	30.06.25	338.612
DiP: OptiLamia - Optimierung von Lamiaceen, einer Gruppe von Arznei- und Gewürzpflanzen, für den Aufbau einer nachhaltigen Wertschöpfungskette von der landwirtschaftlichen Produktion bis zur Verarbeitung zu medizinischen Produkten und Nahrungsmitteln	Otto, L.-G.	BMFTR	01.04.24	31.12.28	227.402
FreeWheat: Auf dem Weg zu fungizidfreiem Weizen durch die Übertragung von Nicht-Wirt-Resistenz	Douchkov	BMFTR	01.01.24	31.12.26	420.724
Bioökonomie International 2024: EXOGENE-Initiative - Erforschung exotischer genetischer Ressourcen zur Verbesseryng von Weizen	Douchkov	BMFTR	29.11.24	31.12.27	252.816
Genebank2.0-P3: Pflanzenzüchtungsforschung-P3-Verbundvorhaben: Genomik-basierte Nutzbarmachung genetischer Ressourcen im Weizen für die Pflanzenzüchtung, TP A	Douchkov	BMFTR	01.11.22	31.10.25	573.499
PrimedPlant-3: Pflanzenzüchtungsforschung-P3-Verbundvorhaben: "Priming für eine verstärkte Abwehr als eine Strategie zur Optimierung der Resistenz und ein mögliches Zuchtziel (PrimedPlant-3) - Teilprojekt A"	Douchkov	BMFTR	01.04.23	31.03.26	497.715
Genebank2.0-P3: Pflanzenzüchtungsforschung-P3-Verbundvorhaben: Genomik-basierte Nutzbarmachung genetischer Ressourcen im Weizen für die Pflanzenzüchtung, TP A	Schnurbusch	BMFTR	01.11.22	31.10.25	215.831
Bioinformatik Infrastruktur (de.NBI)	Scholz, U.	BMFTR	01.01.23	31.12.27	337.500
"MZF: DRIVE - Datengetriebene und genom-editierte Züchtung lokal angepasster Weizensorten zur Steigerung der Agrarbiodiversität, der nachhaltigen Klimaresistenz und der Ressourceneffizienz-TP A"	Arend, D.	BMFTR	01.11.24	31.12.28	324.857
Genebank2.0-P3: Pflanzenzüchtungsforschung-P3-Verbundvorhaben: Genomik-basierte Nutzbarmachung genetischer Ressourcen im Weizen für die Pflanzenzüchtung, TP A	Scholz, U.	BMFTR	01.11.22	31.10.25	1.800
SHAPE-P3: Pflanzenzüchtungsvorhaben-P3-Verbundvorhaben:"Strukturelle Genomvariation, Haplotypendiversität und das Gerste Pan-Genom - Erforschung der strukturellen Genomdiversität für die Gerstenzüchtung (SHAPE3) - Teilprojekt A""	Scholz, U.	BMFTR	01.02.23	31.01.26	335.797
BreedFides: "Verbundprojekt: Entwicklung eines nachhaltigen Datenökosystems für die Pflanzenzüchtung - BreedFides; Teilvorhaben: Förderierte Dateninfrastruktur für eine Datentreuhänderschaft und deren Tests anhand von Use Cases"	Lange, M.	BMFTR	01.01.22	31.12.24	351.526
AVATARS, WP II.12: Pflanzenzüchtungsforschung-Verbundvorhaben: Modernste Virtualitäts- und erweiterte Realitätsverfahren für den Zyklus von Samen zu Samen, TP A	Lange, M.	BMFTR	01.06.19	30.09.24	512.645

Acronym: Project Name	Principle Investigator (Pi) Project Participants at IPK	Funding Agency	Duration (Start)	Duration (End)	Overall budget (Euro)
AVATARS, WP II.5: Pflanzenzüchtungsforschung-Verbundvorhaben: Modernste Virtualitäts- und erweiterte Realitätsverfahren für den Zyklus von Samen zu Samen, TP A	Schippers	BMFTR	01.06.19	30.09.24	616.393
DROMAMED: "PRIMA-Verbundprojekt: Nutzung von mediterranen genetischen Ressourcen von Mais zur Verbesserung der Stresstoleranz; Teilv.: Präzisionsphänotypisierung von Maislienien aus mediterranen Populationen für Trocken- und Hitzestress-bezogenen Mer	Altmann	BMFTR	01.06.21	30.11.24	249.936
DPPN-ACCESS 2.0: Förderung der Nutzung von Anlagen und Technologien zur Pflanzenphänotypisierung, TP D	Altmann	BMFTR	01.01.24	31.12.28	482.065
"MZF: DRIVE - Datengetriebene und genom-editierte Züchtung lokal angepasster Weizensorten zur Steigerung der Agrarbiodiversität, der nachhaltigen Klimaresistenz und der Ressourceneffizienz-TP A"	Altmann	BMFTR	01.11.24	31.12.28	158.839
AVATARS: Entwicklung des VR-Exponates "Plant Journey-3D-Reise in die Pflanze AVATARS" (IdeenExpo)	Freitag	BMFTR	01.06.19	30.09.24	64.130
AVATARS, WP I.1: Pflanzenzüchtungsforschung-Verbundvorhaben: Modernste Virtualitäts- und erweiterte Realitätsverfahren für den Zyklus von Samen zu Samen, TP A	Altmann	BMFTR	01.06.19	30.09.25	426.584
AVATARS, WP II.2: Pflanzenzüchtungsforschung-Verbundvorhaben: Modernste Virtualitäts- und erweiterte Realitätsverfahren für den Zyklus von Samen zu Samen, TP A	Altmann	BMFTR	01.06.19	30.09.24	745.991
AVATARS, WP II.6: Pflanzenzüchtungsforschung-Verbundvorhaben: Modernste Virtualitäts- und erweiterte Realitätsverfahren für den Zyklus von Samen zu Samen, TP A	Altmann	BMFTR	01.06.19	30.09.24	396.922
AVATARS, WP III.1: Pflanzenzüchtungsforschung-Verbundvorhaben: Modernste Virtualitäts- und erweiterte Realitätsverfahren für den Zyklus von Samen zu Samen, TP A	Altmann	BMFTR	01.06.19	31.03.25	182.026
AVATARS, WP III.2: Pflanzenzüchtungsforschung-Verbundvorhaben: Modernste Virtualitäts- und erweiterte Realitätsverfahren für den Zyklus von Samen zu Samen, TP A	Altmann	BMFTR	01.06.19	30.09.25	123.275
AVATARS, WP II.8: Pflanzenzüchtungsforschung-Verbundvorhaben: Modernste Virtualitäts- und erweiterte Realitätsverfahren für den Zyklus von Samen zu Samen, TP A	Blätke	BMFTR	01.06.19	30.09.25	345.938
KABA-2021: "Innovative Technologien für die verbesserte Züchtung und Vermehrung von Kaffee- und Bananenpflanzen in Kuba""	Rolletschek, H.	BMFTR	01.07.21	30.06.24	43.191
DiP: MAGDI - Magnetresonanz für die Digitalisierung der Pflanze - Teilvorhaben A	Borisjuk, L.	BMFTR	01.04.24	31.12.28	982.188
AVATARS, WP II.3: Pflanzenzüchtungsforschung-Verbundvorhaben: Modernste Virtualitäts- und erweiterte Realitätsverfahren für den Zyklus von Samen zu Samen, TP A	Borisjuk, L.	BMFTR	01.06.19	30.09.24	557.367
AVATARS, WP II.7: Pflanzenzüchtungsforschung-Verbundvorhaben: Modernste Virtualitäts- und erweiterte Realitätsverfahren für den Zyklus von Samen zu Samen, TP A	Borisjuk, L.	BMFTR	01.06.19	30.09.24	182.067
DiP: HyperSpace - Digital unterstützte Erweiterung der bioökonomischen Wertschöpfung aus der Arzneipflanze Johanniskraut (Hypericum sp.) TP B	Rizzo	BMFTR	01.04.24	31.12.28	1.076.022
P4ST:WIR! Physics for Food	Neumann	BMFTR	01.01.23	31.12.24	12.872

Acronym: Project Name	Principle Investigator (Pi) Project Participants at IPK	Funding Agency	Duration (Start)	Duration (End)	Overall budget (Euro)
"MZF: DRIVE - Datengetriebene und genom-editierte Züchtung lokal angepasster Weizensorten zur Steigerung der Agrarbiodiversität, der nachhaltigen Klimaresistenz und der Ressourceneffizienz-TP A"	Neumann	BMFTR	01.11.24	31.12.28	208.023
DPPN-ACCESS 2.0: Förderung der Nutzung von Anlagen und Technologien zur Pflanzenphänotypisierung, TP D	Neumann	BMFTR	01.01.24	31.12.28	482.065
AVATARS, WP II.4: Pflanzenzüchtungsforschung-Verbundvorhaben: Modernste Virtualitäts- und erweiterte Realitätsverfahren für den Zyklus von Samen zu Samen, TP A	Gladilin	BMFTR	01.06.19	30.09.24	275.317
Seedmaker: Aufklärung epigenetischer Mechanismen der Endospermbildung für die Entwicklung apomiktischer Kulturpflanzen	Kumlehn	BMFTR	01.07.22	30.06.25	440.172
BIMOTEC: Optimierung von Buchweizen durch moderne Züchtungsmethoden zur Produktion von Nahrungsmitteln und Wertschöpfung biobasierter Rohstoffe	Kumlehn	BMFTR	01.12.24	30.11.28	382.825
FERTIGO: Untersaatmischungen auf Spitzwegerich-Basis als Hilfsmittel zur Verbesserung der N- und P-Ernährung der Zielkultur Mais	Wirén	BMFTR	01.05.24	30.04.27	363.625
BonaRes (Modul A, Phase 3): CATCHY - Zwischenfrüchte als agronomische Maßnahme für nachhaltige Bodenfruchtbarkeit und Ertragssicherheit, SP 2	Wirén	BMFTR	01.04.21	31.03.24	434.913
ALBATROS: Mikrobielle, genetische und metabolische Anpassung verschiedener Weizensorten an Trockenheit	Hajirezaei	BMFTR	01.01.24	31.12.26	399.609
FDCA: Verbundvorhaben: Entwicklung maßgeschneiderter Biokatalysatoren für die Herstellung von 2,5-Furandicarbonsäure auf Basis von Zuckern aus Lignocellulose; Teilvorhaben 2: Herstellung rekombinanter Hefestammefiir die Synthese von FDCA und ...	Wirén	BMFTR	01.04.23	31.03.26	325.872
PREBreed (MZF): Pangenomressourcen-basierte Züchtungsforschung in Gerste-Teilvorhaben A	Stein, N.	BMFTR	15.05.25	14.05.29	1.220.445
POMORROW (MZF): Kartoffeln für morgen: Merkmalsverbesserung mithilfe genetischer Ressourcen der Kartoffel und neuer Züchtungstechniken	Stein, N.	BMFTR	15.05.25	14.05.29	404.711
PREBreed (MZF): Pangenomressourcen-basierte Züchtungsforschung in Gerste-Teilvorhaben A	Mascher, M.	BMFTR	15.05.25	14.05.29	274.412
FABALOUS (MZF): Abiotische Stresstoleranz für Ackerbohne zur Erhöhung der Ertragsstabilität - Teilvorhaben H	Mascher, M.	BMFTR	15.05.25	14.05.29	247.790
POMORROW (MZF): Kartoffeln für morgen: Merkmalsverbesserung mithilfe genetischer Ressourcen der Kartoffel und neuer Züchtungstechniken	Dehmer, K.	BMFTR	15.05.25	14.05.29	615.747
Green ERA Hub Call 2: CerealBio - Exploiting cereal biodiversity in nutrient use and biological interactions in crop resilience breeding - TP B	Douchkov	BMFTR	01.07.25	30.06.28	35.826
INTEGRA: "Implementierung neuer Technologien zur Verbesserung des genetischen Gewinns für widerstandsfähigen Raps-Teilprojekt A"	Lange, M.	BMFTR	15.05.25	14.05.29	256.892
PREBreed (MZF): Pangenomressourcen-basierte Züchtungsforschung in Gerste-Teilvorhaben B	Scholz, U.	BMFTR	15.05.25	14.05.29	303.497
PREBreed (MZF): Pangenomressourcen-basierte Züchtungsforschung in Gerste-Teilvorhaben D	Schippers	BMFTR	15.05.25	14.05.29	93.012
MZF: INTEGRA - Implementierung neuer Technologien zur Verbesserung des genetischen Gewinns für widerstandsfähigen Raps - TP A	Altmann	BMFTR	15.05.25	14.05.29	785.852

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Green ERA Hub Call 2: CerealBio - Exploiting cereal biodiversity in nutrient use and biological interactions in crop resilience breeding - TP B	Neumann	BMFTR	01.07.25	30.06.28	282.737
MZF: INTEGRA - Implementierung neuer Technologien zur Verbesserung des genetischen Gewinns für widerstandsfähigen Raps - TP A	Szymanski	BMFTR	15.05.25	14.05.29	290.640
PREBreed (MZF): Pangenomressourcen-basierte Züchtungsforschung in Gerste	Wirén	BMFTR	15.05.25	14.05.29	461.558
PREBreed (MZF): Pangenomressourcen-basierte Züchtungsforschung in Gerste	Schneider H.	BMFTR	15.05.25	14.05.29	432.577
MZF: INTEGRA - Implementierung neuer Technologien zur Verbesserung des genetischen Gewinns für widerstandsfähigen Raps - TP A	Kumlehn	BMFTR	15.05.25	14.05.29	383.915
MZF: PROGRESS-Präzision und Optimierung von Genom-Editierung für resiliente Kulturpflanzen	Hoffie	BMFTR	01.05.25	30.04.29	1.256.088
Neuland-PLANDT: Neuland gestalten durch Diskurse als Treiber für Innovation und gesellschaftliche Teilhabe – TP1 Naturwissensschaftliche Perspektiven und Impulse am Beispiel Pflanzenforschung	Freitag	BMFTR	01.09.25	31.08.27	311.185
PreLuteus: Entwicklung von ertragreichen und resistenten Prebreeding Linien bei der Gelben Lupine in Deutschland; Teilvorhaben 2: Prüfung der Trockenstresstoleranz	Lohwasser	BMLEH	01.10.22	30.09.25	86.896
CiLaKlima: „Screening genetischer Ressourcen von Kichererbse (Cicer arietinum) und Saat-Platterbse (Lathyrus sativus): Anpassung an den Klimawandel in Deutschland mit alternativen Leguminosen für die menschliche Ernährung (CiLaKlima)“	Lohwasser	BMLEH	01.12.22	30.11.25	122.637
SIMULTAN: Sicherung von Multifunktionalität in der Grobfutterproduktion durch Artenreichtum im intensiven Grasland	Lohwasser	BMLEH	01.04.23	31.05.26	210.016
WiLGeR: Evaluierung genetischer Ressourcen zur züchterischen Verbesserung von Winterlinsen für den Mischfruchtanbau (Winter Lens Genetic Resources)	Lohwasser	BMLEH	01.09.23	31.12.26	82.710
Wick4Pig: Saatwickenkörner (Vicia sativa L.) für Mastschweine als alternatives, proteinreiches Futtermittel unter sich wandelnden klimatischen Bedingungen	Lohwasser	BMLEH	01.12.23	31.01.28	208.651
BOENLE: Vigna-Bohnen und mehr-Screening subtropischer Leguminosenarten für den Anbau in Deutschland	Lohwasser	BMLEH	26.11.24	31.01.28	207.398
ObiVonKnobi: Ökologischer Anbau von Knoblauch-Erweiterung des Sortenspektrums durch Selektion pflanzengenetischer Ressourcen	Nagel	BMLEH	01.04.24	31.03.29	307.701
FUGE: Monitoring der Fusariumarten und Entwicklung genomischer Werkzeuge zur effektiveren Züchtung von Saathafer	Mascher, M.	BMLEH	15.12.20	14.06.24	168.406
Effikar: Selektion und Züchtung nährstoffeffizienter Phytophthora-resistenter Kartoffelzuchtstämme für einen nachhaltigen ökologischen Landbau	Dehmer, K.	BMLEH	01.11.19	31.07.24	339.781
LuzNutz: Erhöhung der Anbauwürdigkeit von Luzerne (Medicago sativa L.) als Futterpflanze - Neue Impulse für die Königin der Futterpflanzen	Dehmer, K.	BMLEH	01.02.21	31.01.24	297.057
KAROLA: Kartoffelzüchtung auf Stresstoleranz und Verarbeitungseignung für den ökologischen Landbau	Dehmer, K.	BMLEH	01.03.24	28.02.29	610.855
HYFLOR: Verbundprojekt: Erforschung der Genetik der Blühbiologie bei Weizen zur effektiven Erzeugung von Hybridweizen, TP 1	Reif, J.	BMLEH	01.10.19	30.09.24	696.077
BigData: Nutzung von Big Data in Weizen zur Präzisionszüchtung	Reif, J.	BMLEH	01.02.20	31.01.25	385.685

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KIBREED: Verbundprojekt Züchtung von Standortangepassten Sorten mittels Algorithmen der Künstlichen Intelligenz-Teilprojekt A	Reif, J.	BMLEH	01.06.21	30.11.24	334.284
Brand-Resist: Verbesserung der Steinbrand- und Zwergsteinbrand-resistenz in Brotweizen durch systematische Nutzung genetischer Variation (Brand-Resist)	Reif, J.	BMLEH	15.09.23	31.08.28	82.228
RustHealth: Genetische Analyse und Modellierung der Weizen-Rostin-teraktion zur Entwicklung stabiler, mehrfachresistenter Weizensorten (RustHealth) - Teilprojekt C	Reif, J.	BMLEH	01.09.23	31.08.26	206.515
Amobila: Verbundvorhaben: Arzneipflanzenanbau als Instrument einer modernen, ertragsorientierten und zugleich biodiversitätsfördernden Landwirtschaft; Teilvorhaben3: Ertragsrelevanz von Bestäubern, Bestäubungswegen und-distanzen an der Echten Kamille	Otto, L.-G.	BMLEH	01.03.23	28.02.26	#NV
HYFLOR: Verbundprojekt: Erforschung der Genetik der Blühbiologie bei Weizen zur effektiven Erzeugung von Hybridweizen, TP 1	Schnurbusch	BMLEH	01.10.19	30.09.24	409.534
BigData: Nutzung von Big Data in Weizen zur Präzisionszüchtung	Scholz, U.	BMLEH	01.02.20	31.01.25	375.253
STRESS-STOPP: Verbundprojekt: Steigerung der Trockenstressadap-tation in Raps: Ertragsstabilität und Stresstoleranz als Selektionstar-gets für Optimierung via physiologischer Phänotypisierung-TP C	Altmann	BMLEH	15.08.23	14.08.26	231.753
ObiVonKnobi: Ökologischer Anbau von Knoblauch-Erweiterung des Sortenspektrums durch Selektion pflanzengenetischer Ressourcen	D'Auria	BMLEH	01.04.24	31.03.29	319.825
KAROLA: Kartoffelzüchtung auf Stresstoleranz und Verarbeitungseig-nung für den ökologischen Landbau	Neumann	BMLEH	01.03.24	28.02.29	44.116
FASTFLOW: Verbundprojekt: Generationsbeschleunigung bei Winter-weizen durch vernalisationsunabhängige Induktion der Ährenbildung - TP 1	Kumlehn	BMLEH	01.04.20	31.03.24	562.892
QUIZ: Züchtung von Quinoa für den Anbau in Deutschland	Kumlehn	BMLEH	01.03.23	28.02.26	204.299
DERUST: Entwicklung dauerhafter und rassenunspezifischer Getreide-resistenz gegen Rostkrankheiten und Mehltau (DERUST) - Teilprojekt A	Kumlehn	BMLEH	01.04.23	31.03.26	399.335
TEAM7: Technologieentwicklung eines breit anwendbaren Genomedi-tierungs-Systems für die Pflanzenzüchtung - Teilprojekt C	Kumlehn	BMLEH	01.04.24	31.03.27	802.693
"Sus-Agri-CC: InnovativeBiodünger zur Ertragssteigerung von Getreide und Gartenbaukulturen unter dem globalen Klimawandel: Aufdem Weg zur Nachhaltigkeit von landwirtschaftlichen Systemen gegen den Klimawandel inariden Zonen"" "	Hajirezaei	BMLEH	01.06.21	31.03.25	170.146
SMARTROOT: Wurzelarchitektur- und Wurzelplastizitätsmerkmale für stickstoffeffiziente und trockenstressresiliente Gerstensorten	Giehl	BMLEH	01.04.23	31.03.26	410.874
NEATWHEAT: Verbesserung physiologischer und morphologischer N-Effizienzmerkmale in Winterweizen für eine nachhaltige Pflanzen-produktion	Wirén	BMLEH	01.10.23	30.09.26	317.433
SWEETDHC: Verbundprojekt: Zuckerreduktion in Lebensmitteln und Getränken durch einen Inhaltsstoff aus Hortensien (Hydrangea.mac. ssp.serrata)	Hajirezaei	BMLEH	01.04.24	31.10.27	338.317
"Evolution und Funktion des Heterostylie-Supergens bei Amsinckia (Boragi-naceae)"	Himmelbach	DFG	01.10.21	31.12.25	47.600
22. Hauptkongress der Euroäischen Gesellschaft für Züchtungsfor-schung (EUCARPIA) "Globale Herausforderung zur Verbesserung von Nutzpflanzen"	Börner, A.	DFG	29.02.24	31.12.24	34.160

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POTEND: „KartoffelEndophyten-Interaktion und die Reaktion auf Stress (POTEND Stress)“	Nagel	DFG	01.11.22	31.10.25	308.750
WILD SIX ROW: "Adaptive Introgressionen in Hybridschwärmen zwischen Wild- und Kulturgerste in Israel"	Mascher, M.	DFG	01.07.22	30.06.25	216.250
ISRAEL: WILD SIX ROW	Mascher, M.	DFG	01.03.22	28.02.25	89.100
Weiterleitung Dr. Abbo: Vetch Nutrition: Agronomische Aufwertung der alten Kulturart Linsenwicke (Vicia erviliaals lokale Eiweißpflanzen in Europa und Israel)	Mascher, M.	DFG	01.04.24	31.03.27	15.000
Weiterleitung Dr. Kerem: Vetch Nutrition: Agronomische Aufwertung der alten Kulturart Linsenwicke (Vicia erviliaals lokale Eiweißpflanzen in Europa und Israel)	Mascher, M.	DFG	01.04.24	31.03.27	49.300
Vetch Nutrition: Agronomische Aufwertung der alten Kulturart Linsenwicke (Vicia erviliaals lokale Eiweißpflanzen in Europa und Israel)	Jayakodi	DFG	01.04.24	31.03.27	274.063
„Modellierung der Mechanismen der mitotischen Chromosomenkondensation mithilfe von Polymersimulationen“	Camara	DFG	01.08.22	31.07.25	333.450
SFB: Sonderforschungsbereich 1211 "Evolution der Erde und des Lebens unter extremer Trockenheit" Köln	Harpke	DFG	01.07.24	31.12.28	49.000
Analyse der komplexen Karyotypevolution in Korkussen	Harpke	DFG	01.04.22	31.03.25	343.203
FAIRAgro: "FAIRe Dateninfrastruktur für die Agrarsystemforschung"	Reif, J.	DFG	01.03.23	29.02.28	280.012
Entwicklung von statistisch-genomischen Werkzeugen zur Entschlüsselung der genetischen Architektur der Heterosis unter Verwendung von tiefen Sequenzdaten	Yong Jiang	DFG	01.08.24	31.07.27	332.877
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 zur Untersuchung der...	Houben	DFG	01.06.21	01.03.25	210.550
"Identifizierung und funktionelle Charakterisierung von Genen beteiligt am Prozess der wurzelspezifischen Eliminierung von B-Chromosomen in Aefilops speltoides"	Houben	DFG	01.06.22	31.05.25	214.950
B-Chromosome: "Chromosomendrive von Roggen B Chromosomen - Analyse der molekularen Grundlagen“	Houben	DFG	01.06.23	31.05.26	216.150
Analyse von Cluster-Holocentromeren - ein neuartige Zentromer Variante der Lililaes Chionographis - Die Evolution von Mono- zu Holozentromeren	Houben	DFG	01.03.23	31.08.25	250.500
Aufklärung des Mechanismus der nicht reduzierten Gametenbildung bei Arabidopsis thaliana	Heckmann, S.	DFG	01.07.21	30.06.24	222.528
Proteomprofiling und funktionelle Analyse des synaptonemalen Komplexes in Arabidopsis thaliana	Heckmann, S.	DFG	01.07.24	30.06.27	244.427
Histon:"Identifizierung der Rolle der H3K9-Demethylierung in der Meiose von Arabidopsis“	Jiang, H.	DFG	01.05.22	15.02.24	107.349
Das Protein-Protein-Interaktionsnetzwerk von KNL2 in Pflanzen	Lermontova	DFG	15.06.21	31.12.24	216.650
Zentromerische Transkripte und ihre Funktion für die Entstehung des zentromerischen Chromatins und den Aufbau des Kinetochors	Lermontova	DFG	01.04.23	31.03.26	225.350
"Emmy-Noether, Phase 1; Meiotische Rekombination, Pollengröße und allelische Selektion im Roggen (Secale cereale) unter Nährtstoffmangel verursacht durch 140 Jahre Monokultur"	Dreißig	DFG	01.01.25	30.06.25	38.400

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MeioTempRes: Meiotische Temperaturbeständigkeit in Wildgerste	Dreißig	DFG	01.01.25	30.06.27	208.010
SFB1664; Quantitative zytologische Charackterisierung und strukturelle analyse von REC8 Proteoformen in der pflanzlichen Meiose	Dreißig	DFG	01.01.25	30.06.28	286.090
"Emmy-Noether, Phase 2; Meiotische Rekombination, Pollengröße und allelische Selektion im Roggen (Secale cereale) unter Nährtstoffmangel verursacht durch 140 Jahre Monokultur"	Dreißig	DFG	01.01.25	31.12.27	850.035
Licorice-Iran: "Genetische Verbesserung und Erhaltung der genetischen Ressourcen von Süßholz (Glycyrrhita glabra)"	Otto, L.-G.	DFG	01.06.23	31.08.24	27.450
CSCS-HvWOXs: "Stammzellsysteme bei Getreide (CSCS): Etablierung, Aufrechterhaltung und Beendigung"	Schnurbusch	DFG	01.07.22	30.06.26	311.500
WILD SIX ROW: "Adaptive Introgressionen in Hybridschwärmen zwischen Wild- und Kulturgerste in Israel"	Schnurbusch	DFG	01.03.22	28.02.25	6.100
Weizenblütchen: Der Blüherfolg eines Blütenstandes hängt von seinem Rückgrat ab – erste Einblicke in das Wachstum und die Entwicklung der Rachis und ihre Auswirkungen auf die Fruchtbarkeit der Weizenblüten und die Kornzahl	Schnurbusch	DFG	01.01.23	31.12.25	238.550
Barley: „Entschlüsselung der wichtigsten Regulatoren der Ährchendeterminierung bei Gerste“	Koppolu	DFG	01.05.23	30.04.26	382.550
NFDI4BioDiversity - A Consortium for the National Research Data Infrastructure (NFDI)	Scholz, U.	DFG	01.01.21	30.09.25	363.910
FAIRAgro: "FAIRe Dateninfrastruktur für die Agrarsystemforschung"	Lange, M.	DFG	01.03.23	29.02.28	903.542
"Identifizierung und funktionelle Charakterisierung von Genen beteiligt am Prozess der wurzelspezifischen Eliminierung von B-Chromosomen in Aefilops speltoides"	Thiel	DFG	01.12.22	30.11.25	11.000
Erscheinung und Funktion von CuZnSOD-Proteinen während der Evolution früher Landpflanzen" im Rahmen des Schwerpunktprogramms SPP 2237 "MAdLand - Molekulare Adaptation an das Land: Evolutionere Anpassung der Pflanzen an Veränderung"	Schippers	DFG	01.09.20	29.02.24	221.290
FloResEng - Engineering endogener Sauerstoffsensoren zur Verbesserung der Überflutungsresistenz von Getreide	Schippers	DFG	25.11.24	31.12.27	62.680
Funktionelle Studien und quantitative Bildgebung zum Stoffwechsel des sich entwickelnden Maiskorns	Rolletschek, H.	DFG	01.01.24	31.12.25	228.750
BRACE: "Reaktion und Adaption der Gerste auf sich wandelnde Umweltbedingungen", SusCrop, ERA-NET	Neumann	DFG	01.06.22	31.05.25	49.800
HETCROP: Vorhersagegestützte Normalisierung der Entwicklungsheterochronie bei parallelen molekularen und phänomischen Studien in Pflanzen	Neumann	DFG	01.10.23	30.09.26	232.400
Identifizierung und funktionelle Charakterisierung von Genen beteiligt am Prozess der wurzelspezifischen Eliminierung von B-Chromosomen in Aefilops speltoides	Szymanski	DFG	01.06.22	31.05.25	9.800
Die Rolle des Mikrobioms bei der Stärkung der Widerstandsfähigkeit in einer von Stress geprägten Umwelt	Szymanski	DFG	25.11.24	31.12.27	217.404
INSIGHT: Untersuchungen der Rolle von Strigolactonen in Gerste als Antwort auf Trockenheit	Melzer, M.	DFG	01.02.20	29.02.24	223.408
CYBDOM: Proteins HYP1 beim Phosphormangel-abhängigen Primärwurzelwachstum	Giehl	DFG	01.03.20	31.03.24	226.799

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WURZELLÄNGE: Verlängerte Wurzeln zur effizienten Erschließung von Stickstoffquellen durch Veränderung der Brassinosteroid- und Auxinbioynthese und Signaltransduktion	Giehl	DFG	01.12.20	31.05.25	344.400
CATCH-BNI: Erhöhte Stickstoffnutzungseffizienz in der Landwirtschaft durch Zwischenfrüchte als Produzenten natürlicher Nitrifikationsinhibitoren	Wirén	DFG	01.04.21	31.12.24	276.050
HvMTP1;2: "Erschließung und Nutzung der genetischen Variation des Metalltransporters HvMTP1;2 in Halmknoten zur verbesserten Organentwicklung, Verlagerung von Spurenelementen und Biofortifikation in Gerste“	Wirén	DFG	01.10.22	30.09.25	442.150
AmmoniumTransport: Molekulare Regulation der wechselseitigen Interaktion zwischen Ammonium- und Nitrataufnahme in Pflanzenwurzeln	Wirén	DFG	01.08.23	30.07.25	267.058
SFB: Sonderforschungsbereich 1664 "Diversität pflanzlicher Proteoformen-SNP2Prot" Halle; TP C02: Bedeutung der allelischen Variation in YUCCA-Genen für die Modulation von Proteoformen, die lokale Auxin-Biosynthese und die phänotypische Variation in	Wirén	DFG	01.10.24	30.09.28	277.752
Auswirkungen der proximalen Internodienverlängerung auf Blütendegeneration, Lagerresistenz und Gemeinschaftsleistung bei Gerste	Yongyu Huang	DFG	01.06.24	31.05.27	1.073.905
OAK: Open Access Publikationen	Winter	DFG	01.02.22	31.01.25	99.100
Weiterleitung Dr. Helmy Youssef	Youssef	DFG	01.02.24	31.01.27	53.783
Dysploidy and Diversifizierung in Crocus, Phase 2	Waminal	DFG	01.10.25	30.09.27	297.223
LONGIDIV:"Kartierung der genetischen Vielfalt von Aegilops longissima mittels eines mehrstufigen Ansatzes und deren Nutzung für die Entwicklung von rostresistentem und salztolerantem Weizen"	Mascher, M.	DFG	01.12.25	30.04.29	390.336
"PreDiMix: Vorhersagen und Verständnis der Diversitätsvorteile von Sortenmischungen"	Reif, J.	DFG	01.09.25	31.08.28	195.804
B-Chromosom: Wie entsteht ein B-Chromosom? - Sind sie ein Produkt der Chromoanagenesis und anschließender schrittweiser Sequenzakkumulation?	Houben	DFG	01.08.25	31.07.27	269.054
"Use Case: ""BrAPI Integration on PSI Hardware"" FAIRAgro: ""FAIRe Dateninfrastruktur für die Agrarsystemforschung"""	Heuermann, M.	DFG	01.01.25	31.12.25	58.584
Gaterslebener Forschungskonferenz "Internationales Symposium Integrative Bioinformatik“, 10.-12.09.2025	Scholz, U.	DFG	01.05.25	31.12.25	33.242
NFDI4BioDiversity-2: A Consortium for the National Research Data Infrastructure (NFDI)	Scholz, U.	DFG	01.10.25	31.12.28	376.797
DataPLANT – Daten in der Pflanzen-Grundlagenforschung (NFDI)	Scholz, U.	DFG	01.10.25	31.12.28	718.340
"PreDiMix: Vorhersagen und Verständnis der Diversitätsvorteile von Sortenmischungen"	El Hanafi	DFG	01.09.25	31.07.28	278.955
Die Rolle des Mikrobioms bei der Stärkung der Widerstandsfähigkeit in einer von Stress geprägten Umwelt (Trilateral)	Rolletschek, H.	DFG	01.10.25	30.09.28	593.652
Funktionelle Charakterisierung des Nuklearfaktors Y für die Kornfüllung und Ertragsbildung bei Gerste	Radchuk	DFG	01.10.25	30.09.28	242.109
AGENT: Activated GEnebank NeTwork	Stein, N.	EU	01.05.20	30.04.25	419.250
TRANSFER: Edaphic adaptation in barley wild relatives and its transfer to the domesticate (ERC)	Börner, A.	EU	01.02.21	31.01.26	51.472

Acronym: Project Name	Principle Investigator (Pi) Project Participants at IPK	Funding Agency	Duration (Start)	Duration (End)	Overall budget (Euro)
CROPDIVA: Climate Resilient Orphan croPs for increased DIVersity in Agriculture	Börner, A.	EU	01.09.21	31.08.25	53.000
Legume Generation: Boosting innovation in breeding for the next generation of legume crops for Europe, TP Lohwasser	Lohwasser	EU	01.09.23	29.02.28	200.000
INCREASE: Intelligent Collections of Food Legumes Genetic Resources for European Agrofood Systems	Oppermann	EU	01.05.20	30.04.26	603.334
AGENT: Activated GEnebank NeTwork	Weise, St.	EU	01.05.20	30.04.25	151.870
PRO-GRACE: Promoting a Plant Genetic Resource Community for Europe	Weise, St.	EU	01.01.23	30.06.25	195.000
COUSIN: Crop Wild Relatives ulilisation and conversation for sustainable agriculture	Weise, St.	EU	01.01.24	31.12.28	417.875
TRANSFER: Edaphic adaptation in barley wild relatives and its transfer to the domesticate (ERC)	Mascher, M.	EU	01.02.21	31.01.26	1.111.557
AGENT: Activated GEnebank NeTwork	Mascher, M.	EU	01.05.20	30.04.25	109.130
AGENT: Activated GEnebank NeTwork	Reif, J.	EU	01.05.20	30.04.25	152.300
PRO-WILD: Protect and promote Crop Wild Relatives	Reif, J.	EU	01.09.24	31.08.29	306.000
MEIOBARMIX: Meiosis in barley: Mixing it up (ERC)	Heckmann, S.	EU	01.02.21	31.01.26	1.497.875
Legume Generation: Boosting innovation in breeding for the next generation of legume crops for Europe, TP Otto	Otto, L.-G.	EU	01.09.23	29.02.28	686.991
AGENT: Activated GEnebank NeTwork	Lange, M.	EU	01.05.20	30.04.25	139.300
AgroServ: Integrated SERvices supporting a sustainable AGROecological translation, EMBL	Arend, D.	EU	01.09.22	31.08.27	30.833
INCREASE: Intelligent Collections of Food Legumes Genetic Resources for European Agrofood Systems	Lange, M.	EU	01.05.20	30.04.26	23.878
CAPITALISE - COMBINING APPROACHES FOR PHOTOSYNTHETIC IMPROVEMENT TO ALLOW INCREASED USTAINABILITY IN EUROPEAN AGRICULTURE	Lange, M.	EU	01.04.20	30.11.24	62.700
CAPITALISE - COMBINING APPROACHES FOR PHOTOSYNTHETIC IMPROVEMENT TO ALLOW INCREASED SUSTAINABILITY IN EUROPEAN AGRICULTURE	Altmann	EU	01.04.20	30.11.24	609.910
MICROBES-4-CLIMATE: Microbial services addressing climate change risks for biodiversity and for agricultural and forestry ecosystems: enabling curiosity-driven research and advancing frontier knowledge	Altmann	EU	01.02.24	31.01.29	531.765
CAPITALISE - COMBINING APPROACHES FOR PHOTOSYNTHETIC IMPROVEMENT TO ALLOW INCREASED USTAINABILITY IN EUROPEAN AGRICULTURE	Altmann	EU	01.04.20	30.11.24	20.788
INCREASE: Intelligent Collections of Food Legumes Genetic Resources for European Agrofood Systems	Neumann	EU	01.05.20	30.04.26	272.825
STARGATE: Sensors and daTA tRainiG towards highperformance Agri-food sysTEms	Neumann	EU	01.01.21	30.06.24	132.171
BOLERO: Breeding for coffee and cocoa root resilience in low input farming systems based on improved rootstocks	Neumann	EU	01.10.22	30.09.26	273.084
Resist: Resilient Oats: Improving Drought Stress Resistance in a Changing Climate	Kumlehn	EU	01.04.24	31.03.29	129.991

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TRANSFER: Edaphic adaptation in barley wild relatives and its transfer to the domesticate (ERC)	Wirén	EU	01.02.21	31.01.26	336.899
FATE: Discovering the developmental transition of cortical parenchyma cells into different cell fates	Schneider H.	EU	01.10.24	30.09.29	1.499.750
Genexpressionsatlas: "Ein Genexpressionsatlas für die wilden Verwandten der Kulturgerste"	Mascher, M.	Land SA	01.07.22	31.12.24	310.000
In Silico: Einrichtung einer Nachwuchsforschergruppe “Insilico Genbank-Proteomik”	Camara	Land SA	01.06.23	31.12.25	250.000
Barley: Veränderung der meiotischen Rekombinationslandschaft in der Gerste (Hordeum vulgare)	Heckmann, S.	Land SA	01.01.23	31.12.25	318.000
UpMix, Freisetzung von Leistung und Nachhaltigkeit durch Genotypen und Pflanzenmischungen	El Hanafi	Land SA	01.06.23	30.06.27	250.000
Aktualisierung und Erweiterung der Mikrokopieplattform des IPK Gatersleben	Melzer, M.	Land SA	13.12.24	31.03.27	1.100.000
SAFE-Verbund Sachsen-Anhalt: Ergänzende Unterstützung zu Patentierungshilfen, Verwertungsförderung, Projektmanagement und Qualifizierungsmaßnahmen	Leps	Land SA	01.01.24	31.12.26	27.896
timsTOF: Weiterentwicklung der Metabolomics-Plattform des IPK mit einem timsTOF HT LC-MS-System	D'Auria	Land SA	01.07.24	30.09.26	971.379
REPLACE: a genomic breeder´s toolkit for faba bean	Jayakodi	Leibniz Association	01.02.22	31.01.27	995.160
MedRhizo: Erfassung der Kulturpflanzen-Wurzelarchitektur in Medium Size-Rhizotronen	Dehmer, K.	Leibniz Association	01.01.23	31.03.24	7.976
SAW AID-CROP: "Amorphous silica in soils and plants Improves Drought stress tolerance of crops"	Wirén	Leibniz Association	01.03.22	28.02.26	312.904
Leibniz-Professorinnenprogramm: Rooting for Resilience: Root Systems for Stress Tolerance and Soil Resource Capture	Schneider H.	Leibniz Association	01.08.24	31.07.29	1.000.000
STIPENDIUM DR. MAHAMMAD ELDAROV	Stein, N.	DAAD	01.08.24	30.10.24	6.189
DAAD Saravanakumar Somasundaram	Houben	DAAD	01.10.20	30.09.24	4.000
Stipendium Dr. Isaac Kodzo Amegbor	Otto, L.-G.	DAAD	01.06.24	31.08.24	6.989
Humboldt-Forschungsstipendium für Postdoktoranden an Dr. Matias Schierenbeck (AvH)	Börner, A.	STIFTUNG	01.03.21	30.06.24	28.800
Forschungskostenzuschuss für Dr. Amira Mourad (AvH)	Börner, A.	STIFTUNG	01.07.21	31.08.24	33.200
Forschungsstipendium für Dr. Olena Kishchenko des Philipp Schwartz-Fellowships (AvH)	Nagel	STIFTUNG	01.09.22	31.08.24	86.129
Forschungsstipendium für Anton Peterson des Philipp Schwartz-Fellowships (AvH)	Nagel	STIFTUNG	01.09.22	31.08.24	85.711
Verlängerung Forschungsstipendium für Anton Peterson und Olena Kishchenko des Philipp Schwartz-Fellowships (AvH)	Nagel	STIFTUNG	01.09.24	28.02.25	35.160
Humboldt-Forschungsstipendium für Postdoktoranden an Herrn Dr. Raz Avni	Mascher, M.	STIFTUNG	01.03.21	31.12.25	32.900
Stipendium Dr. Aleck Kondwakwenda (AvH)	Neumann	STIFTUNG	01.05.24	30.04.26	19.200

Acronym: Project Name	Principle Investigator (Pi) Project Participants at IPK	Funding Agency	Duration (Start)	Duration (End)	Overall budget (Euro)
High-throughput non-invasive root and shoot phenotyping training (Agropolis)	Neumann	STIFTUNG	01.03.23	31.07.24	25.782
Amobila: Verbundvorhaben: Arzneipflanzenanbau als Instrument einer modernen, ertragsorientierten und zugleich biodiversitätsfördernden Landwirtschaft; Teilvorhaben3: Ertragsrelevanz von Bestäubern, Bestäubungswegen und-distanzen an der Echten Kamille	Otto, L.-G.	Firma	01.03.23	28.02.26	10.000
Optimization of gametophytic CENH3 degradation in Arabidopsis	Houben	Firma	01.06.25	31.12.26	65.667
Novel Wheat V: Evalution of wheat plants with altered carbon assimilation, allocation and partitioning	Rolletschek, H.	Firma	01.11.13	30.06.25	9.965
Thüringer Linsensorten: Etablierung einer regionalen Saatgutproduktion der "Kyffhäuserlinse" und der "Dornburger Speiselinse"	Lohwasser	Auftrags-forschung	01.07.23	31.03.25	13.881
Implementing a trans-EUROpean PEPper LANDrace collection for resilient agriculture (EuroPepLand)	Lohwasser	Auftrags-forschung	01.09.24	31.08.26	815
A 100 year Seed Longevity Experiment in the Svalbard Global Seed Vault	Nagel	Auftrags-forschung	12.03.21	11.03.31	26.464
Garlic_CCS: European Cooperative Programme for Plant Genetic Resources - Phase XI	Nagel	Auftrags-forschung	18.08.23	31.08.25	30.000
Maintenance and development of the EURISCO Internet Search Catalogue	Weise, St.	Auftrags-forschung	01.01.24	31.12.28	530.911
Anlage, Pflege und Präsentation eines Lehrgartens für Futterpflanzen	Willner, E.	Auftrags-forschung	01.03.20	31.03.24	7.200
ImprovLoliumCol	Willner, E.	Auftrags-forschungg	01.09.19	31.03.24	725
Gametophytic degradation of CENH3 using engineered E3 ligases for haploid induction	Houben	Auftrags-forschung	01.11.23	31.12.24	30.000
Development of soybean breeding model for water-logging resistance with high-throughput evaluation system of field scanning and Rhizotron platform	Altmann	Auftrags-forschung	01.01.24	31.12.27	68.858
Determination of the inhomogeneous distribution of sugar in sugar beet roots	Borisjuk, L.	Auftrags-forschung	01.06.24	31.05.25	61.750
Chitin Interactions in plant disease mitigation and analysis of Erythroxylum species	D'Auria	Auftrags-forschung	01.06.22	01.06.27	9.129
BayKlimaFit: Genetik der Mykorrhiza vermittelten Stressresistenz in Mais"	Neumann	Auftrags-forschung	01.11.22	31.12.24	29.412
TRORA: Trockentoleranter Raps: Verbesserung der Trockentoleranz von Raps durch ektopische Expression von ABA-Rezeptorgenen	Kumlehn	Auftrags-forschung	01.03.23	28.02.25	10.084
KAUST: "Deciphering the quantitative regulation of host specificity in the barley in the barley-rust pathosystem"	Kumlehn	Auftrags-forschung	01.03.22	30.06.24	91.200
dwarf rye: root trait characterization in dwarf type rye	Giehl	Auftrags-forschung	01.04.23	30.06.24	16.025
Uncovering the biochemical and molecular processes causing growth promotion of plants when exposed to plasma-activated water	Wirén	Auftrags-forschung	01.09.23	31.08.26	351.563
Hopfengarn: "Aufarbeitung von Hopfenfaser-Rohprodukten durch biotechnologische Spaltung von Lignin mit Kupferperoxidasen""	Wirén	Auftrags-forschung	01.09.23	31.08.26	351.563

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RootOptiGrowth: "Optimizing Crop Performance through Root Anatomical Phenotypes for Efficient Soil Resource Acquisition"	Schneider H.	Auftrags-forschung	01.07.24	31.12.27	230.000
Root structure and function traits: Overcoming the root phenotyping bottleneck in cereals	Schneider H.	Auftrags-forschung	01.06.24	31.12.27	115.192
Maintenance and development of the EURISCO Internet Search Catalogue (Projekt hatte 3 Phasen: 2014-2018, 2019-2023, 2024-2028)	Weise, St.	Auftrags-forschung	01.01.19	31.12.23	454.079
KAUST: Scientific collaboration to generate PacBio (HiFi) reads with 25X coverage of long-read data and 50X coverage of long-range scaffolding data (HiC)	Stein, N.	Auftrags-forschung	01.05.25	31.12.26	86.259
Improving abiotic stress tolrerance in wheat	Börner, A.	SONSTIGE	20.07.22	31.12.25	4.303
ExploDiv: Exploring of Grain Legumes diversity for sustainable European Agri-food systems	Lohwasser	SONSTIGE	08.01.24	30.11.25	2.600
SINO-Chinesisch-Deutsches Mobilittätsprgramm: Unlocking genetic basis of cultivated barley to adapt district environments by population genomics	Mascher, M.	SONSTIGE	01.11.22	31.10.25	88.962
Erhaltung der Diversität des Apenninenschwingels	Willner, E.	SONSTIGE	15.10.20	31.03.24	9.377
pollination trials in oilseed crops (Brassica napus)	Willner, E.	SONSTIGE	01.04.23	05.03.24	8.400
Assessing population genetic diversity of crop wild relatives to guide the choice for their conservation in genetic reserves	Harpke	SONSTIGE	01.05.24	30.06.28	6.824
Sequence analysis of a new Hypericum genome	Rizzo	SONSTIGE	01.03.23	29.02.24	4.500
Forschungskostenzuschuss Gast Wirassaya Tobdan	Schneider H.	SONSTIGE	09.12.24	09.04.25	1.800
Getreide-Genomanalyse (Wricke Preis)	Stein, N.	SONSTIGE	01.12.10	31.12.26	11.262
Velux-Stiftung: A tuneable molecular approach to guarantee light-induced flowering for future climates	Dixon	SONSTIGE	01.01.25	30.06.28	17.626
ERASMUS+: Nachhaltige Pflanzenforschung und interkulturellen Austausch erleben	Sehmisch	SONSTIGE	01.06.25	30.11.26	11.665
ELIXIR-HARVEST: Commissioned Service - 2024-SCIENCE-BFSP	Arend, D.	SONSTIGE	01.01.25	31.12.26	24.050
ELIXIR-E-PAN: Commissioned Service - 2024-SCIENCE-BFSP	Scholz, U.	SONSTIGE	01.01.25	31.12.26	13.500
ELIXIR-TECH: Commissioned Service -2024-TECHNOLOGY-DATA	Arend, D.	SONSTIGE	01.01.24	31.12.26	1.800
Seed-Money: Discovery of bioactive natural products from Marchantia liverwort symbionts	Schippers	SONSTIGE	01.05.25	30.06.26	10.000
Seed-Money: Barley Alkaloid- TAS2R interaction study (BATIS)	D'Auria	SONSTIGE	01.05.25	31.08.26	10.000

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Buckwheat: Adapting the orphan crop buckwheat to Swiss agriculture systems by genome editing	Kumlehn	SONSTIGE	01.05.25	30.04.29	205.136
BarrierFates: One cell, three barrier fates – How do cereals use root barriers to survive and thrive?	Schneider H.	SONSTIGE	01.06.25	01.06.31	688.675
Strategische und innovative Erweiterung der Genbank	Stein, N.	Genbank-nachfolge	01.06.23	31.12.25	950.000
Amobila: Verbundvorhaben: Arzneipflanzenanbau als Instrument einer modernen, ertragsorientierten und zugleich biodiversitätsfördernden Landwirtschaft; Teilvorhaben3: Ertragsrelevanz von Bestäubern, Bestäubungswegen und-distanzen an der Echten Kamille	Otto, L.-G.	BMLEH / FNR	01.03.23	28.02.26	43.499
Spitfire/Cornet: Screening of Pisum sativum (pea) accessions for pea necrotic yellow dwarf virus resistance	Lohwasser	BMWE	01.11.21	31.08.24	241.258
Digitalisierung der Verwaltungsprozesse 1.000.000 €	Koehler	Infrastruktur	24.05.22	31.12.27	1.138.600
Laufzeitverlängerungen von Qualifikationsstellen, Vertragsverlängerungen	Deike	Infrastruktur	24.05.22	31.12.25	1.566.050
"""Umgebungskontrollierte Versuchsflächen (Teilmodernisierung des Phytokammernhaus 1)"" 1.410.000 € und ""Umgebungskontrollierte Versuchsflächen (Teilmodernisierung des Phytokammernschränke 1)"" 1.035.000 €"	Fricke, G.	Infrastruktur	25.04.22	31.12.27	2.445.000
bauliche Anpassungen in Arbeits-, Sozialbereichen VUG 100.000 €	Kirsch	Infrastruktur	24.05.22	31.12.25	108.050
Verwaltungsgebäude	Kirsch	Infrastruktur	31.12.24	31.12.26	1.450.000
Anschaffung eines GPS Traktors 150.000 €	Schreiber, P.	Infrastruktur	25.04.22	31.12.27	153.272
Anschaffung eines Parzellenmädreschers (200.000€ in 2023)	Schreiber, P.	Infrastruktur	25.04.22	31.12.27	346.728
Büroplatz- und Home Office -Ausstattung 380.000 €	Miehe, H.	Infrastruktur	24.05.22	31.12.27	380.000
Erweiterung von Serverkapazitäten 670.000 €	Miehe, H.	Infrastruktur	24.05.22	31.12.27	670.000
Erweiterung der Exchange-Mail-Server 100.000 €	Miehe, H.	Infrastruktur	24.05.22	31.12.27	134.000
Erhöhung der Internetbandbreite 160.000 €	Miehe, H.	Infrastruktur	24.05.22	31.12.27	126.000
Einrichtung und Etablierung einer virtuellen Telefonanlage 100.000 €	Miehe, H.	Infrastruktur	25.04.22	31.12.27	100.000
Wricke-Preis zur Förderung der Kulturpflanzenforschung	Mascher, M.	Wricke-Stiftung	01.04.20	31.12.25	30.000

Gatersleben Lectures 2024/2025

Gatersleben Lectures 2024

13. February 2024
Dr. Hernan A. Burbano, Associate Professor of Ancient Plant Genomics & Royal Society Wolfson Fellow, Department of Genetics, Evolution and Environment, University College London, UK
"Plant biotic interactions combining present-day and historical samples"

19. March 2024
Prof. Dr. Rüdiger Simon, Development Genetics, Cluster of Excellence on Plant Sciences, Heinrich Heine University, Duesseldorf, Germany
"Plant Stem Cell Niches"

4. April 2024
Prof. Dr. Nicole van Dam, Director of Research and Head of RG Plants Biotic Interactions, Leibniz Institute of Vegetable and Ornamental Crops (IGZ), Großbeeren, Germany
"Ecological consequences of steroidal glycoside chemodiversity in Solanum dulcamara: A bittersweet story"

7. May 2024
Prof. Dr. Eske Willerslev, University of Copenhagen, Globe Institute Lundbeck Foundation GeoGenetics Centre, Denmark
"Ancient Environmental Genomics Initiative for Sustainability"

11. June 2024
Dr. Matthew J. Moscou, USDA-ARS Research Plant Pathologist & Adjunct Assistant Professor, Cereal Disease Laboratory, University of Minnesota, St. Paul, USA
"Evolution of immunity in the grasses"

20. August 2024
Prof. Dr. Meredith C. Schuman, University of Zurich, Department of Geography and Department of Chemistry, Spatial Genetics, University of Zurich, Switzerland
"Chemical ecology and spatial genetics as tools to help us live and let live"

10. September 2024
Dr. Tom Bennett, Associate Professor of Plant Signalling Development, University of Leeds, Faculty of Biological Sciences, Leeds, UK
"Knowing when to stop: understanding how plants integrate environmental and internal information to optimise their growth and reproductive effort"

19. November 2024
Prof. Dr. Claus Schwechheimer, Plant Systems Biology, Technical University of Munich (TUM), Freising, Germany
"AGC kinases and The Power of Movements in Plants"

3. December 2024
Prof. Dr. Asaph Aharoni, Department of Plant & Environmental Sciences, Faculty of Biochemistry, Weizmann Institute of Science, Rehovot, Israel
"Harnessing Plant Chemical Diversity: From Metabolomes, Metabolons & Metabolic Gene Clusters to Fermenting Start-Ups"

Gatersleben Lectures 2025

11. February 2024
Prof. Dr. Gwyneth Ingram, CNRS, ENS de Lyon, Lyon, France
"Embryo-Endosperm dialogues in developing seeds: Distinguishing in from out, and up from down"

18. March 2025 (Double Lecture)
Prof. Dr. Andrew Leitch, Professor of Plant Genetics and Co-director of MSc Plant and Fungal Taxonomy Diversity, School of Biological and Behavioural Sciences, Queen Mary University of London, UK
"Ecological filtering through genome size and potential mechanisms driving genome downsizing after polyploidy"
and *Dr. Ilia Leitch,*
Trait Diversity and Function, Royal Botanic Gardens, Kew, Richmond, London, UK
"Plant genome size diversity and how this impacts evolution, distribution, and survival."

22. April 2025
Prof. Dr. Jane Langdale, Department of Biology, University of Oxford, Oxford, UK
"Regulation of cell patterning in grass leaves: understanding maize with a view to engineering rice"

13. May 2025
Prof. Dr. Caroline Gutjahr, Director of Dept. Root Biology and Symbiosis, Mycorrhiza and Root Biology, Max Planck Institute of Molecular Plant Physiology, Potsdam-Golm, Germany
"Form and function of a plant-fungal symbiosis"

24. June 2025
Prof. Dr. Sebastian Soyk, Department of Plant Molecular Biology, University of Lausanne, Switzerland
"Decoding the genetic control of meristem transitions for crop engineering"

12. August 2025
Prof. Dr. Stig Uggerhøj Andersen, Department of Molecular Biology and Genetics, Plant Molecular Biology, Aarhus University, Denmark
"Genomics of faba bean agronomic and quality traits"

16. September 2025
Prof. Dr. Zoran Nikoloski, Bioinformatics Department, Institute of Biochemistry and Biology, University of Potsdam, Germany
"Predicting dynamic plant responses using genetic markers"



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