



EPPN Workshop:

Plant Phenotyping

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Organization:

EPSO, (<http://www.epsoweb.org/>)

Roland Pieruschka, Forschungszentrum Jülich, Germany

Why do we need phenotyping?

Plants develop by a complex interaction of genotypes with the environments. The need to characterize the phenome is essential to understand fundamental processes which determine the structure and function of plants. Thus, quantitative analysis of the interaction of plant with the environment will enable us to generate the link to the genotype to understand the genetic basis of this relation. While significant progress has been made in molecular and genetic tools in plant science and breeding in recent years, the quantitative analysis of the phenotype has become a major bottleneck.

What is EPPN doing?

The European Plant Phenotyping Network (EPPN) is an EU-funded infrastructure project with the goal to create structural and functional synergies between the plant phenotyping institutions and users in Europe.

EPPN aims at:

- establishing a close communication between phenotyping experts, user communities and technology development by fostering a discussion between platform operators and the diverse user groups on the needs and opportunities of plant phenotyping,
- developing and implementing of novel instrumentation as well as the establishment of experimental and IT standards for good phenotyping practice,
- enabling transnational access for a diverse user community to the major plant phenotyping facilities in Europe.

How to obtain Transnational Access?

EPPN offers transnational access to eligible scientists to:

- 23 experimental plant phenotyping facilities,
- based on a simple selection procedure.

Eligibility criteria according to the EU guidelines:

- research team members must work in an EU member, associated state, or candidate state,
- the requested access must be transnational,
- only users entitled to disseminate generated knowledge under the project are eligible for access free of charge.

Detailed information at: <http://www.plant-phenotyping-network.eu/>

Programme of the EPPN Plant Phenotyping Workshop

Introduction

- 9:00 – 9:05 Uli Schurr, Forschungszentrum Jülich, Germany
Welcome
- 9:05 – 9:30 Roland Pieruschka, Forschungszentrum Jülich, Germany
What is EPPN and how to obtain Transnational Access to EPPN facilities?

Session 1: Transnational Access: User case studies (Chair: Roland Pieruschka)

- 9:30 – 9:55 Roberto Papa, CRA-CER, Italy
Morpho-physiological evaluation of a collection of tetraploid wheats under different nitrogen levels
- 9:55 – 10:20 Pilar Catalan, Universidad de Zaragoza, Spain
Phenotypic, genotypic and metabolomics analyses within the *Brachypodium distachyon* complex (*Poaceae*): first approaches to phenomics and GWA studies
- 10:20 – 10:45 Ankica Kodnic-Spika, Institute of Field and Vegetable Crops, Serbia
Use of complex stress diagnostic systems to study a combined effect of water nitrogen availability on wheat development
- 10:45 – 11:15 Coffee break

Session 2: Transnational Access: Case studies by operator of plant phenotyping platforms - part 1 (Chair: John Doonan)

- 11:15 – 11:40 Dénes Dudits, Hungarian Academy of Sciences, Hungary
Recent improvements of the Szeged phenotyping platform
- 11:40 – 12:05 Craig Sturrock, University of Nottingham, UK
Phenotyping facilities at Nottingham: past, present and future
- 12:05 – 12:30 Fabio Fiorani, Forschungszentrum Jülich, Germany
Phenotyping platforms at JPPC provide insight into the dynamics of shoot and root growth responses to sub-optimal water, nitrogen and temperature.
- 12:30 – 14:00 Lunch break

Session 3: Transnational Access: Case studies by operator of plant phenotyping platforms

- part 2 (Chair: Dénes Dudits)

- 14:00 – 14:25 Jörg-Peter Schnitzler, HMGU, Germany
Possibilities for plant phenotyping at the phytotron facility of the Helmholtz Zentrum München
- 14:25 – 14:50 John Doonen, Aberystwyth University, UK
Scaling and integrating phenotyping with genetics and genomics
- 14:50 – 15:15 Christophe Salon, INRA, France
Characterizing plant and organisms interactions: challenges and opportunities involving high throughput plant phenotyping
- 15:15 – 15:40 Thomas Altmann, IPK, Germany
Plant Phenotyping at IPK Gatersleben: Installations accessible through EPPN and examples of current applications
- 15:40 – 16:10 Coffee break

Session 4: New developments in plant phenotyping (Chair: Fabio Fiorani)

- 16:10 – 16:35 Jacques Le Gouis, INRA, France
PHENOME: French Plant Phenomic Network
- 16:35 – 17:00 Uli Schurr, Forschungszentrum Jülich, Germany
Establishing phenotyping capacity within the German Plant Phenotyping Network (DPPN)
- 17:00 – 17:25 Uli Schurr, Forschungszentrum Jülich, Germany
Plant Phenotyping: Future perspectives
- 17:25 – 17:30 Uli Schurr, Roland Pieruschka, Forschungszentrum Jülich, Germany
Closing remarks
- 17:30 – 18:30 Open discussion with the EPPN platform operators

ABSTRACTS

Session 1: Transnational Access: User case studies

Morpho-physiological evaluation of a collection of tetraploid wheats under different nitrogen levels

Gioia T.¹, Nagel K.A.², Beleggia R.¹, Ficco D.B.M.¹, Mastrangelo A.M.¹, Platani C.¹, De Vita P.¹, Pieruschka R.², Fiorani F.², Papa R.^{1*}

¹Consiglio per la Ricerca e la sperimentazione in Agricoltura, Cereal Research Centre (CRA-CER), SS16 km 675, 71122, Foggia (Italy),

²Institute of Bio- and Geosciences, IBG-2: Plant Sciences, Forschungszentrum Jülich GmbH, 52425 Jülich (Germany)

Triticum, domestication, root traits, nitrogen fertilization, digital imaging

*roberto.papa@entecra.it

We have analysed if and how domestication and breeding processes have modified shoot and root traits in relation to N availability. A set of 36 inbred lines representing three stages in tetraploid wheat evolution was used: 12 wild emmer lines (*T. dicoccoides*), 12 emmer primitive domestic lines (*T. dicoccum*), and 12 modern varieties (*T. durum*). For each inbred line uniform seeds were selected and after germination in Petri dishes transplanted into rhizotrons filled with peat soil (90x70x5 cm). Plants were grown for four weeks under semi-controlled conditions in the Phytect Greenhouse (Forschungszentrum Jülich GmbH, Germany) and root and shoot traits were quantified using the automated rhizotron robot (GROWSCREEN-Rhizo, Nagel et al. 2012, Functional Plant Biology, 39, 891-904). Additional measurements were performed to quantify the chlorophyll content, photosynthetic performance and biomass. Leaf samples were also taken for a metabolomics analysis with the aim to look for significant differences in metabolites content related to domestication and breeding by a different nitrogen supply. The experiment was arranged in a randomized block design with replications (two replications x two N treatments x three species x 12 genotypes per specie x two plants per genotype). The analysis of a range of traits indicates significant differences between subspecies, genotype, and between the two different N level for several traits. The experiment offered a unique opportunity to relate different type of information to get a deep insight on the process of domestication and in particular on the adaptation to contrasting levels of nitrogen availability among wild emmer, emmer and durum wheat.

This research was enabled by the Transnational Access capacities of the European Plant Phenotyping Network (EPPN, grant agreement no. 284443) funded by the FP7 Research Infrastructures Programme of the European Union.

Phenotypic, genotypic and metabolomics analyses within the *Brachypodium distachyon* complex (*Poaceae*): first approaches to phenomics and GWA studies

Pilar Catalán^{1*}, Diana López-Alvarez¹, Cristina Bellosta¹, Ernesto Pérez-Collazos¹, Fiona Corke², Luis Mur², Hassan Zubair², John Draper², John H. Doonan²

¹Department of Agricultural and Environmental Sciences, University of Zaragoza, Huesca, Spain

²IBERS, University of Aberystwyth, Aberystwyth, UK

*pcatalan@unizar.es

Brachypodium distachyon s. l. has been widely investigated across the world as a model plant for temperate cereals and biofuel grasses. However, this annual plant shows three cytotypes that have been recently recognized as three independent species, the diploids *B. distachyon* (2n=10) and *B. stacei* (2n=20) and their derived allotetraploid *B. hybridum* (2n=30). Within *B. distachyon*, different drought tolerant and drought sensitive lines have been identified.

Phenotypic analysis of Iberian accessions of these taxa using 15 quantitative and discrete characters detected 5 traits capable to significantly discriminate them. Intraspecific variation was also detected for other parameters related to sizes of reproductive and vegetative organs. This variation is correlated with abiotic variables, such as altitude, latitude, and several climatic variables (temperature, rainfall), indicating that the different intraspecific phenotypes might have adapted to distinct environments and stresses. Preliminary genotypic analysis based on SSR and DNA sequences corroborates these findings, showing both geographical-ecologically restricted groupings and largely expanded groupings, each featuring the genetic compositions of the specialist and the generalist wild accessions, respectively. Biochemical variation amongst the accessions was investigated by metabolite fingerprinting using Fourier Transform Infra-Red (FT-IR) spectroscopy. Discriminant Function Analysis (DFA) indicated that variation in metabolites could be linked to geographical origin. Metabolomic approaches (e. g. Mass Spectrometry (ESI-MS)) were also employed to investigate the basis of the variation in drought tolerance; multivariate data indicated that free-fatty acids, polyamine, arginine and antioxidant metabolites were all elevated in the tolerant or arid-climate lines but not in the sensitive ones.

We plan to analyse 50 re-sequenced accessions of *B. distachyon*, sampled across different geographical and ecological clines in the Iberian Peninsula. The overall aim will be to investigate the relationships and their goodness of fit between traditional (manual) vs. automated measurements over this diverse range of genotypes. Drought stress treatments may include 1) water-withholding to wilting point (~20% soil water content) and 2) limited watering to achieve a constant moisture level (~ 30-40% soil water) compared to well watered controls. The traits to be measured (on LemnaTec system) would include: height, estimates of biomass, proxies for tiller number, flowering time, and senescence. Other measurements will include: biomass (fresh and dry weight), plant height, harvest index, relative water content (RWC), and grain yield. Metabolic phenotypes during stress responses will be investigated initially by non-targeted metabolite fingerprinting using high resolution FIE-MS. Integration of metabolomic fingerprinting, morphological and physiological data will be done through statistical multivariate analyses and other correlation analyses. The ultimate aim of this pilot

experiment would be to establish the ground rules for a larger Genome Wide Association experiment where the phenomic output would be correlated with NGS genotyping data, aiming to identify and map genetic loci that control phenotypic variation in drought tolerance traits in *B. distachyon*.

This research was enabled by the Transnational Access capacities of the European Plant Phenotyping Network (EPPN, grant agreement no. 284443) funded by the FP7 Research Infrastructures Programme of the European Union.

Use of complex stress diagnostic systems to study a combined effect of water nitrogen availability on wheat development

Ankica Kondić-Špika¹, Ljiljana Brbaklić¹, Dragana Trkulja¹, Vladimir Aćin¹, Srbslav Denčić¹, Novica Mladenov¹, Nikola Hristov¹, Imre Vass², Dénes Dudits², Janos Pauk³

¹Institute of Field and Vegetable Crops, Novi Sad, Serbia; ²Biological Research Centre, Szeged, Hungary; ³Cereal Research Non-Profit Company, Szeged, Hungary

*kondicspika@gmail.com

Water supply and nitrogen (N) availability are among the major abiotic factors that affect agricultural productivity of important crop species, including wheat, worldwide. Complex interaction of these two important environmental factors and their effects on wheat growth and development were the main objectives of this study.

The experiments were conducted with ten wheat (*Triticum aestivum* L.) cultivars, chosen according to their level of drought tolerance shown in previous field experiments: Siete Cerros (tolerant - T), Panonnia (T), Evropa 90(T), Dunav (T), NS 40S (T), Bezostaja-1 (medium tolerant - MT), Kosuta (MT), Stepa (sensitive - S), Suboticanka (S), NS Avangarda (a promising new cultivar with unknown drought tolerance).

Four growth conditions were checked:

1. Well watered (60 % field capacity) in the presence of sufficient N (60 mg N/kg soil)
2. Well watered (60 % field capacity) in the presence of low N (3-4 mg N/kg soil)
3. Water limited (20 % field capacity) in the presence of sufficient N (60 mg N/kg soil)
4. Water limited (20 % field capacity) in the presence of low N (3-4 mg N/kg soil).

For these experiments soils with defined nutrition levels were used. The water was provided by computer controlled protocols. The shoot growth parameters (plant height, and total green biomass) were analyzed during the whole life cycle of the chosen wheat cultivars by using the HAS-SSDS platform. Water use profiles were recorded at the level of individual plants during the whole cultivation period from which the efficiency of water usage, as well as the effect of N availability on water utilization were determined. The root parameters were analyzed at seedling stage by using the Rhizobox system which is also suitable for detection of S-phase cells by EdU (5-ethynyl-2'-deoxyuridine)-staining of the root tips. The root architecture of adult plants was monitored during the development stages before heading by using the Rhizocolumn system of the HAS-RSDS platform. Digital images were collected from different side angles (bottom view) and from inside the soil, by

using boroscope technology. At the end of the experiment grain production parameters (over ground mass, plant height, no. of spikelets and seeds per spike, thousand kernel weight) were also determined.

A general feature of N limitation was a retardation of total shoot biomass. This effect was observed both under well watered and water-limited conditions. Combination of drought stress and N limitation enhanced the effect of these stress factors relative to their separate applications. However, in case of cv. Siete Cerros the N limitation under drought stressed conditions had only a small additional effect, which occurs also in case of seed production. Based on our results N limitation generally enhances the adverse consequences of drought stress with the exception of cv. Siete Cerros. Plant height was less sensitive to decreased water and N amount than biomass and seed production. Water use efficiency was significantly decreased by N limitation in well watered conditions and also in drought stressed plants. This shows that under N-limitation wheat plants have decreased capacity to use soil water, which could be an important factor in the enhancement of the drought stress. Interestingly, in case of two cultivars (NS Avangarda and Siete Cerros) the water use efficiency at the level of seed production was not affected by N limitation under drought stress. We have also identified a Serbian cultivar (Suboticanka) that was able to continue root growth in soil with limited water supply. These cultivars could be potential candidates for production under conditions when drought and N limitation are combined.

This research was enabled by the Transnational Access capacities of the European Plant Phenotyping Network (EPPN, grant agreement no. 284443) funded by the FP7 Research Infrastructures Programme of the European Union.

Session 2: Transnational Access: Case studies by operators of phenotyping platforms – part 1

Recent improvements of the Szeged phenotyping platform

András Cseri¹, László Sass¹, Ottó Törjék¹, János Pauk¹, Imre Vass¹ and Dénes Dudits¹

¹Biological Research Centre, Hungarian Academy of Sciences, Temesvári krt. 62. H-6701 Szeged, Hungary

*dudits@brc.hu

Genetic improvement of complex traits such as drought adaptation can be advanced by the combination of genomic and phenomic approaches. Semi-robotic phenotyping platform was used for computer-controlled watering, digital and thermal imaging of barley plants grown in greenhouse. In soil with 20% water capacity the reduction in green pixel-based shoot surface area of tested barley variants ranged from 0% to 76 % as compared to control plants grown with 60% water capacity. The EcoTILLING and the subsequent DNA sequencing have defined four (A-D) haplotypes of the HvA1 gene encoding the group 3 LEA protein. The green pixel mean value of genotypes with haplotype D was higher than the mean value of the remaining haplotypes under drought. Thermal images indicated genotype-dependent variation in elevation of the canopy temperature of drought-exposed plants. The drought-induced changes in leaf temperature showed low correlation with the water use efficiency ($r^2 = 0.431$). The haplotype/trait association analysis based on the t-test has revealed a positive effect of the haplotype B of the gene encoding the barley fungal pathogen induced mRNA for pathogen-related protein (HvPPRPX) on harvest index, thousand grain weight, water use efficiency and grain yield. The presented pilot study establishes basic methodology for the integrated use of phenotyping and haplotyping data in characterization of genotype-dependent drought responses in barley.

Phenotyping facilities at Nottingham: past, present and future

Craig Sturrock¹, Tony Pridmore¹, Darren Wells¹, John Foulkes¹, Sacha Mooney¹ and Malcolm Bennett¹

¹Centre for Plant Integrative Biology (CPiB), University of Nottingham, Sutton Bonington Campus, Loughborough, Leics, U.K. LE12 5RD

*craig.sturrock@nottingham.ac.uk

With a rapidly increasing global population and the threat of a changing climate, maximising plant productivity and developing sustainable soil management strategies are vital for food security. At the Centre for Plant Integrative Biology (CPiB) our interdisciplinary team use an integrated approach to research extending from studies at the molecular and biochemical level to physiological analysis and agronomy of whole plants and their environment. The talk will highlight key plant phenotyping approaches currently in use and under development at our facility that encapsulate this vision. These include high resolution analysis of live root cells using vertical confocal microscopy; high-throughput root system structural analysis and growth in agar plates using 'RootTrace'; large plant root analysis system in glasshouses and the field for root architecture in soil-filled columns; and the 4D phenotyping of root geometries and soil properties using Micro Computed Tomography.

Phenotyping platforms at JPPC provide insight into the dynamics of shoot and root growth responses to sub-optimal water, nitrogen and temperature.

Fabio Fiorani¹

¹Forschungszentrum Jülich GmbH, Institute for Bio- und Geosciences (IBG), IBG-2: Plant Sciences, 52425 Jülich

*f.fiorani@fz-juelich.de

The transnational access scheme offered by the EPPN has been established at the Jülich Plant Phenotyping Centre, IBG2 Plant Sciences. During the first two years of funding we have hosted five user groups using three phenotyping installations for non-invasive analyses of shoot and root dynamic responses to key environmental variables such as water, nitrogen and air temperature.

In this presentation we first highlight our current capacities and technical capabilities of our phenotyping infrastructure funded through the EPPN. Next, we present the detailed research questions that user groups have been able to address during the access projects. In particular, we show: i) differential responses sensitivity of shoot and root growth to low water availability in a maize panel selected for tolerance to low water availability (collaboration with University of Antwerp); ii) root architecture responses of durum wheat and domesticated progenitors to low nitrate supply (collaboration with Cereal Research Centre, Foggia); iii) integration of hormonal pathways and sugar signalling in Arabidopsis mutants and transgenic plants, in particular via gibberellin and trehalose 6-phosphate, for acclimation of leaf and root growth to low soil water availability and low air temperature (collaborations with University of Utrecht and Rothamsted Research Centre). In all cases, variability in the analyzed traits and sensitivity of analyses will be addressed.

Taken together, these studies illustrate a high user-driven demand for advanced, automated phenotyping systems for quantitative and non-destructive analyses of plant growth and demonstrate that these approaches are appropriate to study the genetic components underlying trait plasticity to limiting resources.

Session 3: Transnational Access: Case studies by operators of phenotyping platforms – part 2

Possibilities for plant phenotyping at the phytotron facility of the Helmholtz Zentrum München

Jörg-Peter Schnitzler¹

¹Helmholtz Zentrum München - German Research Centre for Environmental Health, Research Unit Environmental Simulation (EUS), Institute of Biochemical Plant Pathology, Ingolstädter Landstr. 1, 85764 Neuherberg, Germany

*jp.schnitzler@helmholtz-muenchen.de

At the Helmholtz Zentrum München (HMGU) the Research Unit Environmental Simulation (EUS) operates a sophisticated environmental simulation platform, which is open for access in the frame of the European Plant Phenotyping Network EPPN. In exposure chambers (ExpoSCREEN) and solar simulators (SunSCREEN) long-term multifactorial experiments can be performed simulating environmental scenarios (gas composition, climate, air pollutants etc.) relevant for understanding plant adaptation, plant-atmosphere and plant-soil interactions under future climate conditions. Globally unique, the sun simulators and exposure chambers allow simulation of irradiation conditions very close to nature, in particular of ultraviolet (UV) irradiation typically for the mid-latitudes. Research of EUS focuses the emission of volatile organic compounds (VOCs) from plants and fungi and their potential functions in biotic interactions. Based on current examples the presentation will give an overview on possible applications of the facility for plant phenotyping. In particular it will be demonstrated how stress-induced VOCs can serve as non-invasive markers in plant-microbe or plant-herbivore interactions.

Scaling and integrating phenotyping with genetics and genomics

John H. Doonan¹, Alan Gay¹, Andreu Alcade-Barrios¹, John Draper¹, Fiona Corke¹, Anyela Camargo¹

¹National Plant Phenomics Centre, IBERS, Aberystwyth University, SY23 3EB, UK

phenotyping, plant growth, grain, traits

*john.doonan@aber.ac.uk

Our capacity to genotype organisms, now vastly exceeds our ability to phenotype those same individuals. Genotyping provides molecular detail at the nucleotide level and can be scaled to deal with whole populations at ever decreasing cost. However, phenotyping of plants is less scalable, is often subjective and measures attributes e.g. yield that can be difficult to relate to the underlying genetic variation. This has been termed the phenotyping bottleneck. The National Plant Phenomics Centre represents a major infrastructural development, funded by Aberystwyth University, the Welsh Government and BBSRC, providing state-of-the-art capabilities for objective plant phenotyping using automated imaging systems combined with computing technologies. The facilities are available to scientists via either the BBSRCs National capability grant (UK) or an FP7 grant (collaborative access from Europe), EPPN. The EPPN project supports development of international standards and protocols for phenotyping analogous to those used in other large scale biology. Automated handling

of over 800 RFID tagged containers allows plants to be moved on a programmable conveyor system between growth, imaging and sampling areas. Each carriage conveys one large plant (up to 2m tall) or a tray of small plants. Environmental, nutrient and watering controls enable the application of single or combinatorial stresses, allowing the dissection of Genotype x Environmental interactions. Other facilities include grain analysis, a large scale nutrient flow glasshouse, photo-physiological analysis, metabolic and genotyping facilities. Access to remote sensing services (i.e. UAV flights for field phenotyping) can be arranged also. The Centre provides a range of imaging techniques and sensors to record plant characteristics non-destructively and dynamically. An early priority will be to develop new high throughput imaging methods to determine key biological parameters. Integration of phenomic data with genomic analyses will be key to exploiting the full value of the NPPC, thus a team of dedicated data analysts assist in this process and will require coordination with trait ontologies that are widely acceptable for use in both controlled environment and field. Different service levels are provided in the NPPC including full service and collaborative projects depending on users' requirements. Academic users will be expected (after a suitable interval to allow for publication) to make experimental and meta-data available to the community. We will discuss early results using various species, including wheat, oats, *Brachypodium* and *Arabidopsis*.

Characterizing plant and organisms interactions: challenges and opportunities involving high throughput plant phenotyping

Christophe Salon¹

¹UMR Agroécologie, GEAPSI Group and High Throughput Phenotyping Platform, INRA, 17 rue Sully, BP86510 Dijon Cedex, France

*christophe.salon@dijon.inra.fr

In the context of climate change, increasing soil degradation and scarcity of water and mineral resources, breeding crops more efficient for resource acquisition is a highly desirable target. This highlights the crucial need to increase knowledge about regulation of shoot and root architecture and to explore it in crop species and in field conditions. To this end, efforts should focus on the understanding of plant plasticity. A major bottleneck for these research fields remains the development of high-throughput, non-invasive and multi-scale phenotyping systems in agronomically relevant conditions. Facing this challenge using the available tools and current developments will help to uncover opportunities for understanding plant response to environmental factors and its interactions with other organisms, including micro-organisms, still poorly known and exploited. The facilities of the High Throughput Plant Phenotyping Platform (PPHD) available in INRA Dijon, developed in response to this challenge, will be presented.

Plant Phenotyping at IPK Gatersleben: Installations accessible through EPPN and examples of current applicationsThomas Altmann¹¹Leibniz-Institute of Plant Genetics and Crop Plant Research (IPK), Corrensstr. 3, 06466 Stadt Seeland OT Gatersleben, Germany.

*altmann@ipk-gatersleben.de

The deliberate utilization of genetic diversity conserved in genebanks such as the German Federal *ex situ* Genebank located at IPK Gatersleben is a key issue to supply a growing world population with food, feed and renewable energy. Beyond conservation of, Knowledge of the structural and functional genetic architecture of agricultural traits is a prerequisite for the systematic exploration and utilization of these genetic resources. Hence, research into basic plant biology and plant biotechnology increasing our understanding of the basic genetic, biochemical and physiological principles underlying plant performance are at the core of the IPK research strategy. Complementary to the assessment of the genetic variation, plant phenotyping is of central importance for mapping and molecular identification of QTL as well as for characterisation of the roles and functions of genes. It is furthermore vital to the elucidation of the mechanisms underlying important biological processes and phenomena in plants as are multidisciplinary and systems-oriented analyses. Owing to the needs and the opportunities of mid to large scale assessment of trait expression, several platforms and procedures for phenotypic assessment have been established or are being installed and used at IPK, ranging from the cellular to the whole plant level.

Dedicated technical platforms have been established and are further upgraded including LemnaTec-based automated transport and imaging systems (IPK-APPP) to monitor plant growth and development properties including performance characteristics displayed under various controlled environmental conditions. IPK-APPP installations are available for small (e.g. Arabidopsis), medium (e.g. barley), or large (e.g. maize) plants. The platforms have capacities for parallel cultivation and monitoring of 384, 2304, or up to 4608 small plants, up to 1584 medium plants, or 396 large plants. Furthermore, infrastructure for processing (grinding and extraction) and non-targeted metabolite profiling (derivatization and GC-MS analysis) of deeply frozen plant material is available. Large-scale genotypic and phenotypic characterisation (including leaf growth, biomass accumulation, and metabolic composition) of Arabidopsis accessions, recombinant inbred line (RIL), and introgression line (IL) populations as well as test crosses thereof opened the opportunity to map per se and heterotic QTL, to uncover relationships between growth and metabolic status, and to identify molecular predictors of plant performance. These investigations are expanded towards analyses of maize diversity collections confirming similar principles and allowing the assessment of further plant performance features such as water use efficiency. Further examples of platform utilization and application to a wider range of plant species will be presented.

Session 4: New development in plant phenotyping

PHENOME: French Plant Phenomic Network

Jacques Le Gouis¹, François Tardieu² (coordinator)

¹INRA-Université Clermont II, UMR GDEC– 5 chemin de Beaulieu, 63039 Clermont-Ferrand Cedex ²INRA-Montpellier SupAgro, UMR LEPSE– 2 place Viala, 34060 Montpellier

*jacques.legouis@clermont.inra.fr

Phenotyping has become the major limitation in programmes aimed at selecting genotypes that maintain or increase their performance under climate change and reduced inputs. The goal of Phenome is to develop an up-to-date, versatile, high-throughput infrastructure and suite of methods allowing characterisation of panels of genotypes of different crops under different environmental scenarios. This project consists in: (1) Building or upgrading five highly instrumented platforms in representative French sites, able as a whole to deal with the most important crop species, biological questions and environmental constraints; (2) Developing sensors, data analysis methods and databases able to cope with the millions of data points that will be generated at different scales and times; and (3) Diffusing techniques and methods towards the French phenotyping community (seed companies, technical institutes, public research groups), and facilitating the emergence of SMEs involved in the development of phenotyping methods.

The Phenome consortium gathers 12 academic groups, two farmer-funded applied research organisations, and subcontractors from public institutions specialized in sensor or imaging developments. It also involves through research projects the major European-based seed companies acting in France and more than 20 SMEs which contribute to methodology developments.

The five locations of Phenome will consist of: (1) two platforms in controlled conditions (capacity of 1900 plants each) with possible controls of soil water content, temperature and CO₂, and the ability to measure individual plant growth, architecture (shoots and roots) and transpiration; (2) two field platforms with strong control of environmental conditions, in particular one free-air carbon enrichment (FACE) system, and large rain-shelters able to control rainfall (capacity 800 individual plots each); and (3) three field platforms with higher throughput (capacity 2000 individual plots each) equipped with soil and climate sensors, and an autonomous 'phenomobile' designed to capture functional images of each individual plot at high throughput. In addition, two supporting "omic" platforms will allow centralising metabolomic and structural measurements associated with the experiments in the phenotyping platforms.

Phenome has made the strategic choice to develop essential methodological projects at the consortium level. The objectives are to: (1) improve our capacity to measure plant traits and environmental conditions with accurate and high throughput methods; (2) organise phenotypic data originating from different platforms, so that they can be analysed jointly through development in ontologies, web services and methods of data representation, all of them compatible with those developed by European and Australian partner projects; and (3) handle very large datasets thanks to

data cleaning via artificial intelligence, analyses of time-related data, and an interface between data collection and plant / crop models.

Phenome is backed by 14 scientific national and European projects and fully integrated to international phenotyping projects. It will be an essential tool for (1) the academic community for original programmes of genetics/genomics; (2) private seed companies, which will have access to the infrastructure via collaborations and bilateral contracts; and (3) French SMEs that will benefit from the project both directly via subcontracts, and indirectly to gain access to the markets of phenotyping and precision agriculture.

Establishing phenotyping capacity within the German Plant Phenotyping Network (DPPN)

Uli Schurr¹, Thomas Altmann², Jörg Durner³, Adi Keßeler¹

¹Forschungszentrum Jülich, ²IPK Gatersleben ³Helmholtzzentrum München

*u.schurr@fz-juelich.de

The ability to quantitatively analyse plant phenotypic traits from single cells to plant and stand level and their dynamic responses to the biotic and abiotic environment is an essential requirement for genetic and physiological research, and the cornerstone for enabling applications of scientific findings to bioeconomy. While significant progress has been made in molecular and genetic tools for plant breeding in recent years, plant phenotyping has become the major bottleneck. The German Plant Phenotyping Network (DPPN, <http://www.dppn.de/>) will establish and run national plant phenotyping infrastructure. The recently started DPPN project develops novel integrated concepts for plant phenotyping infrastructures along roadmaps for the phenotyping of the properties of roots, shoots, plant in the field, seeds, plant-pathogen interaction, and chemical composition. Additionally, the roadmap includes plant panels which cover a wide range of structural and functional properties to be used for validation of the infrastructure and, a technology platform to enable automated phenotyping pipelines throughout the experiment including data management and analysis. The aim is to build the required capacity to address the interrelation between genotypes and their phenotypic representation under the relevant environmental scenarios and to run these platforms with users from academia, breeders and industry. The DPPN is established in cooperation of the Research Centre Jülich (coordination), the Leibniz Institute of Plant Genetics and Crop Plant Research Gatersleben and Helmholtz Zentrum München. In order to integrate national German phenotyping efforts and provide an infrastructure as a nucleus for further expansion of this new research field DPPN will i) improve existing and develop new technologies as well as integrate this technologies into phenotyping platforms, ii) develop and disseminate experimental protocols of Good Phenotyping Practice (GPP) and set benchmarks for future phenotyping efforts and developments, iii) implement a user-oriented portfolio of technologies and methods for phenotyping of complex traits, iv) foster the distribution of knowledge and technologies for adequate phenotyping in plant sciences and its applications. Additionally, an important element of the project is to enable access for the user communities to state-of-the-art phenotyping know-how and technologies.

Plant Phenotyping: Future perspectives

Uli Schurr¹

¹Forschungszentrum Jülich

*u.schurr@fz-juelich.de

Phenotyping sciences are still in a state of infancy while at the same time huge expectations and needs are obvious. While this provides a good environment for the development of phenotyping infrastructures, the real challenge for a sustainable development is to deliver up to the expectations and/or to openly communicate what is possible (today) and what isn't. While continued technological advancements are an essential element of the future development of plant phenotyping, the *ultima ratio* is providing the adequate information that is needed to gain relevant information on the plant-environment interaction. "Relevance" in that context depends strongly on the demand/ user side – with respect to what information is needed as well as what is possible. Here phenotyping sciences and infrastructures must become an integral element of a systemic approach towards understanding genotype-phenotype-environment interactions.

With the dynamic of the development of phenotyping it is hard to predict how the field will be looking like in 5 or 10 years' time. However, I clearly expect significant diversification of approaches, a wider distribution of both special and common technologies – providing new and even larger challenges than today. In this development the existing and emerging national platforms and their interaction will play a crucial role in driving the development in a wise and science-based way.

