ERA-CAPS 1st Grant holders Workshop

Rome, Italy

June 12th,13th 2014

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June 12th-13th 2014 – MIUR, Piazzale Kennedy 20, 00144 Roma, Italy

The 1st Grant-holders workshop is the kick-off event for the ERA-CAPS projects funded in the framework of the first call.

The aim of the workshop is to:

- ✓ gather the grant-holders funded through the first ERA-CAPS call and give them the opportunity to introduce their projects;
- ✓ help researchers to network with each other and share resources, tools and information;
- ✓ get feedback on the call procedures and ERA-CAPS in general.

Each funded ERA-CAPS projects will present their research, clarifying the aim, the facilities and methods they intend to use and their expectations from ERA-CAPS

In addition, there will be a discussion in which each project representatives will give comments on the call procedures, during the session dedicated to call procedures and administrative requirements.

PROJECT REPRESENTATIVES LIST:

Acronym	**Coordinator or representative/s**	**Organisation**	**Country**
ABCEED	Thierry Chardot	Institut National de la Recherche Agronomique, Institut Jean-Pierre Bourgin	France
BARLEY-NAM	Klaus Pillen	University of Halle	Germany
DURESTrit	Patrick Schweizer	Leibniz Institute of Plant Genetics and Crop Plant Research	Germany
	Ulrich Schaffrath	Rheinisch-Westfälische Technische Hochschule	Germany
EURO-PEC	Dolf Weijers	Wageningen University	The Netherlands
Evo-Genapus	Ian Bancroft	University of York	United Kingdom
FLOWPLAST	Prof. Gerco Angenent will introduce Flowplast	Plant Research International	The Netherlands
H.I.P.	Alain Tissier	Leibniz-Institute of Plant Biochemistry	Germany
HotSol	Mark Taylor	James Hutton Institute	United Kingdom
	Christian Bachem	Wageningen University	The Netherlands
N-vironment	Francesco Licausi	Scuola Superiore Sant'Anna	Italy
PER ASPERA	Lorenzo Frigerio	University of Warwick	United Kingdom
	Verena Ibl	University of Natural Resources and Applied Life Sciences, Vienna	Austria
RootBarriers	David E. Salt	University of Aberdeen	United Kingdom
	Rochus Benni Franke	University of Bonn	Germany
SeedAdapt	Kai Graeber	Royal Holloway University of London	United Kingdom
	Joanna Cox	Royal Holloway University of London	United Kingdom

Apologies from BENZEX and DeCOP.

FUNDERS DELEGATE LIST:

Name	Organisation	Country
Paul Wiley	BBSRC (Programme Coordination Office)	United Kingdom
Paul Beckers	ERA-CAPS Call Secretariat	Belgium
Isabelle Hippolyte	ANR	France
Catherine Kistner	DFG	Germany
Karin Metzlaff	EPSO	Belgium
Margit Suuroja	ETAg	Estonia
Marta Abrantes	FCT	Portugal
Arnaud Goolaerts	F.R.S. – FNRS	Belgium
Jean-François Chevalier	F.R.S. – FNRS	Belgium
Dario Zilli	INRA	France
Aldo Covello	MIUR	Italy
Cecilia Bibbò	MIUR	Italy
Maria Uccellatore	MIUR	Italy
Paolo Costantino	MIUR	Italy
Zeljka Dukic	MPNTR	Serbia
Ervin Balázs	MTA-ATK	Hungary
Levente Kiss	MTA-ATK	Hungary

SCIENTIFIC ADVISORY BODY DELEGATES:

Name	Organisation	Country
Gerco Angenent	Plant Research International	The Netherlands
Eva Benková	Institute of Science and Technology	Austria
Atle Bones	Norwegian University of Science and Technology	Norway
Tony Conner	AgResearch Ltd.	New Zealand
Wilhelm Gruissem	ETH Zürich	Switzerland
Klaus K. Nielsen	DLF-TRIFOLIUM A/S	Denmark
Haim Rabinowitch	The Hebrew University of Jerusalem	Israel
Mariana Sottomayor	University of Porto	Portugal
Jens Stougaard	Aarhus University	Denmark
Zofia Szweykowska – Kulińska	Adam Mickiewicz University	Poland

AGENDA

June 12th, 2014

Time	Duration	Content
12.00 – 13.30	90’	Lunch and registration
13.30 – 13.40	10’	Welcome and introduction by host (MIUR) Dr. Maria Uccellatore, Director Unit III – European Research Programmes - DGIR
13 .40 – 14.00	20’	Introduction to ERA-CAPS (coordinator – Paul Wiley – and Call Secretariat – Paul Beckers)
14 .00 – 14.15	15’	ERA-PG questionnaire results – Marta Abrantes (FCT, Portugal)
14.15 – 15.30	25’ x 3	**HotSol** presentation - Mark Taylor, Christian Bachem **DURESTrit** presentation - Patrick Schweizer, Ulrich Schaffrath **H.I.P.** presentation - Alain Tissier
15.30 – 15.50	20’	Coffee Break
15.50 – 17.05	25’ x 3	**RootBarriers** presentation - David E. Salt, Rochus Benni Franke **N-vironment** presentation - Francesco Licausi **BarleyNAM** presentation - Klaus Pillen
18.00 – 19.00		Funders’ meeting – Management Board members only
19.30		Dinner – Ristorante La Glorietta – Hotel dei Congressi, Viale Schakespeare 25, Rome

June 13th, 2014

Time	Duration	Content
9.00 – 9.20	20’	Keynote presentation about "Current research questions in Plant Science” and initiatives of the Global Plant Council – Wilhelm Gruissem (President of the Global Plant Council and ERA-CAPS Scientific Advisory Body member)
9.20 – 9.40	20’	Discussion on ERA-CAPS call procedures, administrative requirements (monitoring and reporting)
9.40 – 10.55	25’ x 3	**EuroPEC** presentation - Dolf Weijers **Per Aspera** presentation - Lorenzo Frigerio, Verena Ibl **Flowplast** presentation - Gerco Angenent
10.55 – 11.15	20’	Coffee break
11.15 – 12.30	25’ x 3	**SeedAdapt** presentation - Joanna Cox, Kai Graeber **ABCEED** presentation - Thierry Chardot **EvoGenapus** presentation - Ian Bancroft
12.30 – 12.40	10’	Conclusions and wrap-up – Paul Wiley (BBSRC – Programme Coordination Office)
12.40 – 14.00	80’	Lunch
14.00 – 16.30	150’	Scientific Advisory Body Meeting – SAB members only

ERA-CAPS 1st Call Projects: Abstracts

Identifying and exploiting genetic variation controlling seed yield and quality in oilseed crops

- **Acronym** **ABCEED**
- **Project leader** **Michael W. Bevan**, John Innes Centre, UK
- **Other project participants** **Michael Lenhard**, University of Potsdam, DE
  Loïc Lepiniec, BAP, INRA, FR
- **Total Granted budget** 934.145 € (funded by BBSRC, DFG, INRA)

Abstract

The provision of sufficient healthy food is critically dependent upon the yield and quality of seed from our crop plants. Oilseed rape is a major EU crop producing oil for human and industrial consumption and protein for animal feed. To meet increased demand in a sustainable manner, new cultivars with increased yield and quality need to be created. Detailed knowledge of the development of seeds and their composition has been achieved in experimental species such as Arabidopsis thaliana. However, a major challenge is to unlock this knowledge for improving crops based on information about gene function and useful genetic variation. In this proposal we will integrate genetic and phenotypic studies of seed development in four closely related Brassicaceae: Arabidopsis thaliana; Capsella rubella; Camelina sativa; and Brassica napus. These species are separated by less than 20 million years of evolution, sufficient time for extensive phenotypic divergence while maintaining high potential for conserved gene function. Each species has complementary genetic resources for understanding and utilizing the knowledge of gene functions that influence critical yield-related traits.

This proposal brings together a unique and complementary set of skills, expertise and genetic resources focused on bridging the gap between a basic understanding of seed formation and exploitation of useful genetic variation underlying this key agronomic process. The research will be carried out in three interdependent Work Packages each led by a PI with an established track record and backed by substantial institutional resources. WP1 focuses on identifying and understanding genes regulating seed size by using induced and natural variation in Arabidopsis. This is linked to association studies in oilseed rape cultivars that will identify genetic variation associated with detailed phenotypic assessment of seed size and seed yield. These two approaches are mutually supportive and provide a framework for integrating phenotype and gene function studies. WP2 focuses on identifying the genetic basis of variation in ovule and thus seed number per fruit. While mutant-based approaches in Arabidopsis have had limited success in understanding this centrally important yield trait, the recent evolution of increased ovule numbers in C. rubella provides a unique opportunity to identify and characterize key genes. Results from Capsella will be integrated with the association study and allele mining in B. napus germplasm. The third WP aims to understand the function of B. napus and Camelina homologues of key seed-development genes from Arabidopsis in regulating seed formation and maturation. This will be coupled to detailed multiscale phenotyping of storage compounds in B. napus and Camelina. When integrated into association analyses in WP1 this will provide an exceptionally informative resource for understanding and exploiting the contributions of genetic variation to seed composition and yield.

BARLEY-NAM: Locating exotic genes that control agronomic traits under stress in a wild barley nested association mapping (NAM) population

- **Acronym** **BARLEY-NAM**
- **Project leader** **Klaus Pillen**, University of Halle, DE
- **Other project participants** **David Jaques Bonfil**, Agricultural Research Organization (ARO), IL
  Andrew John Flavell, University of Dundee, UK
  Eyal Fridman, Hebrew University of Jerusalem, IL
  Frank Ordon, Julius Kühn-Institute (JKI), DE
  William T.B. Thomas, James Hutton Institute, UK. (Self-funded)
- **Total Granted budget** 1.479.350 € (funded by DFG, MOARD, BBSRC)

Abstract

Delivering sustainable food production in the face of climate change requires a revolution in breeding crops that deliver high and sustainable yield under fluctuating disadvantageous environmental conditions. The ancestral wild germplasm of modern crops contains allelic variants that can achieve this goal, yet modern crops are becoming increasingly depleted in biodiversity. The two key obstacles to successful exploitation of wild germplasm are finding the wild-derived alleles needed and testing them in the field.

The BARLEY-NAM project will use wild barley (Hordeum vulgare ssp. spontaneum) as a model and apply novel genomic and breeding tools to improve agronomic performance of elite barley under abiotic and biotic stresses. For this, we will apply the nested association mapping (NAM) approach using the first cereal NAM population, HEB-25. HEB-25 comprises 1,420 BC1S3 lines, sub-divided into 25 families, originating from crosses of the elite barley cultivar Barke with 25 different wild barley donors. The HEB-25 lines will first be assessed for allele content at 21,643 genes (every known high-confidence barley gene), employing state-of-the-art exome capture and next generation sequencing. We expect to map roughly 400,000 SNPs within HEB-25 giving unprecedented levels of gene and genome resolution for barley. Second, all HEB lines will be cultivated in field trials in Germany, Scotland and Israel to assess agronomic performance under nitrogen deficiency, drought and pathogen attack. Yield components and nutrient content will be scored, as well as resistance against the major barley diseases leaf rust, yellow rust and net blotch. In addition, agronomic performance will be modelled by non-invasive remote sensing technology to establish phenotype predictions. Third, the collected data sets will be archived and further processed in a central data warehouse, built around a custom web-accessible relational database. Fourth, genotype and phenotype data of HEB-25 will be combined in a genome-wide association scan (GWAS) to identify wild barley alleles that improve plant performance under stress. Since the gene resolution is extremely high, this study will yield individual high confidence candidate genes that putatively regulate the studied traits. Fifth, to validate the identified trait-improving exotic alleles, segregating high-resolution progeny will be developed from the HEB lines.

The BARLEY-NAM project will be beneficial in two directions. On the one hand, the genes and gene variants regulating agronomic traits in barley will be defined at a level of detail unprecedented for the crop and this will inform future strategies for parallel improvement in wheat and rye. On the other hand, trait-improving wild barley alleles will be available for application in future barley breeding. This will lead to new barley cultivars with improved performance and extend the biodiversity and sustainability of the elite barley gene pool.

Biosynthesis, transport and exudation of 1,4-benzoxazin-3-ones as determinants of plant biotic interactions

- **Acronym** **BENZEX**
- **Project leader** **Matthias Erb**, Max Planck Institute for Chemical Ecology, Jena, DE
- **Other project participants** **Inge S. Fomsgaard**, Aarhus University, DK
  Monika Frey, Technische Universität München, DE
  Georg Jander, Boyce Thompson Institute for Plant Research, USA
  Jurriaan Ton, University of Sheffield, UK
- **Total Granted budget** 1.398.600 € (funded by DFG, DASTI, BBSRC. Co-Funded by NSF)

Abstract

The establishment of a suitable biotic niche is essential for plant survival and agricultural productivity. One important mechanism by which plants shape their environment is the release of phytochemicals. Low molecular weight compounds in particular can initiate the interaction with beneficial microbes in the soil and ward off herbivores. However, the same signalling molecules may also be exploited by specialized pests and pathogens. A detailed understanding of their biosynthesis, transport and release will be essential to disentangle these seemingly contradicting effects and to harness the full potential of secondary metabolite exudation in sustainable cropping systems. Yet to date, no secondary metabolite exporters have been identified in crop model systems.

Here we propose to unite the expertise of different research groups across Europe to study the molecular basis of 1,4-benzoxazin-3-one (BX) exudation in maize. Previous work by the consortium members has identified BXs as important resistance factors in maize and other grasses and has elucidated their biosynthesis in detail. We have also shown that BXs are the dominant secondary metabolites in maize root exudates and the leaf-apoplast and that they are important recruitment signals for beneficial microbes as well as for one of the most damaging pests of maize, the western corn rootworm Diabrotica virgifera. Given their obvious importance for crop productivity and their strong involvement in extracellular signalling, BXs are an ideal and relevant model to study the molecular ecology of secondary metabolite exudation.

The overall aim of BENZEX is to create the most advanced molecular toolkit in extracellular plant-environment interactions to date. First, a comprehensive population of maize genotypes that are altered in BX biosynthesis will be established by interrupting or enhancing the expression of three important biosynthetic enzymes. Second targeted and untargeted reference methods to identify and quantify BX production, storage, exudation and transformation will be established using HPLC-MS and 13C-labelled BX precursors. Third, BX transporters will be identified by a combination of proteomics, quantitative PCR and phytochemically guided QTL-mapping. Fourth, the generated resources will be used to analyse the role of extracellular BXs in the interaction with the soil microbiome, plant growth promoting bacteria, arbuscular mycorrhizal fungi, root herbivores and leaf-feeding aphids. Taken together, our project will substantially increase knowledge about the biological relevance of secondary metabolite exudation. It will furthermore enhance the competitiveness of European molecular plant sciences by providing an array of new tools and resources, including transgenic plants and mutants, analytical methods as well as molecular and microbial markers for maize as an important agricultural model system.

Delineating the crossover control networks in plants

- **Acronym** **DeCOP**
- **Project leader** **Peter Schlögelhofer**, University of Vienna, AUT
- **Other project participants** **Chris Franklin,** University of Birmingham, UK
  Ian R. Henderson, University of Cambridge, UK
  Karl Mechtler, Institute of Molecular Pathology, Vienna, AUT
  Holger Puchta, Karlsruhe Institute of Technology (KIT), DE
  Eugenio Sanchez-Moran, University of Birmingham, UK
- **Total Granted budget** 1.982.640 € (funded by FWF, BBSRC, DFG)

Abstract

Meiosis is a specialized type of cell division required for sexual reproduction. It ensures the reduction of the genome and the recombination of maternal and paternal chromosomal segments prior to the formation of generative cells. The process of meiotic recombination is initiated by programmed DNA double-strand breaks (DSBs), introduced by the conserved Spo11 protein. Ultimately, the positions of the DSBs define loci of mutual genetic exchange. However, in a single meiotic cell only a small sub-set of DSBs are destined to form genetic crossovers (COs), while the remainder are repaired via non-CO pathways. CO formation itself is subject to stringent control, which ensures that each homologue pair receives at least one obligate CO. A phenomenon known as CO interference then ensures that most (~85%) additional COs do not occur in an adjacent chromosomal region. As a result multiple COs are spaced well apart along the homologues. Understanding the factors that control DSB formation and processing to form COs is of fundamental scientific interest, moreover this knowledge will have important implications for manipulating meiotic recombination in crop plants.

In recent years meiosis research in plants has largely focussed on the identification of meiotic genes/proteins involved in recombination pathways or the organization of the chromosome axes and synaptonemal complex. Although these studies clearly demonstrate the importance of these proteins, it remained mostly enigmatic how their activities are coordinated to ensure the controlled formation of COs. Hence this collaborative project (DeCOP) seeks to shift emphasis to focus on how recombination, chromosome organisation and remodelling are orchestrated to control the frequency and distribution of COs. Specifically, we seek to identify the protein networks that determine the fate of individual DSBs and establish when CO interference is established. We propose to 1) perform an innovative screen to identify novel factors that modulate CO formation and interference, 2) investigate the role of chromosome axis-associated proteins in CO maturation and interference, 3) determine the role of (ATM/ATR mediated) phosphorylation in coordinating meiotic DNA repair and CO formation and 4) to identify proteins involved in the final step of CO formation.

The factors and processes studied in the DeCOP project will significantly enhance our understanding of the networks that govern crossover formation in plants. We therefore anticipate that our findings will strongly stimulate future crop breeding programmes.

Functional characterisation and validation of nonhost components in Triticeae species for durable resistance against fungal diseases

- **Acronym** **DURESTrit**
- **Project leader** **Patrick Schweizer,** Leibniz Inst of Plant Genetics and Crop Plant Research, DE
- **Other project participants** **Lesley Boyd,** NIAB, UK
  Adam Bogdanove, University of Cornell, USA
  Jochen Kumlehn, Leibniz Inst of Plant Genetics and Crop Plant Research, DE
  Rients Niks, Wageningen University, NL
  Ralph Panstruga, Rheinisch-Westfälische Technische Hochschule, DE
  Brigitte Ruge-Wehling, Julius-Kühn Institute, DE
  Ulrich Schaffrath, Rheinisch-Westfälische Technische Hochschule,DE
  Pietro Spanu, Imperial College London, UK
  Nils Stein, Leibniz Inst of Plant Genetics and Crop Plant Research, DE
  Emma Wallington NIAB, Cambridge, UK
  Roger Wise, USDA-ARS, Iowa State University (ISU), Ames, USA
- **Total Granted budget** 2.213.100 € (funded by DFG, BBSRC, NWO. Co-funded by NSF)

Abstract

Nonhost resistance (NHR) is the most durable and broadly acting form of resistance plants possess to ward off the majority of pathogens regularly occurring within the environment within which they live. In order to exploit NHR in future crop protection concepts we need to understand why the minority of adapted host pathogens can circumvent or suppress NHR and what defense- or accommodation-related proteins, signalling pathways or structural components of their host plants are targeted in order to establish disease. A major obstacle to the rapid exploitation of NHR in crop breeding is related to the fact that NHR is operating at the species level, and only in exceptional cases corresponding sources of resistance can be crossed with related crop plants. Therefore, gene technological approaches to transfer NHR components across species barriers are an attractive alternative to traditional or molecular breeding.
In the ERA-NET consortium TritNONHOST, plus a number of related projects e.g. funded within the German GABI program (BMBF), we identified a number of genes and genetic loci in barley and wheat that are associated or correlated with NHR to three major fungal pathogens including powdery mildews. A limited set of those belonging to the group of receptor-like kinases were successfully validated in functional transient assays in barley and wheat and will provide an important source for the proposed work in the DURESTrit consortium, in addition to resistance loci derived from the wild barley species Hordeum bulbosum or from experimental barley populations segregating for NHR strength. In DURESTrit, we propose to functionally validate three promising receptor-like kinase genes plus a limited number of genes with outstanding regulation behaviour in host- versus nonhost interactions by generating and characterizing stable transgenic lines in barley and wheat. We also propose to fine map and isolate NHR genes from H. bulbosum introgressions and from segregating barely populations. All these materials will either carry transgenes or genome fragments from NHR donors, or have potentially important resistance components silenced by RNAi or genetically modified using TALEN technology. Candidate genes of barley will be tested for molecular interactions with secreted effector molecules of the barley powdery mildew, and this part of the project will be linked to a planned investigation of effector function during barley-powdery mildew interactions funded by NSF.
The project will result in the deeper characterization and validation of previously identified strong NHR candidates, with a special emphasis on receptor-like kinases, and in the identification of new NHR components introduced into barley or wheat by wide crosses or genetic engineering. This will deepen our understanding of NHR in cereals and provide materials and know-how for the exploitation of NHR by translational research.

European Plant Embryology Consortium

- **Acronym** **EURO-PEC**
- **Project leader** **Dolf Weijers,** Wageningen University, NL
- **Other project participants** **Gerd Jürgens,** Max-Planck-Institute for Developmental Biology, Tübingen, DE
  Thomas Laux, University of Freiburg, DE
  Michael Nodine, Gregor Mendel Institute, Vienna, AUT
  Ben Scheres, Wageningen University, NL
- **Total Granted budget** 1.277.600 € (funded by NWO, DFG, FWF)

Abstract

Embryogenesis lays down the foundations of the plant body on which postembryonic development elaborates in a repetitive manner. The early embryo of Arabidopsis is a highly suitable system to study key developmental regulators and the context in which they act because of the limited number of cells and their predictable division patterns. This collaborative research project (CRP) addresses molecular mechanisms underlying each of four critical differentiation events that occur consecutively in early embryogenesis: (1) differential specification of embryonic identity versus extra-embryonic, (2) generation of epidermis versus inner cells, (3) formation of vascular tissue and ground tissue precursors, and (4) specification of shoot and root identity including their respective stem-cell system. We will use previously identified key regulators of these events as starting points and identify the context in which they act. We will also perform genome-wide approaches, including transcript profiling in mutant embryos and chromatin immunoprecipitation followed by next-generation sequencing to identify binding sites and biologically meaningful target genes of key transcriptional regulators. Furthermore, we will employ independent cell-type specific transcriptome profiling approaches to help define the global molecular landscape of these key differentiation events. Finally, we will characterize microRNA-mediated post-transcriptional control as a novel layer of regulation in early embryogenesis. This collaboration will identify regulatory frameworks governing embryonic cell differentiation events and interactions between them. In addition to the advanced genome-wide approaches, genetic analysis as well as 3D- and live embryo imaging will be used to define the role of newly identified regulators in early embryonic patterning.

The consortium comprises five international partners each with a strong record in studying developmental decisions in the embryo. The partner labs have been instrumental in identifying the key developmental regulators that form the starting point of this CRP. While sharing a strong interest in understanding early plant embryogenesis, all partners study a different key step and have complementary methodological expertise. Findings, materials and technologies will be shared among the partners to create a common basis for dissecting the developmental decisions. Coordination of individual efforts is critical to prevent duplication of work and will enable identification of links between developmental steps. This collaborative project will help to organize and consolidate a competitive European research base for studying the most fundamental building blocks of plant development. This will be the only way forward in generating a comprehensive understanding of the earliest formative events in plant life, and will provide the much-needed basis for rational applications in plant breeding, propagation and biotechnology.

Evolution of genomes: Structure-function relationships in the polyploid crop species Brassica napus

- **Acronym** **Evo-Genapus**
- **Project leader** **Ian Bancroft,** University of York, UK
- **Other project participants** **Anne-Marie Chèvre,** INRA (BAP), FR
  Rod Snowdon, University of Giessen, DE
  Denis Tagu, INRA (SPE), FR
- **Total Granted budget** 1.430.759 € (funded by BBSRC, INRA, DFG)

Abstract

The genomes of all plants have evolved through cycles of polyploidy (during which whole genome duplication occurs) and diploidisation (during which those duplicated genomes stabilise). This cycle represents a fundamental mechanism by which the genetic control of biological processes evolve and is a key driver of diversity and performance in almost all crop species. Most of our understanding of the diploidisation process is based on analyses of its outcomes following ancient polyploidy events. Recent results, however, have suggested that the genome evolution mechanisms involved in diploidisation may be having effects on traits in important crop species now, i.e. thousands of years after the most recent polyploidy events in their ancestry.

As a model for a complex polyploid with variable rates of genome evolution we will study Brassica napus, which includes the principal oilseed crop in Europe, oilseed rape. A wide range of accessions are available, of both B. napus formed in nature (an allotetraploid formed by spontaneous hybridization of B. rapa and B. oleracea species; the main source of genetic diversity for rapeseed breeding) and resynthesised B. napus (formed by induced hybridization of the same species in the laboratory), which undergoes rapid genome change.

We hypothesise that the genome evolution observed in resynthesised B. napus represents an accelerated form of the genome evolution that is ongoing in cultivated B. napus derived in nature. We aim to test this hypothesis by characterising molecular evolution on a genome-wide scale in a large panel of natural and resynthesised B. napus, including derived populations, relating the observed variation in genome structure to trait variation of relevance for rapeseed as a crop. Our specific objectives are: (1) Establish the B. napus pan-transciptome, comprising ordered unigenes (EST assemblies) representing the nascent B. napus genome. (2) Quantify the frequency of copy number variation (of transcribed sequences) and homoeologous exchanges present in B. napus formed in nature. (3) Quantify the frequency of copy number variation (of transcribed sequences) and homoeologous exchanges present in resynthesised B. napus, comparing it with the frequency observed in B. napus formed in nature. (4) Understand how genome structural evolution affects trait variation, for a range of traits of importance in this crop.

The research will be conducted by an international consortium with partners from UK, Germany and France. The partners are world-leading experts in their fields and have complementary expertise, enabling multidisciplinary investigation of shared material. The results will provide important insights into the fundamental molecular biology of plant genome evolution. Importantly, it will do this in the context of material that can be used for the improvement of one of the most important crop species in Europe.

Plasticity of flowering time in response to environmental signals in Arabidopsis thaliana

- **Acronym** **FLOWPLAST**
- **Project leader** **Markus Schmid,** Max Planck Institute for Developmental Biology,Tübingen, DE
- **Other project participants** **George Coupland,** Max Planck Institute for Plant Breeding Research, Cologne, DE
  Brandon Davies, Leeds University, UK
  Richard Immink, Wageningen University, NL
  Pawel Krajewski, Polish Academy of Sciences, PL
- **Total Granted budget** 1.495.700 € (funded by DFG, BBSRC, NWO, NCBiR)

Abstract

Flowering is precisely controlled by diverse environmental cues. These responses contribute to the adaptation of plants to different environments and to the optimisation of crop yields. Genetic and molecular analyses performed mainly in Arabidopsis thaliana have identified regulatory pathways that confer different responses to the environment and integrate endogenous and environmental cues to control the floral transition. These pathways act in different tissues of the plant but ultimately influence flowering at the shoot meristem. A complete understanding of these pathways and how they are integrated will decipher how plasticity in flowering response is conferred among plants of the same genotype and how genetic variation between varieties impacts on this plasticity. In turn such knowledge will increase our capacity to breed crops for changing environmental conditions. We propose to investigate the molecular basis of plasticity in flowering-time control in A. thaliana, with a focus on two crucial environmental cues, increases in ambient temperature and different day lengths. As the pathways mediating these responses ultimately converge on the shoot meristem to initiate transcriptional reprogramming we will develop the INTACT system to describe the transcriptional changes that occur in defined spatial zones of the meristem through a temporal series in response to changes in day length. Then, we will use the data from the INTACT profiling to address specific issues related to signal integration at the meristem. We will investigate the chromatin landscape at the shoot apical meristem (SAM) during the transition to flowering and correlate this to transcriptional activity and splicing patterns in response to high ambient temperatures. Such analyses will allow comparison of these data with those obtained during the day-length series identifying common and distinct processes. In addition, we will investigate the integration of different signalling pathways in the rib meristem, where photoperiod and gibberellic acid (GA) signalling converge. Thus, this project will employ flowering and advances in genomic technologies as a platform for dissecting basic mechanisms that govern developmental plasticity on a whole-genome scale. Our results will be of interest to a wide audience, and will help to answer the evolutionarily important questions of how environmental signalling pathways are prioritized and integrated at the shoot meristem as well as how much epigenetic regulation and alternative splicing contributes to the floral transition. Ultimately such knowledge will help predict the mechanisms available to plants to manipulate the timing of the floral transition in response to environmental changes and will contribute to sustainable agriculture.

Homeostasis of Isoprenoids in Plants: understanding compartmentalization, flux and transport of isoprenoids in glandular trichomes for non-crop and crop species

- **Acronym** **H.I.P.**
- **Project leader** **Alain Tissier,** Leibniz-Institute of Plant Biochemistry, DE
- **Other project participants** **Marc Boutry,** Université catholique de Louvain, BE
  Yoram Eyal, Volcani Center ARO, IL
  Robert C. Schuurink, University of Amsterdam, NL
- **Total Granted budget** 934.050 € (funded by DFG, FRS-FNRS, MOARD, NWO)

Abstract

Isoprenoids constitute a wide range of metabolites with diverse functions as plant hormones (gibberellins, abscisic acid, strigolactones, brassinosteroids) or house-keeping constituents (e.g. sterols), but also contain a large group of structurally diverse secondary metabolites with roles in plant protection against insects and pathogens, attraction of pollinators or seed dispersal. Furthermore, some plant terpenoids are used industrially as pharmaceutics, flavour or fragrance ingredients. The co-existence, in the same metabolic network, of signalling molecules in extremely low concentration (nM range), of structural components, and of secondary metabolites which can be produced in high concentrations in specific tissues or even specific organelles, raises the issue of how plant cells manage to appropriately balance the flux towards these distinct isoprenoid classes with highly divergent concentrations and in competition for the same building blocks. In plants the universal isoprenoid precursors, isopentenyl diphosphate (IPP) and dimethyl-allyl diphosphate (DMAPP), are produced via two distinct routes, the cytosolic mevalonate pathway (MEV) and the plastidic deoxy-xylulose phosphate pathway (DXP). Although the allocation of precursors from these two sources is relatively strict, there is now mounting evidence that cross-talk exists, implicating most likely the transport of isoprenyl diphosphates (IPP, DMAPP, GPP or FPP) between compartments. The identity of these putative transporters is however still elusive. The production of industrially relevant terpenoids often resides in specialized cells or structures, such as the glandular trichomes. The study of isoprenoid flux in glandular trichomes is advantageous, since they are separated from the rest of the plant and are not vital organs, thus allowing the study of components of isoprenoid pathways which are otherwise essential for plant growth and development. Using two species of the Solanaceae, tomato (food) and tobacco (non-food), as model plants with glandular trichomes, we will implement a multi-disciplinary approach, including proteomics, interactomics, cell biology, biochemistry and molecular genetics, to deepen our understanding of isoprenoid metabolism. The major objectives of this project are to 1) identify transporters of intracellular isoprenoid intermediates and of terpenoid secretion; 2) determine flux through the two isoprenoid biosynthesis pathways in different types of glandular trichomes; 3) establish a complete and detailed map of sub-cellular localization of all enzymes involved in isoprenoid precursor pathways; 4) explore the interactome of isoprenoid pathway enzymes. This research programme will shed new light on how glandular trichomes achieve such massive flux towards specialized terpenoid metabolites while maintaining homeostasis, and establish new ground for a knowledge-based exploitation of these natural cell factories.

Future-proofing potato: Mechanisms and markers for global-warming tolerant ideotypes

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- **Total Granted budget** 1.117.889 € (funded by DFG, NWO, BBSRC)

Abstract

Potato is the third most important food crop in the world after rice and wheat. Because of its widely distributed cultivation and high yields, it is considered a critical species in terms of food security in face of a growing world population. However, potato is particularly vulnerable to high temperature during various stages of its life cycle. Elevated temperatures strongly suppress tuberisation, negatively affect storage and shelf life of tubers and reduce fitness of seed potatoes. Breeding new heat-stress tolerant cultivars is an urgent need for sustainable increases in potato production, given the negative impact of the rises in temperature due to global warming.

In this project, an integrated approach will be used by combining physiology, genetics, genomics, metabolomics and natural variation studies to analyze the impact of elevated temperatures on (1) sink-source relations of potato plants, (2) potato tuber development, (3) starch accumulation and tuber quality and (4) tuber dormancy. To achieve these aims both unbiased and targeted approaches will be employed. The unbiased approaches include the elucidation of phenotypic, biochemical and molecular responses to varying environmental conditions of selected potato genotypes (diploid populations, and a panel of tetraploid varieties and GMPs). Environmental conditions will include elevated and ambient temperatures in combination with different day lengths and light intensities. The plants will be phenotyped with respect to assimilate allocation, tuberisation, tuber yield, quality and dormancy. The genetic approach aims at identifying polymorphisms of candidate genes from diploid populations exhibiting a wide response to elevated temperatures. This will lead to the identification of genes and allelic variants that confer heat tolerance. The targeted approach is based on recent breakthroughs of the partners, which show that two linked regulators (StCDF_V and StSP6A) play a central role in the initiation of tuberisation. Our unpublished work suggests that StSP6A over-expression confers heat tolerance in transgenic potato plants. Therefore, the role of these regulators will be investigated in more detail in order to identify key components of the multiple signal transduction pathway(s). In addition levels of phytohormones known to regulate tuber initiation and dormancy will be modified and their impact on heat tolerance will be investigated.

The role of the N-end rule pathway in controlling plant response to the environment

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- **Other project participants** **Andreas Bachmair,** University of Vienna, AUT
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- **Total Granted budget** 1.273.860 € (funded by BBSRC, FWF, DFG)

Abstract

Manipulation of plants to provide stability of yield under unpredictable growth conditions will be essential to respond to the effect of climate change in increasing the uncertainty of the agricultural environment. Selective and conditional removal of regulator proteins by proteolysis is emerging as a major regulatory principle in plants. The aim of the N-vironment project is to provide a complete mechanistic understanding of the role of the N-end rule pathway of targeted proteolysis in controlling plant responses to the environment. To achieve this goal consortium partners have been selected that represent internationally leading European teams with complementary expertise in the pathway´s multiple facets, including the biochemical basis of the pathway, hypoxia, transcriptional regulation of stress and metabolic signalling. The project will bring together six research groups with complementary expertise in fundamental molecular plant science, biochemistry and chemistry, in four institutions. The research programme of the N-vironment consortium will be achieved through six inter-related Work Packages (WPs) carried out by the four consortium partners (three funded by ERA-CAPS, one associated laboratory). The objectives of these work packages are related to three fundamental questions that arose after integration of the recent discoveries by consortium members of the role of the N-end rule pathway of targeted proteolysis as a major regulator of plant development and response to the environment. Question 1: What are the substrates and enzymatic components of the N-end rule pathway? Question 2: How is the N-end rule pathway integrated into cellular signaling pathways? Question 3: What is the extent of the role of the N-end rule pathway in plant response to the biotic and abiotic environment? The proposed research has highly innovative measurable outcomes that address this newly discovered area of plant biology, and will uncover: New mechanisms regulating protein stability, new mechanisms of environmental stress sensing, new functions for proteins in stress sensing, the importance of the N-end rule in a key EU crop, tomato. This fast-developing area of plant molecular science is led by N-vironment members (including discovery of substrates, methods of entry into the N-end rule pathway, biochemical components of the pathway), and together with the availability of a large number of unique resources within the consortium, makes the N-vironment proposal highly novel and timely. The synergistic value of this collaborative programme will be the development and exploitation of a highly novel area of plant biology of key importance to agriculture, in which Europe has the capacity to take a world lead through ERA-CAPS funding.

Plant Endoplasmic Reticulum Architecture and Seed Productivity - ERA

- **Acronym** **PER ASPERA**
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- **Total Granted budget** 1.584.218 € (funded by BBSRC, FWF)

Abstract

The plant endoplasmic reticulum (ER) is the cellular organelle that regulates the flux of proteins and lipids into the secretory pathway, and is responsible for storing large amount of proteins for human and animal nutrition. The ER has a unique and dynamic architecture, which changes to allow for different biosynthetic functions. Building on our collaborative work over the last 5 years, our team combines expertise in plant molecular and cell biology, biochemistry, microscopy and cereal genetics to bring understanding of ER structure/function relationships to the next level.

We aim at understanding the key molecular determinants of ER shape by studying their function, regulation and interactions. We also propose to investigate interorganellar cooperation by analysing putative contact points between ER and plasma membrane and ER and protein storage vacuoles. We will manipulate the key ER morphogens and assess how changes in ER shape affect protein and lipid biosynthesis and storage. This work will be perfomed in model plants and, importantly, in seeds of cereals (barley, weat and maize) in order to test directly the ER structure/function relationships in these crop models.

Plant root diffusional barriers: genesis and implications for nutrient efficiency and stress tolerance

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- **Total Granted budget** 2.071.500 € (funded by BBSRC, NWO, INRA, DFG, DASTI)

Abstract

Casparian strips and suberin limit extracellular diffusion in plant roots by providing tight seals between adjacent cells, and between the cell wall and the plasma membrane, respectively. Such diffusional barriers are vital to enable the root endodermal cell layer to act as a selectivity barrier allowing controlled uptake of water and solutes into plants. Further, these barriers are also thought to provide a chemical or physical block to pathogen penetration into roots, including plant-parasitic nematodes accessing the vascular system for feeding. The molecular mechanisms that drive the biosynthesis of these critical barriers are poorly understood, limiting our ability to fully characterize their function and manipulate their properties for agricultural benefit. We have designed an ambitious interdisciplinary research programme integrating molecular plant science with analytical chemistry, whole plant physiology and modelling. This programme aims to deliver a complete understanding of the biology of Casparian strips and suberin, across scales, from molecules to the whole plant. Such information will enable a molecularly directed manipulation of Casparian strips and suberin, providing new pathways for the development of crop varieties with improved nutrient and water use efficiencies, and enhanced resistance to root pathogens, salinity and water stress. Such traits are essential if we are to develop crops that are more resilient to the predicted impacts of climate change on soil fertility, and to improve yields in a more sustainable manner to deliver the yield gains required to meet future population growth. By employing genomic, molecular genetic, chemical, biochemical and cell biological approaches we will discover and characterize the genes and molecular mechanisms involved in the biosynthesis of Casparian strips and suberin. Genetic resources characterized and developed through this mechanistic investigation will be leveraged to understand, at the root and whole plant level, the role of these physical and chemical barriers in mineral nutrient and water uptake, and root parasitic nematode infection. The ecological and adaptive function of these barriers to agriculturally relevant abiotic stresses such as water, mineral nutrient (deficiency and excess) and salinity will also be established. Building on this new understanding, mathematical models integrating molecular mechanistic knowledge with physiological processes at the tissue and whole plant level will also be built, providing predicative capacity to connect barrier properties with whole plant function.

Dimorphic fruits, seeds and seedlings as adaptation mechanisms to abiotic stress in unpredictable environments

- **Acronym** **SeedAdapt**
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- **Total Granted budget** 1.750.073 € (funded by BBSRC, FWF, DFG, NWO)

Abstract

The aim of the SeedAdapt project is to elucidate the molecular mechanisms of fruit/seed-related early-life history traits that evolved in annual plant species as adaptations to abiotic stresses. Higher plant dispersal units - diaspores, here: fruits and seeds - support the distribution and early life history of the progeny. Our project will use a comparative approach to understand the dimorphic diaspore (fruit/seed) syndromes produced on the same plant of annual Aethionema species (sister of all core Brassicaceae, cabbage family) and provide distinct adaptations as a dormancy bet-hedging strategy. The availibility of the Aethionema arabicum genome will facilitate our comparative investigation of the epigenomes, hormonomes and transcriptomes in relation to abiotic stress during sensitive developmental processes. We propose that investigating the regulatory basis of fruit, seed, and seedling trait diversity is ideal for integrating new technologies and complementary expertise in order to study a field with utmost importance in ecology, evolution, seed industry and crop breeding.