



HAL
open science

Recent progress in drought tolerance from genetics to modelling : Conference Handbook

Claude Welcker, Roberto Tuberosa, Francois F. Tardieu

► To cite this version:

Claude Welcker, Roberto Tuberosa, Francois F. Tardieu. Recent progress in drought tolerance from genetics to modelling : Conference Handbook. Recent progress in drought tolerance from genetics to modelling, Jun 2015, Montpellier, France. 164 p., 2015. hal-02799350

HAL Id: hal-02799350

<https://hal.inrae.fr/hal-02799350>

Submitted on 5 Jun 2020

HAL is a multi-disciplinary open access archive for the deposit and dissemination of scientific research documents, whether they are published or not. The documents may come from teaching and research institutions in France or abroad, or from public or private research centers.

L'archive ouverte pluridisciplinaire **HAL**, est destinée au dépôt et à la diffusion de documents scientifiques de niveau recherche, publiés ou non, émanant des établissements d'enseignement et de recherche français ou étrangers, des laboratoires publics ou privés.



Recent progress in drought tolerance

from genetics to modelling

CONFERENCE HANDBOOK

June 8, 9 & 12, 2015

Le Corum – Montpellier - France



Scientific Committee

F. Tardieu (INRA-LEPSE, France) – President, DROPS Coordinator

X. Draye (Université Catholique de Louvain, Belgium)

A. Charcosset (INRA - Le Moulon, France)

G. Hammer (University of Queensland, Australia)

B. Usadel (RWTH Aachen University, Germany)

R. Tuberosa (Università di Bologna, Italy)

C. Welcker (INRA-LEPSE, France)

A. Boerner (IPK, Germany)

D. Simic (PIO, Croatia)

B. Boller (President Eucarpia, Agroscope, Switzerland)

Organizing Committee

C. Welcker (INRA LEPSE, France) - President

P. Lucas (INRA-Transfert, France)

J. Vouillamoz (Eucarpia Agroscope, Switzerland)

Z Bedo (MTA-ATK, Hungary)

M-A. Cané (UNIBO, Italy)

A. Pasquier (INRA LEPSE, France)

O. Mackre (INRA Transfert, France)

Acknowledgements

*This conference was partly funded by **DROPS** and has received funding from the European Community's Seventh Framework Programme (FP7/ 2007-2013) under the grant agreement n° 244374.*

The conference was financially supported too by Agropolis Fondation under the reference ID 1400-024 through the « Investissements d'avenir » programme (Labex Agro:ANR-10-LABX-0001-01).

The financial support of two INRA divisions "Environment and Agronomy" and "Plant Biology and breeding" and the Region Languedoc-Roussillon is gratefully acknowledged.



Table of contents

Welcome message.....4

Keynote speakers.....5

Session 1: Coping with drought in crop improvement: a global perspective.....15

Session 2: Traits-base strategies for dealing with drought.....18

Poster session 3: Variation for target traits and phenotyping methods.....32

Session 4: Dealing with Genotype x Environment interaction.....85

Poster session 5: QTL, functional genomics, allelic diversity and breeding application.....91

Session 6: Breeding for drought, strategies, choices.....152

List of posters session 3.....157

List of posters session 5.....160

Program technical session: phenotyping for the responses to environmental conditions163

Conference program.....164



Welcome message

The conference is at the crossroad of plant and crop physiology, genetics and breeding. It aims at presenting an accurate view on recent advances in the mechanisms associated with plant response to water deficit, on these mechanisms phenotyping, on their genetic variability and on the modelling of relevant allelic effects on plant behavior under changing climates.

A large space will be dedicated to discussion, with two forums on opportunities and limits of breeding for drought tolerance, and the link between upstream disciplines and breeding. This will foster dialogue between academic and private sector, young scientist and senior breeders, initiatives from the Northern regions where the impact of climate change is becoming visible and the developing countries that already face drought-prone conditions.

This conference is jointly organized by the DROPS (FP7 EU project) and the sections Cereals, maize and sorghum of Eucarpia. It will present results obtained in the project DROPS and in related projects.

This conference will be twined to the 23th Eucarpia Maize and Sorghum conference on "Genomics and phenomics for model-based maize and sorghum breeding", to be held at the same venue, June 10 and 11.

Attendance is free, but registration is mandatory, associated with a questionnaire on attendee's expertise, current activity and main interests. Applications from Mediterranean, African, Asian and South American participants are highly encouraged.

Claude Welcker (INRA-France)
Conference Chair

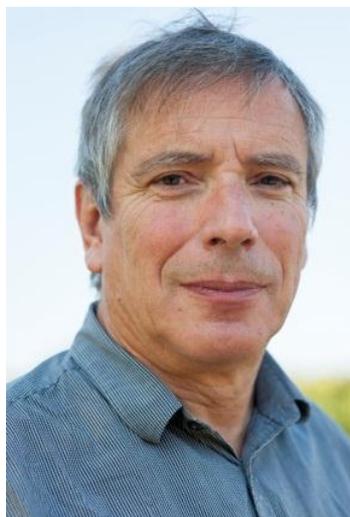
Roberto Tuberosa (University of Bologna -Italy)
Conference Vice- chair

François Tardieu (INRA, France)
Coordinator of EU-DROPS project and
President of the international scientific committee of the conference



Keynote speakers

François Tardieu - INRA, France



François Tardieu leads the Research Group "Analysis and modelling of the genotype x environment interaction" of LEPSE at INRA Montpellier. His group deals with the modelling of plant responses to environmental conditions, especially water deficit: stomatal control, leaf growth, root growth in relation with hydraulic and chemical signalling. Since 2000, he has developed an approach aiming at modelling the genetic variability of plant responses to environmental cues linked to climate changes, by combining ecophysiological modelling, high throughput phenotyping and genetic analyses. The group has developed novel phenotyping platforms for temporal analyses of growth, architecture and transpiration of hundreds of genotypes. He coordinates the UE project DROPS that links genetic analyses in the field and in phenotyping platforms via modelling, and the French National infrastructure of phenotyping (Phenome-FPPN)

Claude Welcker - INRA, France



Claude Welcker, plant breeder and geneticist, joined the LEPSE at INRA Montpellier in 2003 to develop a program at the interface between genetic and ecophysiology after having lead research on adaptation of maize to acid soils in the tropics (1992-2002).

His research topic is the analysis of the genetic control of growth under fluctuating conditions and its impact on grain yield in drought-prone environments and implication in breeding. He coordinates maize activities within the UE project DROPS that links genetic analyses in the field and in phenotyping platforms via modelling, and coordinates the work on drought tolerance in the PIA-ANR project Amaizing (including GWAS, functional genomics and field testing of historical series and novel genetic formula).

He is deputy director of Montpellier plant phenotyping platform (M3P).



Roberto Tuberosa - Università di Bologna, Italy

Roberto Tuberosa, Ph.D. from the University of Minnesota and Fellow of the Crop Science Society of America, teaches Plant Biotechnology Applied to Plant Breeding at the University of Bologna, Italy. He represents Europe in the Board of the International Crop Science Society (ICSS) and regularly serves as a member of review panels of research programs funded by the EU and EU countries. His research program focuses on genomics of resistance to drought and fungal diseases in durum wheat and maize. He coordinates the Italian Technological Platform "Plants for the Future" and collaborates with seed companies to improve durum wheat and maize yield via marker-assisted selection. He has published over 120 manuscripts in peer-reviewed journal and has edited 7 volumes. He has organized 8 international Congresses and has presented invited lectures at over 40 Congresses and workshops. Additional details are available at www.distagenomics.unibo.it.



Elias Fereres - Universidad de Cordoba, Spain

Professor of the University of Cordoba, Spain and researcher, Institute for Sustainable Agriculture, IAS-CSIC, Cordoba, Spain. Currently Chief Editor of the Irrigation Science Journal



Xavier Draye - Université Catholique de Louvain, Belgium

Professor at Université Catholique de Louvain and group leader at Earth and Life Institute. Our team originally focuses on the phenotyping (SmartRoot, RSML), modelling, physiology and genetics of root system architecture. We are currently collaborating with molecular biologists and soil hydrologists to design root system ideotypes for water deficit conditions based on concepts of the hydraulic architecture of the soil-plant system at various scales



Boris Parent - INRA, France

Currently working in the INRA-LEPSE laboratory (Montpellier, France), I am focusing in the analysis and modelling of the genetic variability of plant responses to water deficit and temperature in cereals.



David Jordan - University of Queensland, Australia

David Jordan is a Professor in plant breeding and genetics at the University of Queensland. He has 23 years experience as a sorghum breeder geneticist in both the public and private sectors. For the last decade he has led the public sorghum pre-breeding program in Australia.



Charlie Messina - Pioneer, USA

Charlie Messina is Senior Scientist with DuPont-Pioneer. He leads a Crop Physiology and modeling group that supports the development of maize products. His research focuses on understanding and using native and transgenic sources of genetic variation to improve drought tolerance in maize. His work contributed to the development of AQUAmax drought tolerant maize.



Bill Davies - Lancaster University, UK

Bill Davies developed his interest in plants when working on the family horticultural holding in Buckinghamshire, UK. He has a degree in Horticultural Science from Reading University and a PhD from Forestry and Botany from the University of Wisconsin, USA. For the whole of his professional career in the UK he has worked at Lancaster University, most recently in the Lancaster Environmental Centre. He has a general interest in interventions that might enhance global food security, while his research group focuses on understanding how crop plants cope with adverse environmental conditions. The focus of much work has been exploitation of novel understanding of plant hormone relations, both in crop improvement and crop management programmes, aimed at increasing crop yield as the climate changes.



François Chaumont - Université Catholique de Louvain, Belgium

François Chaumont is Professor at Institut des Sciences de la Vie Université catholique de Louvain.

François Chaumont studies the function and the regulation of plant aquaporins combining complementary approaches of molecular and cellular biology, biophysics and physiology. He has contributed to the isolation and characterization of a large number of different plant aquaporins



Yves Gibon - INRA, France

Yves Gibon has a PhD in Biology (1998, Rennes University, France) and an HDR (2007, Rennes University), has been postdoc at the Botanical Institute at Heidelberg University (1999-2001, Germany), then principal investigator at the Max Planck Institute of Molecular Plant Physiology (2001-2008, Golm, Germany). Directeur de Recherche at INRA-Bordeaux since 2008, he leads the Metabolism Team at BFP, which is interested in improving our understanding of metabolism, in particular the way it contributes to biomass production and quality.



Fred van Eeuwijk - Wageningen Universiteit, Netherlands

Fred van Eeuwijk is head of the Applied Statistics department of Wageningen University. His research focusses on statistical methods for GxE and QTL mapping. Two important characteristics of his work are the use of mixed models and the integration of statistical approaches to GxE with crop growth modelling approaches. He published more than 130 refereed papers. Currently, he is president of the Biometric Section of Eucarpia and chairman of the Scientific Programming Committee of the International Biometric Conference in Vancouver, July 2016. He is also editor of Genetics.



Delphine Fleury - ACPFG, Australia

She obtained her PhD in 2001 at the Plant Biotechnology Institute of Toulouse (INP-ENSAT, France). She constructed a genetic map of sunflower and identified QTL for resistance to a pathogen and for photosynthesis for two breeding companies (Maisadour and Caussade semences). She worked as a postdoctoral fellow with Mieke Van Lijsebettens at VIB in Ghent (Belgium) on a European collaborative project named DAGOLIGN. She cloned and analyzed the function of several genes involved in plant development of Arabidopsis.

In 2006, she joined the ACPFG working first on comparative genomics in wheat and barley, on an ARC international science linkage project associated to the EU project TriticeaeGenome. She runs now the forward genetics program aiming to improve the tolerance of wheat and barley to drought using quantitative genetics and omics data. Delphine worked as a consultant for Generation Challenge Program in 2011-2012 on the Integrated Breeding Platform. She is Genetics leader of ACPFG since 2012.



Professor Graeme Hammer - University of Queensland, Brisbane, Australia

Graeme is a Professor in Crop Science and Director of the Centre for Plant Science (CPS) in the Queensland Alliance for Agriculture and Food Innovation (QAAFI), which is a research institute of The University of Queensland, Australia.

Graeme conducts research on the physiology and genetics of complex adaptive traits in field crops with a focus on water productivity in cereals. His research underpins the development of mathematical models of crop growth, development and yield that enable simulation of consequences of genetic and management manipulation of crops in specific target environments. He has played a leading role in the design and on-going development of the APSIM crop modelling platform. He is a Fellow of the Australian Agriculture Institute and was awarded the Australian Medal for Agricultural Science in 2013 and Farrer Memorial Medal in 2012.



Adam Price - University of Aberdeen, UK

Adam Price is Professor of Plant Molecular genetics at the Institute of Biological and Environmental Sciences, University of Aberdeen. He has an educational background in biochemistry. He has been researching rice genetics for 24 years with an overriding interest in roots and plant-soil interactions which includes biotic interactions. An important additional area is elemental composition of grain, most specifically arsenic. Originally he worked mostly with the Bala x Azucena mapping population which I made in 1995 and more recently been exploiting association mapping using the Rice Diversity Panel and a population for NE India and Bangladesh which we are making ourselves. The latter involves contributing the global effort of rice genome sequencing.



Scott Chapman - CSIRO, Australia

Dr Chapman is a Senior Principal Research Scientist in the CSIRO Agriculture Flagship, and an Adjunct Professor with The University of Queensland. He works across the areas of plant science from genetics through physiology to breeding methodology and design to agronomy and climate analysis in order to provide insights and tools to help breeders and farmers. In recent years, he has also led projects to use UAVs to capture image and spectral data for in-season decision-making in breeding



Jean-Marcel Ribaut – GCP, Mexico

Director of the Generation Challenge Program (GCP). He is responsible for leading and coordinating a large network of partners in modern crop breeding for food security. Jean-Marcel has cumulative experience in agriculture biotechnology and plant breeding, project and finance management and policy formulation, as well as leadership skills for dispersed global R&D teams. Since December 2014 Jean-Marcel is the Director of the Integrated Breeding Platform: <https://www.integratedbreeding.net>

Jean-Marcel holds a PhD in Plant Physiology from Lausanne University, Switzerland. His scientific background is in plant physiology and genetics, with main research interest being understanding the genetic basis and underlying physiological and metabolic pathways that influence plant performance under abiotic stress– particularly drought – as well as innovations in molecular breeding.



Alain Murigneux - Limagrain Europe, France

Head of Marker assisted Selection with Limagrain Europe from 1991 to 1999; Head of Maize and Wheat Genomics with Biogemma from 1999 to 2008. Since 2011, he is Head of Native Trait in the Field seeds Division of Limagrain Europe.

He has worked in the development of improved varieties in Maize, wheat, Rape Seed of varieties with improved traits of agronomic interest: Drought tolerance – Nitrogen Use Efficiency; the development of a portfolio of breeding projects in Maize and Wheat to increase genetic diversity in the breeders germplasm but also in building and implementing Genomic activities within Biogemma/Limagrain and coordinating the French national effort (Genoplante)



Javier Betrán - Syngenta, France

Head of Corn Breeding EAME. Syngenta Seeds. Javier has a Ph.D. in plant breeding from Iowa State University. He is currently the Head of the Maize Breeding Europe, Africa and Middle East for Syngenta. Before he was professor at Texas A&M University in the US and scientist at CIMMYT. He is interested in plant breeding, quantitative genetics, biotechnology, environment, abiotic and biotic stresses, and people development. He has collaborated with international organizations like the Rockefeller Foundation, CGIAR centers and private consortiums. As R&D lead, he has developed research and development teams internationally and manage R&D portfolio fostering innovation and new technologies.



Mark Cooper - Pioneer, USA

Mark Cooper leads a team responsible for maize product development research utilizing transgenic and native sources of genetic diversity. The research spans understanding the genetic architecture of drought tolerance, application of molecular breeding using native and transgenic diversity and precision phenotyping technologies to develop hybrids with improved yield, stress tolerance and agronomics. The team enabled the delivery of the DuPont-Pioneer Optimum AQUAmax® line of drought tolerant maize hybrids.



Björn Usadel - University Aachen, Germany

Full Professor since 2011, joined RWTH after having led a research group at the Max Planck Institute of Molecular Plant Physiology between 2008 and 2011. He additionally holds a position as a director in the research center Jülich and is leader of the German Plant Primary Database and PI in the German Bioinformatics infrastructure network (de.NBI). His research topics are analysis and storage of large data sets as well as cell walls and carbon metabolism. He has published more than 85 ISI papers, has an (ISI) h-factor of 39 and has been named an ISI highly cited researcher in Plant and Animal Sciences. He leads the WP4 Data Analysis and Integration of DROPS



Session 1: Coping with drought in crop improvement: a global perspective

Keynote speaker

The Nature and Patterns of Agricultural Drought in Europe

E. Fereres and F. J. Villalobos

*Institute for Sustainable Agriculture (IAS-CSIC) and University of Cordoba,
Cordoba Spain.*

ag1fecae@uco.es

Drought is an unusual water scarcity that occurs periodically in most regions of the Planet. It is not a major feature of the overall European climate, as the area affected by drought varies widely among years between 3 and 30% of the total EU27 area. Over the last decade, about 15% of Europe has been affected by drought, but this figure masks strong spatial and temporal variations. While Southern Europe experiences frequent droughts of significant intensity and duration, Northern Europe is hardly affected by drought, and Central Europe has periodic events of variable duration. The impacts of drought on European agriculture will be documented using studies of recent droughts. Accurate seasonal rainfall predictions are crucial for strategic decisions in farming that would greatly assist in coping with drought, and advances in this area are badly needed. There is a panoply of genetic and management options to mitigate the impacts of drought on rain fed agriculture of variable relevance. Many of them have been explored in the past but there are some areas that deserve new attention, based on advances in simulation modelling and in plant breeding. In the current global warming trend, the combination of absence of rainfall with hot spells is particularly dangerous for crop production in Europe and needs to be examined in detail. Although the relations between climate and hydrological variability are complex and not fully understood, many biophysical and socio-economic indicators suggest that drought will be an increasingly important threat to European agriculture in the future.



Keynote speaker

DROPS, a multi-scale, multi environment project on drought tolerance

Tardieu F¹, Cané, MA², Draye X³, Charcosset⁴, Hammer GL⁵, Fleury D⁶ Tuberosa R², Usadel B⁷, Welcker C¹

1 INRA, Montpellier France, 2 Unibo Italia 3 U.C. Louvain Belgium, 4 INRA Le Moulon France, 5 U. Queensland Australia, 6 ACPFG, Australia, 7 Aachen U, Germany

francois.tardieu@supagro.inra.fr

DROPS develops novel methods and genetic strategies aimed at yield improvement under water deficit, based on the premise that drought tolerance and water-use efficiency have a high genotype x environment interaction (any trait can have positive, negative or no effect depending on the drought scenario). It uses a knowledge-based approach involving the modeling of plant performance in environmental scenarios representing current or future European climates. DROPS involves specialists of several disciplines (physiology, modeling, genetics, statistics, breeding) of 11 public research groups in Europe and Australia, and of 5 seed companies. The project focuses on four key traits, namely seed abortion rate and vegetative growth maintenance in dry conditions, root system architecture and transpiration efficiency in maize, bread wheat and durum wheat. The main goals are :

- To develop indicators that (i) are stable characteristics of genotypes, (ii) characterize the sensitivity of genotypes to water deficit, (iii) are genetically related to the four target traits and (iv) allow prediction of plant performance in the field via simulation models. These indicators are based on the progress in understanding of the physiological bases of responses of target traits to water deficit. They involve trait-specific phenotyping platforms in controlled condition, omic platforms and a network of field experiments across Europe.
- To explore the allelic variation of the four target traits by identifying genomic regions that control them in diverse drought scenarios. We aim at (i) linking these traits to physiological pathways, genes or genomic regions, (ii) assessing the effects of allelic diversity on the four target traits and on their responses to environmental conditions. Panels of lines (durum and bread wheat) or hybrids (maize) have been evaluated in phenotyping platforms and in field experiments. Association genetics is based on a dense genotyping (e.g. 500,000 SNP markers in maize) and involves phenotypic data in fields and platforms, including variables determined by model-assisted phenotyping.



- To support crop improvement strategies by estimating the comparative advantages of relevant combinations of alleles under contrasting drought scenarios in Europe. This is performed by (i) developing a generic crop model incorporating novel understanding of the physiology and genetics of the four target traits, and enabling us to estimate the effects of alleles affecting these traits on crop growth, yield and water-use efficiency, (ii) simulating yields of genotypes that differ by traits or alleles at specific loci, over the variability of drought scenarios occurring across Europe.

A dedicated information system secures and gives access to the whole dataset of DROPS. It includes tools for assessing the validity of phenotypic measurements and for relating them with environmental variables. This allows joint analysis of (i) all phenotypic data (field and platforms) together with environmental conditions, and (ii) phenotypic and genotypic data for genetic analyses, essentially association genetics. After publication, data will be made available to the whole academic community.



Session 2: Traits-base strategies for dealing with drought

Keynote speaker

Root traits beyond architecture

Draye X, Orman B, Ligeza A, Faget M, Meunier F, Couvreur V, Javaux M

Université catholique de Louvain, Belgium

xavier.draye@uclouvain.be

Increasing attention is being devoted to root system architecture (RSA) for the improvement of drought tolerance. The focus is generally set on deep roots, expected to grant access to soil water resources during water deficit episodes. Surprisingly, our quantitative understanding of the role of RSA in the uptake of soil water remains limited, which is mainly due to the complexity of the soil-plant continuum. However, although soil and roots consist of very different media, understanding the distribution of water uptake is a matter of quantifying resistances and gradients of water potential in a common spatial and highly dynamic framework. There are therefore several reasons to adopt a fine-grained 3D modelling approach to explore how the interplay between RSA, root and soil hydraulics determines water uptake patterns.

Using such quantitative models coupling the hydraulic behaviour of soil and roots in an explicit 3D framework, we show that the contribution of RSA to root water uptake is hardly separable from the hydraulic properties of the roots and of the soil. Simulations have been run in which major attributes of the soil/plant system thought to influence water uptake and its spatial distribution have been varied separately: the soil hydraulic conductivity (K_s), the root hydraulic conductivities (K_r and K_x , respectively radial and axial) and the root architecture. These simulations indicate that the soil hydraulic properties impact the spatial distribution of the root uptake term and therefore the distribution of soil hydraulic gradients over a wide range of soil water potential. They show that it is difficult to analyze the effect of soil hydraulic conductivity without taking into account the geometric configuration of water flows from the bulk soil to the rhizospheric compartments, which depend heavily on root system architecture.

The contribution of hydraulic architecture was analysed with the same model by varying the ratio of the radial to axial conductivities. Under a small ratio, the



water potential gradient in the xylem is expected to be very small and water tends to be taken up everywhere in the profile. If the radial conductivity is larger than the soil conductivity, water is then taken up as a function of the soil water distribution. Under a high ratio, the xylem limits the water flow through the root system and important water potential gradients build up in the xylem. In this case, the water is preferably extracted from the upper layers where large gradients between soil and roots develop and where root xylem conductance is high enough to transfer water to the collar. We are currently dissecting *in silico* the radial hydraulic conductivity of a root segment as a function of its anatomy and of patterns of aquaporin expression.

Making these models compatible with crop growth models is under way and will help explore how water fluxes driven by soil and plant processes affect soil water availability and uptake *throughout a growth cycle*.

The conclusion that local soil and roots properties significantly affect whole plant patterns of water uptake calls for a better consideration of rhizosphere processes and root plasticity (e.g. hydropatterning) in the design of root ideotypes for water-limited environments.



Selected talk

Quantitative imaging of root water uptake

Mohsen Zarebanadkouki, Mutez A. Ahmed, Eva Kroener, Andrea Carminati

Division of Soil Hydrology, Georg-August University of Göttingen, Germany

mzareba@gwdg.de

Better understanding of root water uptake could help to optimize irrigation and identify optimal traits for the capture of water from the soil, in particular under dry condition. Our study aimed to develop a new non-destructive method to measure the local fluxes of water in roots and to estimate the axial and radial conductivities of different root segments.

We used neutron radiography to trace the transport of deuterated water (D2O) into roots. The radiographs showed that the radial transport of D2O from soil to roots depended similarly on diffusive and convective transport, while the transport of D2O along the root xylem was largely dominated by convection.

To quantify the convective fluxes from the radiographs, we introduced a numerical convection-diffusion model of D2O transport. The model takes into account different pathways of water across the root tissue and the endodermis as a layer with distinct properties. Water uptake by branching roots, such as laterals or root hairs, is included as a sink term into the xylem. The diffusion coefficients of the root segments were inversely estimated by simulating the experiments at night under the assumption that convection was negligible. Inverse modeling of the experiment at day gave the water fluxes into the roots.

We applied the method to lupine and maize. In 4-weeks-old lupines, root water uptake was higher in the proximal parts of lateral roots and decreased toward the distal parts. The function of the tap root was to collect water from laterals and transport it to the shoot. Similarly, in 2-weeks-old maize water uptake was higher in lateral roots, while the uptake of distal, unbranched segments of seminal and primary roots was small. Based on the measured fluxes and using a 3D model of water uptake we estimate the axial and radial conductivities of the different root segment.

Keywords: Root water uptake, Maize, Lupine, Diffusion convection model.



Selected talk

Linkage mapping for root system architecture in durum wheat

Ghasemali Nazemi^{1,2}, *Marco Maccaferri*², *Roberto Tuberosa*², *Silvio Salvi*²

¹ *Department of Agriculture, Haji abad Branch, Islamic Azad University, Haji abad, Iran;*

² *Department of Agricultural Sciences (DipSA), University of Bologna, Viale Fanin 44, 40127 Bologna, Italy*

nazemigh@gmail.com

Root system architecture (RSA) is of great agronomic importance and it has emerged in recent years as an important focus for plant genetics and breeding study. The genetic basis of variation for RSA traits were investigated using a population of 176 recombinant inbred lines (RILs) derived from the cross between two Italian elite durum wheat cvs. Meridiana and Claudio, in order to identify QTLs for RSA and compare their overlaps with other QTLs identified in other experiments and environments. The following seedling-stage RSA and seed traits were: seminal root angle, primary root length, total root length, root number, thousand kernel weight, shoot length, root and shoot dry weight. The results indicated a wide range of variation for RSA traits. The largest heritability was observed for thousand kernel weight (78.6%) and seminal root angle (65.4%). In total, 48 novel QTLs for RSA traits were identified on all chromosomes, with the exception of chromosome 4A. Both parents contributed favorable alleles at QTLs. Among the considered RSA traits, seminal root angle appears the most promising for undertaking further studies on the role of RSA traits. The most important QTLs for seminal root angle identified in this study mapped on chromosomes 4B and 6B.

Keywords: Durum wheat, Root system architecture, QTL, Linkage mapping



Keynote speaker

Control of expansive growth in water deficit: from phenotyping to field simulations.

Boris Parent^{1,2}, Llorenç Cabrera¹, Maria Angela Cané³, François Chaumont⁴, Santiago Alvarez-Prado¹, Cecilio Caldeira¹, Sebastien Lacube¹, Delphine Fleury², Claude Welcker¹, Roberto Tuberosa³ and François Tardieu¹

¹ **INRA, LEPSE, Montpellier, France,**

² **ACPGF, Adelaide, SA, Australia;**

³ **UNIBO, Bologna, Italy,**

⁴ **Université Catholique de Louvain, Louvain-la-Neuve, Belgium**

boris.parent@supagro.inra.fr

Maintenance of expansive growth under water deficit has been selected as a key target trait of DROPS because of its early response in drying conditions, its large genetic variability, its partially common control with reproductive growth and its consequences on light interception and transpiration.

Development of methods to measure shoot growth in Phenotyping platforms (PhenoArch and Phenodyn, M3P, Montpellier, France; The Plant Accelerator, Adelaide, Australia) allowed identification of a large genetic variability in maize, wheat and durum wheat. Three-D characterization of individual plant architecture and of the spatial distribution of light in phenotyping platforms allowed calculation of light interception and of Radiation Use Efficiency (RUE) of hundreds of genotypes. Measurements of leaf elongation rate with a temporal definition of a few minutes allowed comparison of time courses of growth and of physiological variables that are candidate for the control of expansive growth. Overall, these methods resulted in progress in physiological understanding and in dozens of QTLs identified for shoot growth in bread wheat and maize, peduncle in durum wheat, RUE, transpiration and phenology in all three species.

The importance of hydraulics in the control of leaf expansion rate (LER) has been demonstrated. Changes in LER occurred over a few minutes upon changes in evaporative demand and soil water status. LER also varied with circadian-driven changes in plant hydraulic conductance in continuous light. Rapid changes of LER with water deficit and evaporative demand are due to stomatal movements and changes in hydraulic conductivity related to aquaporin Plasma Membrane Intrinsic Proteins (PIPs). Both PIP expression and plant hydraulic conductance rapidly changed with environmental conditions and with the circadian clock. In addition to its value, this result was essential to establish a protocol for



comparing transcript amounts of PIPs in genotypes of the maize panel (eQTLs). A large genetic variability has been observed for the progression of shoot development (phyllochron), for whole-plant leaf growth and for their responses to water deficit. Accurate QTLs have been identified for each of these variables, which are compared with the positions of QTLs of PIP transcript amounts, and of accumulation of abscisic acid and of metabolites in the leaf. This will result in new insights on the control of growth under water deficit.

The position of QTLs of growth in response to drought has been compared to the positions of QTLs of yield in the field in the three species. In addition, the effects of introgressed genomic regions have been analyzed on the growth of several organs (leaf, peduncle, roots) and on yield of durum wheat and maize. The analysis of impact on yield of growth QTLs is based on collocation of QTLs between platforms and fields, and on a model for scaling up the effects of growth in the field. We have designed for that a model of shoot development that takes into account the responses of individual leaves to water deficit and evaporative demand, with parameters that are measured in a phenotyping platform for all genotypes of the panels. The model is incorporated into the crop model APSIM-maize, for estimation of the effect of QTLs of leaf growth on crop yield in hundreds of climatic scenarios, current or future.

Overall, (i) the development of new methods and screen for expansive growth of wheat and maize in phenotyping platform resulted in the (ii) determination of mechanistic and genetic determinisms of plant response to drought and evaporative demand and (iii) the simulation of its effects on crop production in different climatic scenarios.



Selected talk

Using modelling and GWAS for the phenotypic and genetic dissection of a complex trait, toward ideotype exploration : Case of rice early vigor response to drought

Delphine Luquet ¹, Maria Camila Rebolledo ², Jean Christophe Soulié ¹, Brigitte Courtois ¹, Michael Dingkuhna ³

**¹ CIRAD, UMR AGAP
F-34398 Montpellier, France**

luquet@cirad.fr, soulie@cirad.fr, courtois@cirad.fr, dingkuhn@cirad.fr,

² CIAT, Agrobiodiversity

AA 6713, Cali Colombia - m.c.rebolledo@cgiar.org

**³ IRRI, CESD Division
DAPO Box 7777, Metro Manila, Philippines**

By formalizing elemental traits, their compensations and their genetic variability, crop modelling can support the phenotypic and genetic dissection of complex agronomic traits. It can accordingly be used to predict optimal trait combinations and theoretical margin for genetic improvement for a given environment (Cooper et al. 2014). The present study aims to develop and provide a proof of concept of such modelling approach applied to the case of rice early vigor and its response to drought. The plant growth model Ecomeristem (Luquet et al. 2012) was heuristically parameterized for each of 136 accessions constituting a japonica rice diversity panel, using phenotypic data acquired in a greenhouse at IRRI under two water conditions (well-watered vs. dry-down, Rebolledo et al. 2013).

Model parameters controlling leaf morphogenesis, transpiration rate, light conversion efficiency and their drought regulation, were in silico recombined within the range explored by the 136 accessions in order to generate a virtual population of 9000 individuals. Simulations of real and virtual phenotypes under three water treatments pointed out strong and similar tradeoffs between constitutive vigor and drought tolerance, estimated as shoot growth maintenance. A substantial margin for potential genetic improvement of vigor and drought resistance was however pointed out, depending respectively on parameter related to C sink strength and water or light use efficiency (Luquet et al., in press). These results are theoretical as they rely on the prediction of phenotypes from virtual genotypes, based on simple modelling (particularly on gas exchange) and genetic (free, additive trait combinability) assumptions. However they provide further insight into the way genetic and physiological information should be further combined into models toward ideotype exploration. This will be discussed with respect to the results of the Genome Wide Association Study recently performed using 12,221 single-nucleotide polymorphisms and model parameters estimated for the abovementioned 136 rice accessions.

Keywords: Model assisted phenotyping, C source-sink regulation, genetic diversity, heuristics



Keynote speaker

Modeling kernel abortion in maize

Charlie Messina¹, Graeme Hammer², Francois Tardieu³, Greg McLean⁴, Scott Chapman⁵, Erik van Oosterom², Jeff Schussler¹, Mark Cooper¹

¹ **DuPont-Pioneer, 7250 NW 62nd Avenue, PO Box 552, Johnston, IA 50131, USA**

² **The University of Queensland, Queensland Alliance for Agriculture and Food Innovation, Brisbane, QLD 4072, Australia.**

³ **INRA, UMR759 - Laboratoire d'Ecophysiologie des Plantes sous Stress Environnementaux. 20 Place Viala, F-34060 Montpellier, France**

⁴ **Department of Agriculture and Forestry, Toowoomba, QLD 4350, Australia.**

⁵ **CSIRO Plant Industry, Queensland Biosciences Precinct, 306 Carmody Rd, St Lucia, QLD 4067, Australia**

charlie.messina@pioneer.com

Drought stress is ubiquitous in maize production environments. Its impact on maize production and physiology has been studied in depth, in particular at flowering time. However, a quantitative synthesis in the form of a simulation model that can be applied to enable genetic improvement for maize is lacking. We present a model to simulate reproductive processes that affect kernel determination in maize and its response to drought stress. Results from exercising the model demonstrate it can generate emergent properties and functional mathematical relations that were previously utilized to model kernel number, recapitulate historical breeding trends, discriminate among elite commercial hybrids for levels of tolerance to drought stress and provide a framework to interpret reproductive failure in maize. The model provides an advanced framework that can inform phenotyping strategies targeted to investigate the genetic architecture of traits that contribute to improved drought tolerance, and can inform decisions on how best to use diverse sources of genetic variation to develop new maize products.



Selected talk

Grain abortion and yield stability under drought: a key role for growth processes in reproductive organs

Olivier Turc, Vincent Oury, François Tardieu

**INRA LEPSE
2 place Viala 34060 Montpellier, France**

olivier.turc@supagro.inra.fr

Yield maintenance under drought in maize (*Zea mays*) is associated to flowering synchrony which requires the rapid extension of styles and stigma (silks) to be accessible for pollen. Most analyses of the control of grain abortion in maize conclude that abortion is linked to a carbon shortage in ovaries, but they have been performed with a common protocol avoiding the impact of water deficit on silk growth. A series of recent works attempt to reconcile the developmental view that abortion is due to the timing of silk growth, with the molecular view that abortion is linked to the sugar metabolism in ovaries. They analyse expansive growth, transcript abundances, concentrations/amounts of sugars and enzyme activities in silks and ovaries located at different positions along the ear. A switch to abortion occurs 2-3d after first silk emergence in water-stressed plants, when silk growth stops simultaneously for all ovary cohorts, and explains abortion rates in different treatments and positions on the ear. The metabolic analysis supports the view that the first molecular events occur in silks rather than in ovaries, and involve genes affecting expansive growth rather than sugar metabolism. Sugar availability is preserved in ovaries until the switch to abortion, and the disruption of carbon metabolism only occurs after this switch. Hence, changes in metabolite contents, transcript amounts and enzyme activities involved in ovary sugar metabolism would be a consequence rather than a cause of the beginning of ovary abortion. Patterns of silk growth responses to environment share common features with those of leaf growth and suggest that both physiological and genetic controls under drought involve mechanisms associated to cell wall properties and water entry into growing cells, rather than carbon metabolism. Those findings have large consequences for breeding drought tolerant maize, and for modelling grain yields in water deficit.

Keywords: maize, water deficit, silk growth, ovary abortion, carbon metabolism



Selected talk

Predicting maize kernel number using genetic information

Agustina Amelonga¹, Brenda L. Gambín², Lucas Borrás³

*Facultad de Ciencias Agrarias, Universidad Nacional de Rosario
Campo Experimental Villarino S/N, Zavalla S2125ZAA, Santa Fe, Argentina*

¹ *agusamelong@gmail.com*

² *bgambin@unr.edu.ar*

³ *lborras@unr.edu.ar*

Most maize yield variations are explained by changes in the number of established kernels. Kernel number is dependent upon ear biomass accumulation around flowering. Both are quantitative traits highly influenced by the environment. Determining the genetic basis of quantitative traits is complex because of genetic \times environment interactions (G \times E). Crop physiology models are proposed to help overcome this problem, as they are structured to predict G \times E interactions based on dynamic responses. In our previous work (Amelong et al., 2015) we studied the genetic basis of maize kernel number determination by conducting two quantitative trait loci (QTL) analysis: (i) on final traits per se (kernel number per plant, KNP, and ear biomass, EB) and (ii) on specific model parameters of well documented curves describing KNP and EB response to plant growth around flowering.

Our objective was to predict EB and KNP based on QTL information. QTL information of model parameters helped predict accumulated EB and KNP with higher accuracy ($r^2 = 0.13$ and 0.12 , $n=207$, $p < 0.001$, for EB and KNP, respectively) than trying to predict EB and KNP based on QTL information from final traits per se ($r^2 = 0.01$ and 0.01 , $n=207$, $p > 0.10$, for EB and KNP, respectively). However, all predictions showed very low accuracy. At present we are evaluating if using genotype specific information of model parameters estimated with genomic predictions can provide better estimations. Preliminary results indicate higher prediction accuracies when using genomic predictions for our crop physiology model parameters ($r^2 = 0.43$ and 0.36 , $n=207$, $p < 0.001$, for EB and KNP, respectively). Genetic information helped predict KNP at different environments with different accuracies depending on the approach, although overall accuracies were all quite low.

Keywords: modeling, crop physiology, Zea mays, QTL, genomic prediction



Keynote speaker

Genotypic variation in water use efficiency and related physiological traits

William J. Davies, Arnauld A. Thiry and Ian C Dodd

The Lancaster Environment Centre, Lancaster University, Bailrigg, Lancaster, LA1 4YQ, UK

w.davies@lancaster.ac.uk

A faster selection of genotypes resistant to and productive under abiotic stress is needed if agriculture is to cope with global warming and the increase in food demand by a growing world population. Here we discuss screening for water use efficiency at various scales and the identification of related traits that might be useful in phenotyping for stress resilience. Variation in hormone balances that impact gas exchange and the development of both vegetative and reproductive plant parts is considered. We also discuss a new method for evaluation of genotypes in terms of their resilience to drought stress and their production capacity. The method, based on a combination of previously-discussed stress indices, offers the possibility of identification of new physiological traits that can be associated with different drought tolerance mechanisms.



Selected talk

High resolution mapping of traits related to whole-plant transpiration under increasing evaporative demand in wheat

Rémy Schoppach¹, Julian D Taylor², Elisabeth Majerus¹, Elodie Claverie², Beata Sznajder³, Delphine Fleury³, Walid Sadok¹

¹ **Stress Agronomy Group, Earth and Life Institute, Université catholique de Louvain, Croix du Sud 2, L7.05.14, 1348 Louvain-la-Neuve, Belgium.**

² **School of Agriculture, Food and Wine, Waite Research Institute, The University of Adelaide, PMB 1, Glen Osmond, South Australia SA 5064, Australia.**

³ **Australian Centre for Plant Functional Genomics (ACPGF), The University of Adelaide, PMB 1, Glen Osmond, SA 5064, Australia.**

walid.sadok@uclouvain.be

Atmospheric vapor pressure deficit is a key component of drought and strongly influences yields (Sinclair et al. 2005). Whole plant transpiration (TR) sensitivity to vapor pressure deficit (VPD) has been linked to better yield performance under drought in wheat (Schoppach and Sadok 2012), but the genetic basis of this sensitivity remained unexplored. Further, the genetic control of other key traits potentially linked to daytime TR such as nighttime TR, whole plant leaf area, whole plant specific leaf area and abaxial/adaxial stomata densities remains unknown. Considering the presence of phenology genes that often interfere with drought tolerance in wheat (e.g., Foulkes et al. 2004) and the often too low resolution of genetic maps, the aim of this investigation was to identify the genetic basis of the above key traits at a high genetic resolution while taking into account the effects of phenology related genes Ppd-D1 and Ppd-B1. Virtually all traits were highly heritable (heritabilities from 0.61 to 0.91) and the genetic analysis revealed a total of 68 QTL the majority of which were trait-specific with peaks located in regions covering less than 0.5 cM. Six QTL were detected for TR sensitivity to VPD, collectively explaining 83.4% of the genetic variance. One of these (QSLP.ucl-5A) explained 25.4% of the genetic variance and harbors several genes involved in drought tolerance. Nocturnal TR and abaxial/ adaxial stomata densities were characterized by different and robust QTL, indicating that they have a physiological role that was not discarded by wheat domestication. The traits were also intercorrelated genetically and phenotypically while being influenced differentially by Ppd-D1 and Ppd-B1, shaping drought tolerance strategies that depend more subtly on phenology and development than previously thought. The study will be useful in identifying molecular mechanisms that underlie drought tolerance strategies operating over the course the entire crop cycle in wheat.

Keywords: vapor pressure deficit, stomata, leaf area, QTL, drought



Keynote speaker

Aquaporins: physiological roles and variability

François Chaumont

Institut des Sciences de la Vie, Université catholique de Louvain, Croix du sud 4-L7.07.14, 1348 Louvain-la-Neuve, Belgium

francois.chaumont@uclouvain.be

Maize (*Zea mays*) is a major crop for which drought poses a crucial problem, and it has been used as a paradigm for water relations at physiological level. Water diffusion across cell membranes is facilitated by aquaporins that provide plants with the means to rapidly and reversibly modify water permeability (Chaumont and Tyerman, 2014). Our laboratory is studying the function and regulation of maize plasma membrane aquaporins (PIPs, plasma membrane intrinsic proteins) which control cellular water movement in many different physiological processes. Using molecular and biophysical approaches, we showed that the expression and activity of PIP aquaporins are regulated in maize roots, leaves and stomatal complexes according to the developmental stages, day and night cycle and/or in response to osmotic, nitrogen or salt stress.

In the frame of the European DROPS project, we quantified the mRNA levels of 12 PIP aquaporins in the leaf elongation and mature zones from 30 maize genotypes grown in well watered and water deficit conditions. Data indicate an important variability of PIP expression levels according to the isoforms, leaf zones, genotypes and growing conditions. These expression data are currently analyzed together with different physiological parameters including biomass, water use efficiency and transpiration to evaluate the contribution of specific aquaporins in the natural variation of these traits.

Keywords: Aquaporins, Maize, Plasma membrane intrinsic proteins, Variability, Water relations,



Keynote speaker

Investigating drought resistance using metabolic phenotyping

Duyên Prodhomme^{1 2}, Daniel Jacob^{1 2}, Stéphane Bernillon^{1 2}, Catherine Deborde^{1 2}, Annick Moing^{1 2} and Yves Gibon^{1 2},

**¹ UMR1332 Fruit Biology & Pathology
INRA & Bordeaux University, France
yves.gibon@bordeaux.inra.fr**

**² Bordeaux Metabolome Platform
INRA & Bordeaux University, France
amoing@bordeaux.inra.fr**

Metabolomics have emerged as a powerful tool able to diagnose a range of diseases in humans, in particular cancer, which can be detected earlier than with any other technology (Righi et al., 2015). In plants, evidence is also emerging that the metabolome, which represents highly integrated information at the cellular level, can be used to predict plant performance (Steinfath et al., 2010). Central metabolism includes the pathways generating, using and interconverting major carbohydrates and amino acids that are necessary for biomass production. A recent study has shown that levels of central metabolites are determined by genetic variation in C4-metabolism genes that could be useful for breeding (Zhang et al., in press). In DROPS we hypothesised that levels of central metabolites and related enzymes activities could also be used as markers for plant performance under stress. Taking advantage of a recently established platform enabling high throughput measurement of a range of major metabolic traits we investigated seed abortion and leaf metabolism. A subset of maize hybrids of the DROPS panel was used to search for ear metabolic traits that would be associated with grain yield. We found significant differences between genotypes for several metabolites and enzyme activities (difference between tip and basis of the ear, response to water stress) measured in ears at silk emergence. We then found that some of these traits are potentially associated to yield. Leaf samples taken from plants of the full maize DROPS panel growing under optimal or water-limited conditions in an automated greenhouse (PhenoArch, Montpellier) were analysed in order to search for associations between metabolic profiles and resistance to water stress. So far, we identified 3 metabolic strategies related to N-assimilation and C-use that could also be associated to yield.

Keywords: ears, leaves, metabolism, metabolic phenotyping, yield



Poster Session 3: Variation for target traits and phenotyping methods

Short talk

Genotypic variability of maize growth and developmental traits under semi-controlled conditions

Alvarez Prado S¹, Grau A¹, Cabrera-Bosquet LI¹, Welcker C¹, Tardieu F¹

¹ INRA, UMR 759, LEPSE

2 Place Pierre Viala, Montpellier 34060, France

santiago.alvarez-prado@supagro.inra.fr; grau@supagro.inra.fr

cabrera@supagro.inra.fr; welcker@supagro.inra.fr; francois.tardieu@supagro.inra.fr

DROPS develop strategies for yield improvement under dry environments and for enhanced plant water-use efficiency. An association panel of 255 maize hybrids was genotyped with 50K and 600K chips of Single Nucleotide Polymorphism (SNPs) and phenotyped in a network of fields, in platforms and via omic data. In particular, three experiments with two water treatments were carried out in the phenotyping platform PhenoArch to assist those in the field in view of possible confusions of effects in the field. Hybrids were characterized via the progression of phenological stages (phyllochron), those of leaf area, plant height and plant volume dynamics, and finally metabolites concentrations and aquaporin activity at key developmental stages. Phyllochron ranged from 0.19 to 0.26 leaves per day at 20°C, plant height ranged from 705 to 1756 cm, leaf area from 0.13 to 0.54 m² and plant fresh weight from 117 to 577 g. All traits showed high heritability values along the vegetative phase ($H^2 = 0.60-0.91$). Variations in plant volume were closely and positively related to changes in plant evapotranspiration in all situations. Genotypic variability for water use efficiency ranged from 34.6 to 73.4 g FW/l and from 40.3 to 64.9 g FW/l for well-watered and water deficit scenarios, respectively. Plant growth traits were linked to alleles of genes through Genome Wide Association Studies (GWAS). Significant SNP were detected for all traits in all situations showing several SNP co-location for phenotypically correlated traits. The results will be useful to (i) assist field experiments, in particular for the timing of plant development, (ii) compare QTLs in the field and in the platform and (iii) modelling for selecting specific genotypes for drought scenarios : several variables measured in the platform can serve as parameters of a crop model.

Keywords: maize, growth traits, SNPs, water use efficiency, phenotyping platform.



Short talk

PhénoField®, a high-throughput phenotyping PHENOME (FPPN) platform

***Katia Beauchene, Alain Bouthier, Benoit De Solan, Jean-Charles Deswarte,
Yann Flodrops, Antoine Fournier, David Gouache, Josiane Lorgeou, Benoit
Piquemal, Samuel Thomas***

***ARVALIS, Institut du vegetal ;
45, voie Romaine 41240 Ouzouer le MarchéOuzouer-le-marché, France
Station expérimentale 91720 Boigneville, France
Route de Châteaufort, ZA des graviers, 91190 VILLIERS LE BACLE, France
228 Route de l'aérodrome, 84914 Avignon, FranceAvignon, France
Domaine du Magneraud, 17700 St Pierre d'Amilly, France***

k.beauchene@arvalisinstitutduvegetal.fr

Drought is projected to be an increasing problem for crops in France and evaluating drought tolerance is a complex task. Using rain-out shelters, PhénoField®, the ARVALIS platform of PHENOME project (French Plant Phenotyping Network) can control drought stress condition in field with high capacity for housing large genotype panels. Using a suite of validated and novel sensors, we propose frequent and non-destructive measurement of canopy to understand what the physiology behind drought tolerance is. We present the PhénoField® Platform as a key element for deep characterisation of germplasm, evaluation of technology sensors, and tool for quantitative genetics.

Around PhénoField®, an ecosystem of expert researchers in agronomy, crop physiology, robotics, biophysics, bio-informatics make possible to:

- Cultivate the major field crop species properly in the platform
- Estimate soil water holding capacity at microplot level
- Propose adapted experimental designs
- Control and calibrate sensors
- Analyze sensor data to provide physiological/agronomic indicators
- Connect environmental, soil and plant canopy data
- Model relations between plant and environmental factors to extract complex traits

To date, we provide frequent, rapid, non-destructive measurements of:

- Canopy architecture
- Leaf area expansive growth
- Senescence
- Radiation Use Efficiency (RUE)
- Water Use Efficiency (WUE)

Factors targeting climate change adaptation requires an integration of multiple tools. We combine in PhénoField® controlled environments and environmental sensors with high-throughput phenotyping capacity in a fully implemented data analysis pipeline. That's why, PhénoField® house in 2015 a corn field trial for AMAIZING and for 2016 a wheat field trial for BREEDWHEAT project.

Keywords: High-throughput Phenotyping, rain-out shelters, dynamics measurements, sensors



Short talk

Genetic architecture of water use efficiency in grapevine: a key role for night transpiration

**Aude COUPEL-LEDRU¹, Eric LEBON¹, Angélique CHRISTOPHE¹, Agnès DOLIGEZ²
& Thierry SIMONNEAU¹**

**1 UMR LEPSE,
2 UMR AGAP,
2 Place Viala, F-34060 Montpellier, France**

aude.coupel-ledru@supagro.inra.fr

Improving water use efficiency (WUE, the balance between biomass production and water costs) in crops becomes crucial to match increasing needs for food in a context of global change. Reduction of water loss at night could be a good strategy to limit waste of water without altering photosynthesis rate in the daytime. However, genetic and physiological bases of night transpiration and its contribution to WUE remain poorly documented. This study first aimed at deciphering the genetic determinants of WUE in grapevine, a woody crop of economic importance in drought prone areas. It further explored a possible role for night transpiration in WUE variability. A four-year experiment was run on a F1 progeny from a cross between Shiraz and Grenache. A greenhouse phenotyping facility (PhenoArch, Montpellier) was used to dissect determinants of WUE in potted plants and results were compared to those obtained in vineyard conditions under two soil water regimes. In PhenoArch, a high genetic variability was found and QTLs were detected for whole plant WUE under both watering regimes. Interestingly, these QTLs co-localized with those found for proxys of WUE ($\Delta 13C$ in musts) measured in the field, highlighting the promising avenues offered by phenotyping facilities. Furthermore, a genetic control of water losses at night was detected and supported for the first time by QTL detection. Night transpiration could reach 30% of daytime one depending on genotype and conditions. Furthermore, we found common QTLs to WUE and night transpiration. This, together with significant negative correlations between both traits, strongly suggested that lower WUE relies, at least partly, on higher water losses at night. Through further physiological characterization of the determinants of night transpiration, we showed that both residual stomatal aperture and cuticle losses are genetically controlled. These results open new avenues to breed grapevine for lower water losses at night.

Keywords: Water use efficiency, night transpiration, QTL, stomata, cuticle



Short talk

Image-Based Precision Phenotyping of Maize Ear Morphology and Kernel Size

Nicholas Haase¹, Nathan D. Miller², Edgar P. Spalding³, Shawn Kaeppler⁴, Natalia de Leon⁵

¹, **Department of Agronomy, University of Wisconsin-Madison, Madison, WI 53706, USA**

^{2, 3} **Department of Botany, University of Wisconsin-Madison, Madison, WI 53706, USA**

^{4, 5} **Department of Agronomy and Department of Energy Great Lakes Bioenergy Research Center, University of Wisconsin-Madison, Madison, WI 53706, USA**

nhaase@wisc.edu; ndmiller@wisc.edu; ndeleongatti@wisc.edu; spalding@wisc.edu; smkaeppl@wisc.edu

Grain yield in maize is a complex trait that is highly affected by environmental conditions. This complexity leads to lower heritabilities and makes the mapping of quantitative trait loci (QTL) for grain yield relatively difficult. However, grain yield can be separated into component traits, such as kernel number and kernel weight. Finding and characterizing genic regions contributing to these yield component traits could prove to be important for developing higher yielding cultivars. In order to better understand the relationships between kernel number, kernel size, and cob and ear morphology we have implemented a machine vision platform. This platform uses custom algorithms to extract information contained in digital images to quantify maize ear, cob, and kernel phenotypes. Ear, cob, and kernel images were collected using Epson Perfection V700 Photo flatbed scanners. Ear and cob images were processed to generate width profiles and estimate maximum width, average width, and length. Principal components analysis (PCA) of the width profiles was then used to generate quantitative proxies describing ear and cob morphology. A Fourier transform-based analysis of ear images was used to estimate the average height per kernel along the length of the ear. From images of loose kernels, average kernel width and depth were also estimated. To date, more than 26,000 ears have been analyzed with this imaging platform. Genotype to phenotype associations are being explored using genome wide association (GWA) and joint-linkage mapping.

Keywords: maize, ear, kernels, high-throughput phenotyping, image analysis



Short talk

Insights in water loss and uptake in coffee plants

Cecilio Frois Caldeira Jr, Christiane Noronh Fernandes Brumb, Antonio Chalfun-Jr.

**Biology Department, UFLA,
Lavras, Minas Gerais, Brazil**

cecilio.frois@gmail.com; chalfunjunior@dbi.ufla.br; chrisbioufla@gmail.com

Because water scarcity accounts for more than 20% of coffee yield lost in the Brazil's major producing regions last years, we decided to explore the natural coffee diversity aiming at finding genotypes displaying drought tolerance related traits. A first screening revealed that *Coffea arabica* L. progeny Siriema kept higher leaf water potential (LWP) under drought amongst different coffee genotypes. Osmotic adjustment may be involved (Brum et al. 2013), however our field studies have shown that 4-year-old Siriema plants saved water by drastically reducing stomatal conductance (gs) and transpiration rate (TR) when compared to the standard genotype Catuai IAC-144. In addition, Siriema plants sustained higher TR and ACO₂ along the dry season, which are linked to a more favorable water status. These results suggest the role of stomatal control. In accordance, similar results were obtained at greenhouse conditions with 6-month-old plants subjected to soil drying, in which the midday LWP reached -3.3 and -4.0 MPa for Siriema and Catuai IAC-144, respectively. LWP full recovering was observed at 48 hours after rewatering both genotypes, however, Siriema and Catuai's ACO₂ completely and partially (21%) restored the ACO₂ of well watered plants. In addition to the water relations studies, gene expression analysis have shown that desiccation responsive genes (CaRD29 and CaNACRD26) are regulated in a similar way in both genotypes, being upregulated under drought, however the lower transcript levels observed in Siriema plants suggest that they are under lower stress level than Catuai plants. Putative genes related to cell wall relaxation, abiotic stress and carbon metabolism were also differentially regulated in rewatered Siriema plants. Considering that only a few coffee plantations are under irrigation in Brazil, the exploitation of natural genetic variability for drought tolerance traits, such as those observed for Siriema, is of paramount importance.

Keywords: *Coffea arabica*, drought, stomatal conductance, genetic diversity, gene expression.



Short talk

Evaluation of a high throughput phenotyping method for drought tolerance in rainfed lowland rice based on infrared thermography

A.K. Konaté¹, Audebert²

¹ INERA FaraKo-Ba, 01 BP 910 Bobo-Dioulasso, Burkina Faso

² Cirad, UMR AGAP, TA A-108/01, BP 34398 Montpellier cedex 5, France

alain.audebert@cirad.fr; kadougoudiou@yahoo.fr

Drought is one of the major constraints for rice production when cropped in lowland conditions. Lowland rice indeed depends only on rainfall and thus suffers from frequent water deficits. AfricaRice leads a GCP supported project to develop rice varieties for rainfed lowland conditions combining high yield potential and drought tolerance using marker assisted recurrent selection in collaboration with national partners in Burkina Faso, Mali and Nigeria. Among methods used for characterizing plant response to drought, canopy temperature is known to be related to plant transpiration and thus drought tolerance. This study aims to confirm the relevance of a drought phenotyping method base on infrared thermography standardized with the Crop Water Stress Index (CWSI). In 2013 and 2014, 250 lines coming from the cross between IR64 X IITA212 were phenotyped in 2 West African locations. Drought was applied for 15 days at reproductive stage (45 days after sowing) and characterized soil humidity (monitoring with diviner). Drought response was evaluated with canopy temperature using a numerical infrared thermographic camera. Canopy temperature was normalized (CWSI) according to micro-meteorological variation collected through an on-site weather station. Results confirm the relationship between water deficit and canopy temperature. A large genetic variability of the drought response (CWSI) was observed in each site revealing some drought tolerant and sensitive lines. Some lines showed a stable tolerance and response to drought across the three sites. A classification of the lines with respect to their sensitivity to stress could be established by the use of the Crops Water Stress Index (CWSI). This strategy, once adopted, will enable a high throughput field phenotyping of a large number of genotypes and be useful to plant breeders.

Keywords: Canopy temperature, CWSI, Drought, Infrared thermography, Rainfed lowland Rice.



Short talk

Identifying physiological traits for drought tolerance in adapted and ancestral wheat germplasm

Yadgar Mahmood ^a, Ian King ^a, Julie King ^a, Simon Griffiths ^b, Luzie Wingen ^b and John Foulkes ^a

^a Division of Plant and Crop Sciences, University of Nottingham, Sutton Bonington Campus, Loughborough, Leicestershire LE12 5RD, UK.

^b John Innes Centre, Norwich Research Park, Norwich, NR4 7UH, UK.

John.Foulkes@nottingham.ac.uk; jic.communications@jic.ac.uk

Wheat (*Triticum aestivum* L.) is globally one of three most important crops. Drought stress is the most important factor limiting grain yield in wheat and a major goal of wheat breeding is improved drought tolerance. Physiological traits including leaf transpiration and photosynthetic efficiency, canopy temperature, leaf senescence parameters and grain ^{12/13}C isotope discrimination (CID; Farquhar and Richards, 1984) are important selection criteria for improving yield under drought and genetic variation associated with yield has been identified in wheat (Foulkes *et al.*, 2007; Reynolds and Tuberosa, 2008; Aravinda Kumar *et al.*, 2011).

This study aims to identify genetic variation for physiological traits determining water-use efficiency and drought tolerance in wheat and underlying mechanisms. A field experiment was carried out at Nottingham University, UK examining 94 Rialto x Savannah DH lines in 2012-13 under irrigated and unirrigated conditions. Overall drought reduced yield by 22% ($P=0.068$). Amongst genotypes under drought there were positive linear relationships ($P<.001$) between yield and canopy temperature ($R^2=0.15$) and flag-leaf senescence duration ($R^2=0.30$). For a sub-set of 8 genotypes under drought, grain CID correlated positively with yield ($R^2=0.47$; $P=0.06$), photosynthetic rate ($R^2=0.57$; $P=0.03$) and stomatal conductance ($R^2=0.63$; $P=0.02$).

A glasshouse experiment was carried out in 2012-13 comparing 6 representative Rialto x Savannah DH lines, 7 amphidiploid lines (durum wheat x *Thinopyrum bessaribicum*), and 3 accessions of each of *T. bessaribicum*, *T. uratu* and *Aegilops speltoides*. One *T. bessaribicum* accession had significantly higher leaf photosynthetic and transpiration rate and chlorophyll content under irrigation than R x S DH lines. Post-anthesis photosynthetic and transpiration rate in the glasshouse were correlated with those in the field for the R x S DH lines. QTL analysis is ongoing for traits and yield data for the R x S DH population using an existing genetic map (2000+ KASP).

Keywords: Wheat; drought; wild relatives; physiological traits; QTL.



Short talk

Optimizing root system hydraulic architectures for water uptake

*Félicien Meunier^a, Valentin Couvreur^b, Xavier Draye^c, Jan Vanderborght^d,
Mathieu Javaux^{a,d}*

^a **Université catholique de Louvain, Earth and Life Institute - Environment
Louvain-la-Neuve, Belgium**

^b **University of California, Davis, Department of Land, Air and Water
Resources, Davis, USA**

^c **Université catholique de Louvain, Earth and Life Institute - Agronomy
Louvain-la-Neuve, Belgium**

^d **Forschungszentrum Jülich GmbH, Agrosphere (IBG-3) Jülich, Germany**

felicien.meunier@uclouvain.be

In this study we started from local hydraulic analysis of idealized root systems to develop a mathematical framework necessary for the understanding of global root systems behaviors. The underlying assumption of this study was that root systems are naturally optimized for the water uptake. The root system is thus a pipe network dedicated to the capture and transport of water. The main objective of the present research is to explain the fitness of major types of root architectures to their environment.

In a first step, we developed links between local hydraulic properties and macroscopic parameters of (un)branched roots. The outcomes of such an approach were functions of apparent conductance of entire root system and uptake distribution along the roots. We compared our development with some allometric scaling laws for the root water uptake: under the same simplifying assumptions we were able to obtain the same results and even to expand them to more physiological cases. Using empirical data of measured root conductance, we were also able to fit extremely well the data-set with this model.

In a second stage we used generic architecture parameters and an existent root growth model to generate various types of root systems (from fibrous to tap). We combined both sides (hydraulic and architecture) then to maximize under a volume constraint either apparent conductance of root systems or the soil volume explored by active roots during the plant growth period. This approach has led to the sensitive traits for the macroscopic parameters (conductance and location of the water uptake) of each single plant selected for the study.

The next (and ultimate phase) will be to validate our conclusions with real architectures data and with a physical model of the water fluxes in the soil-plant continuum.

Keywords: Root system, Water uptake, Macroscopic parameters, optimization, GxE



Short talk

Lateral root growth: A framework to analyse the variability among elongation patterns and the impact of auxin and sugar signals

Beatriz Moreno-Ortega ^a, Bertrand Muller ^b and Yann Guédon ^c
^a UMR LEPSE, INRA, Montpellier, France

^b UMR LEPSE, INRA, Montpellier, France

^c AGAP, CIRAD and Inria Virtual Plants, Montpellier, France

ortegab@supagro.inra.fr; yann.guedon@cirad.fr, muller@supagro.inra.fr

A remarkable facet of lateral root (LR) behavior is variability affecting root development, leading to a large range of LR lengths and branching densities along the primary root. It has been argued that such variability among LRs could be a strategy to optimize soil exploration in a context of spatial and temporal heterogeneity of soil resources (Forde 2009).

In order to characterize variability in LR growth and evaluate the role of hormonal and biochemical signals that might influence it, we analyzed the patterns of development of hundreds of lateral roots in a set of maize seedlings grown in rhizotrons. The SmartRoot software (Lobet et al. 2011) was used to provide a comprehensive recording of individual root elongation dynamics.

Using a multivariate clustering method based on traits such as growth rates and apical root diameters, we identified a number of coherent growing states in maize LRs. This approach allows to quantify the variability of LR growth patterns in a root system in a probabilistic manner by computing the initial and transition probabilities among the different LR growing states.

Moreover, the molecular and cellular characterization of apical root samples revealed consistent variations in meristem size, as well as sugar and auxin status relative to the growing state of the root.

Keywords: lateral root growth, developmental pattern, probabilistic modelling, auxin, sugar signaling



Short talk

Optimizing transpiration by rhizosphere management

Mutez A. Ahmed ^a, Mohsen Zarebanadkouki ^a, Andrea Carminati ^a

^aDivision of Soil Hydrology, Georg-August University of Göttingen, Göttingen
37077, Germany

mahmed@gwdg.de

Increasing plant drought tolerance is fundamental to sustain the increasing food demand. Our objective was to test the effects of selected additives (*Aquatrols*) on root water uptake during repeated drying/wetting cycles.

Lupine and maize were grown in a sandy soil. The plants were kept irrigated by capillary rise from the bottom for two weeks. Then, the samples were let dry. When the plants showed wilting symptoms, they were irrigated by capillary rise. Half of the samples were immersed in water and half in a solution of the additives. Then another drying cycle was applied. In total we applied 6 drying cycles.

The results showed that the plants treated with additives had higher water content after irrigation. The reason was that the additive rewetted the rhizosphere, while in the samples irrigated with water the rhizosphere remained dry. In both treatments, transpiration increased during 1-2 days after irrigation. Interestingly, transpiration in the plants irrigated with water was higher than in the plants irrigated with the additive. Our hypothesis is that the lower transpiration upon irrigation with additives was caused by a quick pulse of ABA from the roots to the shoot. On the contrary, in the plants irrigated with water, the hydrophobicity of the rhizosphere delayed root rehydration and limited ABA transport to the shoot. The higher water content of the samples irrigated with additives and the lower transpiration during the first 1-2 days after irrigation delayed plant wilting.

We propose a method to manage the wetting dynamics of the rhizosphere. The tested additives increased rhizosphere rewetting. This resulted in faster root rehydration upon irrigation and to larger volume of water available to plants. Remarkably, the larger water volume was also used more slowly, as transpiration was suppressed. The transpiration suppression was probably the consequence of enhanced ABA transport (*Patents are pending*).

Keywords: transpiration, ABA, root water uptake, additive, irrigation



Short talk

Addressing drought tolerance in sugarcane varieties through leaf physiological traits

Nayara Cristina de Melo^a, Fernando Henrique Silva Garcia^b, Florent Mouillot^c, João Paulo Rodrigues Alves Delfino Barbosa^d

^a Universidade Federal de Lavras - Department of Biology – Plant hysiology
P.O. Box 3037. ZIP Code 32700-000. Lavras, Minas Gerais, Brazil

^b Universidade Federal de Lavras - Department of Biology – Plant Physiology
P.O. Box 3037. ZIP Code 32700-000. Lavras, Minas Gerais, Brazil

^c Institut de La Recherche pour le Developpement - Centre d'Ecologie
Fonctionnelle et Evolutive - Montpellier, France

^d Universidade Federal de Lavras - Department of Biology – Plant Physiology
P.O. Box 3037. ZIP Code 32700-000. Lavras, Minas Gerais, Brazil

nayaramelobio@yahoo.com.br

Tracking the drought impacts defining yield potential using fast screening leaf traits are important to crop management and breeding. We addressed sugarcane tolerance to drought using temporal patterns of net photosynthesis (A) and minimum leaf water potential (P) of four sugarcane varieties (1 to 4 – 1 and 3 more tolerant) that were submitted to two cycle of water shortage followed by rehydratation. Drought tolerance was associated with the ability of the plant to i) keep leaf traits stable under water shortage, ii) quickly recover patterns observed before water shortage when rehydrated, and iii) reduce to maximum the negative impacts of a new stress event. Those characteristics were used to estimate the stress intensity (SI), defined as the area between curves observed for watered and stressed plants. Plants (240/variety) were cultivated in greenhouse for 2 months in 8L pots. After this period, 120 were kept watered and 120 were submitted to two cycles of water shortage (15 days) followed by rehydratation (15 days). We measured A and P every 3-5 days (IRGA LiCOR-6400XT and Pressure chamber PMS-1000, respectively) in five plants. We observed the following SI in the first/second cycles for A (1- 160.4/56.5; 2- 153.3/149.2; 3-183.1/112.4; 4- 126.5/103.0) and for P (1- 41.1/6.5; 2- 40.0/8.5; 3-40.5/7.7; 4- 39.0/9.0). For P, there was an overall reduction in the SI of 80% between cycles, indicating mechanisms to reduce the impacts on P in a second stress event. For A, the great SI reduction was observed for varieties 1 and 3 (65% and 39%, respectively) indicating a low plasticity of the photosynthetic apparatus of 2 and 4. Although those results are preliminary they drive to high-throughput methods for: i) crop monitoring strategies, ii) sugarcane yield forecasting, and to crop management and breeding.

Keywords: net photosynthesis, leaf water potential, plasticity, stress intensity, rehydration.



Short talk

Growth angle of seminal roots in wheat correlates with drought responsive physiological traits and grain yield evaluated in fields with contrasting soil moisture regimes

Madhav Pandey^a, Kiran Baral^b, Amrit Poudel^c

**^aDepartment of Genetics and Plant Breeding, Agriculture and Forestry University
- Chitwan, Nepal**

^{b, c} Nepal Agricultural Research Council - Kathmandu, Nepal

mppandey.pb@gmail.com

Seedling root growth angle (RGA) is a potential surrogate trait for mature root system in wheat. The practical value of RGA has not been established yet and it is unclear whether RGA correlates with physiological traits and grain yield in field conditions. We measured the RGA of 50 wheat (*Triticum aestivum* L.) cultivars and landraces and analyzed its association with canopy temperature depression (CTD), leaf chlorophyll content (SPAD), and grain yield. The field experiments were conducted in Chitwan (84.34° E and 27.65° N) and Nawalparasi (83.77° E and 27.56° N) during 2009 and 2010 wheat seasons and with different soil moisture regimes: irrigated– 2009 and 2010 in Chitwan, rainfed– 2009 and 2010 in Chitwan and in Nawalparasi, and managed drought– 2009 in Chitwan. The soil texture class of Chitwan was a sandy loam and Nawalparasi was a silt loam. In terms of mean annual precipitation both sites were comparable.

RGA varied significantly among the studied cultivars and landraces (range: 64.1–158.4 degree). RGA was negatively correlated with grain yield in all the experiments in Chitwan ($r = -0.29$ to -0.39), irrespective of the soil moisture regimes. It did not show a relationship with the grain yield in Nawalparasi. Interestingly, RGA was positively correlated with CTD in Nawalparasi in 2009 ($r = 0.27$ to 0.34) and negatively correlated in the managed drought and rainfed experiments in Chitwan in 2009 ($r = -0.3$ to -0.34). RGA had negative correlations with SPAD in the managed drought and irrigated experiments in Chitwan in 2009 ($r = -0.28$ to -0.44). Plant height and maturity did not affect RGA, except for the Nawalparasi experiment in 2010 (RGA vs. maturity, $r = 0.32$). The results suggest that RGA can be selected for wheat improvement as it showed consistent association with the grain yield, CTD, and SPAD. We speculate that the synergistic effects of the narrow RGA on yield, CTD, and SPAD seen in the sandy loam soil of Chitwan correspond with deep and robust root system. The silt loam soil of Nawalparasi might have restricted the vertical root growth as compaction layers are common in this type of soil.

Keywords: Root growth angle, wheat, SPAD, CTD, drought



Short talk

Using rapid fluorescence for phenotyping C source regulation by drought and its relation with growth regulation in contrasted biomass sorghum genotypes

Lisa Perrier¹, Sandrine Roques¹, Pascal Sartre², Delphine Luquet¹, Denis Fabre¹

¹ CIRAD, UMR AGAP, F-34398 Montpellier, France

²INRA, UE DIASCOPE, Domaine expérimental de Melgueil 34130 Mauguio, France

Lisa.perrier@cirad.fr

Biomass sorghum diversity offers the opportunity to develop multipurpose genotypes combining high grain and ligno-cellulosic biomass productions. It also provides a large spectrum of adaptive traits, particularly to drought. Sorghum breeding is thus of major interest for semi-arid, drought prone cropping environments as met in West Africa, to improve conjointly food and feed productions. This is the objective of the BIOSORG project that firstly aims to understand the elemental traits contributing to combine biomass and grain production and their stability under drought.

Sorghum biomass accumulation depends both on C source (photosynthetic) and sink (organ development rate, number, size) processes. While sink strength related traits are commonly phenotyped and known to vary across sorghum genetic diversity, it is not the case regarding photosynthetic processes, much more difficult to measure to a large scale. Accordingly the impact of drought on C source-sink balance is in general not apprehended in the process of large population phenotyping.

The present study aims to explore the relevance of modulated fluorescence for a large scale phenotyping, as a proxy of photosynthetic performance, of biomass sorghum genotypes under contrasted water situations. A field trial comparing two water treatments during stem elongation phase was carried out in 2013 and 2014 on 4 biomass sorghum hybrids in order to explore the relationship between leaf chlorophyll fluorescence (measured with a Walz PAM-2500) and photosynthetic level (measured with a Walz GFS-3000), their regulation by drought and their genotypic variability. 2014 trial was extended considering 12 more contrasted genotypes to confirm the relation on a larger diversity. The confirmation of the relationship between fluorescence and photosynthetic parameters, the genotypic variability of the Drought Factor Index (DFI) will be presented as well as a first appraisal of its relationship, across genotypes, with sink organ growth regulation by drought.

Keywords : *Biomass sorghum, fluorescence, photosynthetic performance, C source-sink balance, drought*



Short talk

Effect of water shortages on yield and yield components of maize

Tamás Spitkó*, Zoltán Nagy, Zsuzsanna Tóthné Zsubori, Csaba Szőke, Tamás Berzy, Janos Pintér, Judit Bányai, Csaba L. Marton

Agricultural Institute, Centre for Agricultural Research, Hungarian Academy of Sciences

2 Brunszvik street, 2462 Martonvásár, HUNGARY

spitko.tamas@agrar.mta.hu

The timing and form of drought changes from year to year, so under non-irrigated conditions it is difficult to design experiments that will give reproducible results suitable for the selection of genetic materials with resistance to water deficit. Plants may be exposed to the various components of drought stress in many forms and combinations. The components of drought stress are the following: the duration and starting date of drought; the relative humidity, temperature and movement of the air; the intensity of solar radiation; the quantity and distribution of precipitation; the texture, water content and temperature of the soil, and the groundwater depth; the species, variety, age and developmental stage of the crop, the plant density and the length of the vegetation period. When investigating drought tolerance, it must not be forgotten that drought stress is a complex phenomenon exhibiting quite different characters in different years and locations. For this reason, the plant response to drought is also a complex process. In our study, 83 maize hybrids originating from various countries were investigated over a period of two years, under irrigated and non-irrigated conditions. The drought tolerance of plants in the non-irrigated plots was analysed in terms of flowering synchrony and yield components. It could be concluded from the results that in response to long-term water deficit the period between tasselling and silking became longer, while the analysis of yield components revealed the greatest reductions in the number of kernels per ear and in the proportion of seed set. As the degree of proterandry increased, there was a decline in the grain yield, confirming that the analysis of this trait could be a way of predicting drought tolerance. Considerable differences in drought tolerance were observed between the genetic materials included in the analysis, suggesting the presence among these parental lines and hybrids of genotypes resistant to long-term water deficit, suitable for cultivation under dry conditions. An analysis of correlations between the traits revealed that proterandry should be treated as a priority trait when investigating drought stress tolerance, as better predictions can be made of both drought tolerance and potential yields, leading to more reliable selection for higher yields.

Keywords: maize, drought, yield components, proterandry



Short talk

Using Field-based aerial imaging platform to improve selection efficiency in breeding for drought tolerance in Maize

Zaman-Allah M^a, Cairns J^a, Araus JL^b, Tarekegne A^a, Magorokosho C^a, Zarco-Tejada PJ^c, Hornero A^c, Das B^d, Olsen M^d, Prasanna BM^d,

^aInternational Maize and Wheat Improvement Center (CIMMYT) PO Box MP163, Harare, Zimbabwe

^bPlant Physiology Unit, Dpt. of Plant Biology, University of Barcelona, 08028, Barcelona, Spain

^cLaboratory for Research Methods in Quantitative Remote Sensing, Cordoba, Spain

^dInternational Maize and Wheat Improvement Center (CIMMYT), PO Box 1041, Nairobi, Kenya

Z.MainassaraAbdou@cgiar.org

Constraints in field phenotyping capability is still limiting the efficiency of conventional breeding as well as preventing molecular breeding from delivering all its potential (Araus et al. 2008; Cabrera-Bosquet et al. 2012; Cairns et al. 2012; Cobb et al. 2013). To overcome this limitation, the use of aerial phenotyping platforms is becoming an interesting option because they offer the possibility to simultaneously and cost-effectively phenotype large numbers of plots and upscale the measurements, from a single plot basis to dissecting an entire trial. In addition, data can be collected in a dynamic way using time series.

We present the use of an unmanned aerial platform equipped with sensor for multispectral imaging in spatial field variability assessment and phenotyping for drought stress tolerance in maize. Multispectral aerial images were used to characterize experimental fields for spatial soil variability and derive indices for crop performance under drought stress.

Results showed that the aerial platform enables to effectively characterize spatial field variation that can be used to select appropriate experimental designs and improve repeatability. Selection index using the Normalized Difference Vegetation Index (NDVI) data derived from spectral imaging increased the predicted response of grain yield by 11 to 18% compared with direct selection for grain yield alone. This work suggests that the aerial sensing platform designed for phenotyping has the potential to effectively assist in maize breeding targeting stress environments where heritabilities for grain yield are low (Bolafios and Edmeades, 1996).

Keywords: Maize, phenotyping platform, drought, remote sensing, selection efficiency



Interactive exhibit

Growth and genome-wide transcriptional analysis reveal that elevated CO₂ mitigates the impact of drought stress in *Arabidopsis thaliana*

Hamada Abdelgawad, Gaurav Zinta, Marios Nektarios Markakis, Viktoriya Avramova, Gerrit T.S. Beemster, Han Asard

Laboratory for Molecular Plant Physiology and Biotechnology, Department of Biology, University of Antwerp, B-2020 Antwerp, Belgium.

hamada.abdelgawad@uantwerpen.be

Future climate scenarios indicate increasing CO₂ in combination with more frequent drought. Elevated CO₂ (eCO₂) reduces drought impact by inducing stomatal closure, preventing water loss, as well as by non-stomatal factors, e.g. effects on enzymes, photorespiration and defense responses. Mechanisms underlying non-stomatal effects remain unclear. We investigated growth, physiological, biochemical and transcriptome responses of *Arabidopsis thaliana* to mild (MD) and severe drought (SD) under ambient (aCO₂, 360 ppm) and eCO₂ (620 ppm). Drought reduced leaf growth by inhibiting cell division and expansion. eCO₂ reduced the impact of MD on cell division and expansion, and the impact of SD on cell size. Transcriptome analysis showed that photosynthesis and defense processes are more strongly affected by SD compared to MD. These results were mirrored at the physiological and biochemical levels, where SD inhibited photosynthesis and stomatal conductance and induced defense responses (antioxidants, hormones, osmolytes). Accumulation of antioxidants and osmolytes were not sufficient to counter the SD damage impact. Stress alleviation by eCO₂ can result from enhanced (antioxidant) defenses, and/or of reduced ROS generation. The transcriptome and metabolite analyses did not implicate the antioxidant defenses in the effect of eCO₂, with a down regulation, or no impact on most antioxidant parameters. However, we found that eCO₂ reduced photorespiration, resulting in lower stress-induced H₂O₂ generation. Thus, the antioxidant relaxation in eCO₂ could be a consequence of lower oxidative pressure. Remarkably, we also noted a rather strong eCO₂-specific effect on the gene cluster supporting glucosinolate metabolism. The functional role for the glucosinolates in the drought stress response remains to be elucidated. Compared to aCO₂, higher induction of osmolytes was observed and could be associated with high turgor pressure under drought and eCO₂.

We conclude that eCO₂ mitigates the effects of drought by maintaining plant turgor and reduced H₂O₂ production.

Keywords: Drought, Elevated CO₂, Oxidative stress, Redox network, *Arabidopsis thaliana*.



Interactive exhibit

Identification of stress response and recovery mechanisms by a multi-scale analysis of the effect of drought in the growth zone of maize leaves

Viktoriya Avramova , Hamada AbdElgawad , Han Asard, Gerrit T.S. Beemster

**Laboratory for Molecular Plant Physiology and Biotechnology,
University of Antwerp, Groenenborgerlaan 171, B-2020 Antwerp, Belgium**

Viktoriya.Avramova@uantwerpen.be

Drought is presumably the most important yield-limiting factor under natural and agricultural conditions and therefore detailed knowledge of its impact on plant growth regulation is crucial. The maize leaf represents an attractive system for growth studies, because of its spatial gradient, allowing simultaneous sampling of dividing, expanding and mature cells. At the same time, because of its relatively big size (~10 cm), it provides enough material for extensive biochemical and molecular analyses of each developmental state.

By means of a kinematic growth analysis we showed that drought inhibits leaf growth in maize by reducing cell division rates in the meristem and cell expansion rates in the elongation zone. Transcriptome analysis provided a molecular basis for the observed inhibition of cell division rates, but also pointed at distinct effects on the development of the photosynthetic machinery, and antioxidant and redox systems. The effects on these regulatory pathways were subsequently confirmed by detailed biochemical analysis of the activity of key enzymes (peroxidase, catalase, superoxide dismutase, lipoxygenase, and NADPH oxidase) and quantification of metabolites (H_2O_2 and malondialdehyde (MDA)).

We demonstrated the functional significance of the identified transcriptional and physiological changes, showing that 1. Increasing the antioxidant capacity in the growth zone, by overexpression of iron superoxide dismutase, increases leaf growth under control and drought conditions. 2. Increased expression of photosynthesis genes under stress facilitates faster growth upon re-watering compared to unstressed controls.

Keywords: maize, drought, transcriptomics, leaf growth, redox enzymes



Interactive exhibit

Monitoring phenotyping platforms using UAV borne sensors: PHENODRONE

F. Baret¹, A. Comar^{1,3}, B. de Solan², G. Colombeau¹, S. Madec¹, F. Toromanoff², F. Tison¹, S. Thomas², S. Liu¹

¹INRA, EMMAH, UMT CAPTE¹ Avignon, France

²Arvalis institut du végétal, UMT CAPTE Avignon, France

³HIPHEN, Avignon, France

Monitoring the dynamics of crop growth in field conditions is highly desired to evaluate a number of structural and functional traits of accessions within phenotyping experiments. The rapid technological improvements in UAV and sensor technology allowed to develop UAV based systems with several advantages as compared to ground based systems: a very high throughput, and the capacity to image concurrently a large number micro-plots. Such a system called PHENODRONE was developed within the framework of the PHENOME project. It is based on an hexacopter vector with an autonomy around 15 to 20 minutes. It is equipped with tilt compensated mount where several payloads could be setup. They include a SONY Alpha5100 24 Mega pixel RGB camera equipped with a 60 mm focal length lens for plant or organ counting, a multispectral camera with 6 bands (450, 530, 570, 670, 730, 780 nm) with a resolution of 1280x960 pixels and a thermal infrared camera with a resolution of 640x480 pixels. The thermal infrared camera is designed to be operated concurrently with the multispectral camera.

An automatic processing chain has been developed to ingest the large number of images acquired and provide two main outputs: a mosaic of the experiment, and an HDF5 file containing the extracts of the micro-plots from each image. This HDF5 file is then further exploited to transform the digital numbers into higher level products including

- Plant or organ counting and characterization (position, projected area, shape) from the SONY camera,
- a series of vegetation indices (NDVI, MTCI, PRI, ...), the green fraction, FIPAR (fraction of intercepted photosynthetically active radiation), GAI (green area index), Canopy chlorophyll content from the multispectral camera,
- the canopy height/volume from the multispectral camera,
- the foliage temperature derived from the thermal infrared camera combined with the multispectral camera.

The poster presents the main characteristics of the PHENODRONE (vector+sensors) as well as the first results obtained over a range of experiments covering several species that includes plant counting and the dynamics of some biophysical variables over the whole growth cycle of the canopy.



Interactive exhibit

Influence of soil moisture stress on vegetative growth and root yield of some selected cassava genotypes under greenhouse condition

Bello, A.A.^{1, 2}, Adetoro, N.A.¹, Kulakow, P.¹

¹International Institute of Tropical Agriculture (IITA), Ibadan, Nigeria

²Agronomy Department, University of Ibadan, Ibadan, Nigeria
Cassava Breeding Unit, IITA, Ibadan, Nigeria.

¹International Institute of Tropical Agriculture (IITA), Ibadan, Nigeria
Cassava, Breeding Unit, IITA, Ibadan, Nigeria

¹International Institute of Tropical Agriculture (IITA), Ibadan, Nigeria
Cassava, Breeding Unit, IITA, Ibadan, Nigeria

a.bello@cgiar.org-www.iita.org

Improving root yield has always been one of the major thrusts in cassava improvement programmes, and the wide variability among genotypes for shoot and root characteristics can be utilized as an important tool. This study was carried out to determine how variation in shoot and root characteristics affect root yield and the influence of soil moisture stress on the vegetative growth and yield of cassava genotypes. In the greenhouse, twelve genotypes selected on the basis of field performance for root yield and root number were evaluated at three moisture conditions of 75% (control), 50% and 25% field capacity (FC) using a Completely Randomized Design with factorial arrangement (variety and moisture level) and replicated three times. Moisture stress affects the vegetative growth and root yield. Significant differences ($P < 0.05$) existed among genotypes and moisture regimes for plant height stem girth, root weight, root number and shoot weight from which estimates of variance components were generated. The higher stress level (25% FC) resulted in a greater reduction in vegetative growth than the moderate stress level of 50% FC, but moisture levels was uniform over time for plant height and stem girth but the response to moisture levels varied widely among genotypes for root weight at harvesting 24 Weeks After Planting (WAP) indicating that genotypes experience a higher stress condition. Genotypes IITA TMS IBA 010040,011086 and 920326 were identified as having good drought tolerant abilities.

Keywords: moisture stress, genotypes, green house, field capacity, field performance.



Interactive exhibit

Implication of root parameters in drought tolerance at the early germination stage for bread wheat

Sahar Bennani^a, *Birouk Ahmed*^b, *Nsarellah Nasserlehaq*^a

^a National Institute of Agricultural Research
INRA Avenue Ennasr Rabat, Morocco

^b Hassan II Veterinary and Agronomy institute
Madinat Al Irfane, BP 6202, Rabat Instituts, 10101, Rabat, Morocco

sahar.bennani@gmail.com

Drought is the main abiotic stress constraining wheat productions. In order to understand the roots traits which can be used as quick criteria for drought tolerance, the response of 3 national bread wheat varieties (*Arrehane*, *Aguilal* and *Radia*) compared to 2 international elite lines (*Attila* and *Sokoll*) to drought stress imposed at germination stage during 7 days was investigated in a laboratory experiment using polyethyleneglycol-6000 (PEG 6000). Three water stress levels were considered: control (0% PEG-6000), 15% PEG-6000 and 25% PEG-6000. Germination percentage (GP), root system (primary root length, roots number and dry weight, coleoptile length and dry weight) and shoot parameters (leaf number, length and dry weight) were evaluated. In control conditions, there were significant differences for all parameters except GP, roots and coleoptile lengths. In moderate stress conditions (15% PEG-6000), all parameters were not significant with 16% decrease in GP. We observed a significant increase in root dry weight and length, while shoot system was significantly reduced. When the stress became more severe (25% PEG), we recorded 32% as mean decrease of GP associated to root and shoot parameters reduction. Significant differences were recorded for GP, roots and coleoptile dry weights and coleoptile length. The cultivars responded variably to stress treatments. *Attila* and *Sokoll* were the most resistant cultivars in severe drought conditions which developed highest levels of all roots and coleoptile parameters. However, even if *Radia* root parameters were reduced in severe stress conditions, it showed high GP. In conclusion, root parameters have a relevant role in drought tolerance and may be considered as selection criteria, especially roots and coleoptile dry weights and coleoptile length. However, further tests should be taken to prove their contribution in consideration of largest genetic base and interaction with the other mechanisms involved in drought tolerance aiming to deliver accurate selection criteria.

Keywords: Bread wheat, drought tolerance, selection criteria, roots



Interactive exhibit

Hyperspectral imaging for phenotyping plant root systems

**Gernot Bodner^a, Alireza Nakhforoosh^a, Hans-Peter Kaul^a, Daniel Leitner^b
Raimund Leitner^c, Thomas Arnold^c**

^a Department of Crop Sciences, University of Natural Resources and Life Sciences BOKU Vienna

Konrad-Lorenz-Strasse 24, 3430 Tulln, Austria
gernot.bodner@boku.ac.at – www.dnw.boku.ac.at

^b Computational Science Center, University of Vienna
Oskar Morgenstern-Platz 1, 1090 Vienna, Austria

daniel.leitner@univie.ac.at – www.csc.univie.ac.at/index.php?page=rootbox

^c CTR Carinthian Tech Research

Europastraße 4/1 Technologiepark Villach, 9524 Villach/ St. Magdalen, Austria
thomas.arnold@ctr.at – <http://www.ctr.at>

A new phenotyping method for plant root systems grown in soil filled rhizoboxes using hyperspectral imaging is presented. Hyperspectral imaging should provide an improved segmentation of plant roots from the growth medium and provide additional information such as water extraction profiles of roots. The objective of the study is to present the technical setup, and establish an experimental protocol for root phenotyping with a hyperspectral scanner. Durum wheat (cv. Floradur) is grown in three different substrates (two types of soil and sand) and two water regimes in rhizoboxes with a transparent glass front window. Hyperspectral scans in the near infrared range are made weekly until plants reach the bottom of the rhizobox. Scans are evaluated for root architectural and morphological traits as well as water uptake profiles. First results are presented and discussed in terms of information to be obtained from hyperspectral imaging of rhizoboxes, and challenges using hyperspectral imaging as an advanced method for root phenotyping to distinguish stress resistance between crop genotypes.

Keywords: phenotyping, hyperspectral imaging, root system, water stress, experimental protocol



Interactive exhibit

Photosynthetic parameters in screening of wheat genotypes for tolerance to drought and high temperature

Marian Brestic^a, Marek Zivcak^a, Katarina Olsovska^a, Pavol Hauptvogel^b

^a Faculty of agrobiological and food resources, Slovak University of agriculture in Nitra, Slovak Republic, marian.brestic@uniag.sk

^b National Agricultural and Food Center - Research Center of plant production in Piešťany, Piešťany, Slovak Republic, hauptvogel@vurv.sk

The study was aimed at the evaluation of several photosynthetic methods and technical approaches in assessment of tolerance to drought and high temperature in wheat genotypes. The post-anthesis drought stress was induced by withholding of irrigation under a rainout shelter. The set of physiological parameters was monitored regularly, including the leaf water content and osmotic adjustment. Using the values of CO₂ assimilation and transpiration, the leaf transpiration efficiency was calculated; moreover, the stomatal conductance was measured by porometer. The numerous measurements of rapid chlorophyll a fluorescence kinetics in wheat leaves were recorded and the drought stress-associated changes at the chloroplast level were analysed. This technique was used also for assessment of photosynthetic thermostability. The drought tolerance of genotypes was classified according to harvested grain yield in non-stressed and stressed conditions. The correlations of physiological traits with yield-based drought tolerance of genotypes were assessed. Our results indicated that the drought-tolerant genotypes had higher transpiration efficiency due to lower stomatal conductance in non-stressed conditions, but higher stomatal conductance associated with higher osmotic adjustment in drought. The analysis of chlorophyll fluorescence kinetics based on numerous measurements enabled to identify parameters, which well reflected the drought stress level and hence, they correlated well with genotypes' drought tolerance. In contrary, the commonly used fluorescence parameters were fully insensitive until the sub-lethal drought level. The simple methodical approach enabled to identify also the significant genotypic differences in heat resistance. The results confirmed the link between the leaf transpiration efficiency and yield in conditions of post-anthesis drought stress in wheat. Moreover, the rapid, non-invasive easy-to-do measurements of chlorophyll fluorescence kinetics in wheat leaves were shown to be useful in assessment of drought stress severity and the drought stress tolerance.

Keywords: drought, genotypes, photosynthesis, wheat, chlorophyll fluorescence

Supported by grant APVV-0197-10 and EU project no 26220220180: Building of AgroBioTech Research Centre ".



Interactive exhibit

How to estimate maize sensitivity to water deficit in field? A method consistent with the estimators measured in a phenotyping platform

R. Chapuis^a, C. Delluc^b, R. Debeuf^b, F. Tardieu^a, C. Welcker^a

^a **INRA, UMR LEPSE**
IBIP 2 Place Viala, 34060 Montpellier, France

^b **Limagrain Europe**
Ferme de l'Etang, 77390 Verneuil l'Etang, France

Tolerance to soil water deficit is a priority of many maize breeding programs. Its genetic analysis requires estimators that characterize each genotype in a reproducible way. For that, we have tested and compared the abilities of hybrids to maintain leaf growth in a large range of soil water potentials (i) in a phenotyping platform that measured leaf elongation rate and (ii) in a network of field experiments via an estimator of the sensitivity of grain number to water deficit.

Tolerance to soil water deficit was estimated in a network of 14 field experiments via the regression between yield components and soil water potential measured with tensiometers.

A drought index was obtained by averaging soil water potential, measured with tensiometers, for the phenological phase during which grain number was determined (evaluated for each individual hybrid in each site). It closely correlated with grain number in each of the 19 hybrids that were analyzed over 14 environmental situations in France, Hungary and Chile. The slope of the regression line between drought index and grain number, established for each hybrid, was taken as an estimate of the sensitivity to soil water deficit of that hybrid. Sensitivity estimated in this way varied 2-fold in the set of studied hybrids, and correlated with that of leaf growth to soil water deficit in short-term experiments in the phenotyping platform.

This method is promising for the evaluation of hybrids in the context of a breeding program with a minimum amount of environmental measurements and can be extended to a large number of genotypes compatible with a genetic analysis.

Keywords: Zea mays, Drought tolerance, Model-assisted phenotyping, Grain yield, Growth



Interactive exhibit

Transcriptomic analysis of drought responses of elite barley cultivar Scarlett and Spanish landrace SBCC073

Carlos P Cantalapiedra^a, María J García-Pereira^a, Bibiana Macarulla^a, Ana M Casas^a, Ernesto Igartua^a and Bruno Contreras-Moreira^{a,b}

^a Estación Experimental de Aula Dei (EEAD-CSIC)
Av. Montañana, 1005, 50059 Zaragoza, Spain

^b Fundación ARAID, Calle María de Luna 11, 50018 Zaragoza, Spain

bcontreras@eead.csic.es

Traditional cultivars and landraces of the Spanish Barley Core Collection harbour genetic variability of potential interest for breeding elite varieties adapted to Mediterranean environments. Here, local landrace SBCC073, with high yield under drought conditions, and European elite cultivar Scarlett, which performs poorly with low water supply, were subjected to different watering regimes both in growth chamber and greenhouse and compared to infer differential adaptive responses. Measurements taken during plant growth confirm the impact of the drought treatments on physiology in terms of water potential, relative water content and stomatic conductivity. Tiller and spike counts also suggest that drought affected grain yield.

RNA of control and water-deprived plants was extracted from several tissues, sequenced and used to build *de novo* transcriptomes. Over 100,000 transcripts were obtained for both cultivars, of which near 90% align to barley sequences, revealing large sets of transcripts expressed in one genotype but not in the other, and also novel contributions of these two cultivars to the barley pangenome. Transcripts were quantified and expression profiles on leaf (LF) and young inflorescence (YI) obtained. There were more differentially expressed (DE) isoforms in YI than in LF in chamber experiments, while the opposite was observed in the greenhouse. Similarly, we report more DE protein kinases than transcription factors in the chamber, while the reverse was observed in the greenhouse. Analyses of putative regulatory motifs within promoters and altered metabolic pathways reveal phenotypic differences between tissues and genotypes, and provide molecular details of adaptation and tolerance responses. Both cultivars shift their expression profiles and metabolic networks towards mechanisms such as reduction of water-loss, accumulation of osmoprotectants or flowering-related processes. We argue that genetic components underlying the adaptation of Mediterranean landraces, such as SBCC073, should be considered in breeding programmes.

Keywords: barley, drought, transcriptome, adaptation, metabolism



Interactive exhibit

Mediterranean durum wheat landraces as potential donors for early vigor improvement

Conxita Royo, Leila Haddouche, Dolors Villegas

**Institute of Agriculture and Food Research and Technology (IRTA)
Field Crops Program, Rovira Roure 191, Lleida, Spain**

conxita.royo@irta.cat

Rapid development of seedling leaf area early in the season is a major factor affecting resource acquisition, water use efficiency and grain yield of wheat. Dwarfing genes introduced during the Green Revolution not only reduced plant height, but they also decreased the early vigor (leaf area) of seedlings. The current study was conducted to compare the variability existing for early vigor in a set of 185 durum wheat (*Triticum turgidum* L. var *durum*) landraces and 133 modern varieties from 25 countries, and to identify potential donors for the improvement of early vigor in breeding programs. Genotypes were grown in 2013 in plots of 3.6 m², arranged in an augmented design with 2 replicated checks, at Gimenells (North of Spain) under rainfed conditions. Early vigor was estimated by repeated digital image sampling as percentage of green coverage. Zenital pictures of the plots were captured periodically from the top of the plots at about 120 cm from the soil. The green fraction (GA, green pixels divided by total pixels) of images was obtained for each plot and sampling date with the free software Breedpix, and data of each plot were integrated from sowing to the beginning of jointing. A mixed model was used to estimate the BLUPs and to determine the differences between landraces and modern varieties. The range of values of GA was 20.5 in landraces and 16.2 in modern varieties. On average landraces had 22.4% ($P < 0.0001$) more early vigor than the modern varieties. Around 10% of the studied landraces showed higher early vigor than the best modern variety, thus suggesting that Mediterranean landraces may be a potential source of alleles for improving early vigor in breeding programs. The estimation of early vigor through analysis of digital images was a useful method to evaluate a large number of plots under field conditions.

Keywords: drought, durum wheat, landraces, modern varieties, Mediterranean environment.

This study was partially funded by the Spanish Government under projects CICYT AGL2012-37217 and RTA2012-00011.



Interactive exhibit

Forage grass species root distribution in long term field trials

Tom De Swaef^a, Mathias Cougnon^b, Peter Lootens^a, Dirk Reheul^b, Isabel Roldán-Ruiz^a

^a **Institute for Agriculture and Fisheries Research (ILVO)
Caritasstraat 21, B-9090 Melle, Belgium**

^b **Department of Plant Production, Ghent University
Proefhoevestraat 22, B-9090 Melle, Belgium**

tom.deswaef@ilvo.vlaanderen.be

A sustainable forage grass production in the future implies that more drought-tolerant varieties should be bred as global change will cause more frequent and more intense dry periods in NW Europe. Therefore, interest is currently increasing towards root phenotypic traits. Many root phenotyping experiments occur in rather artificial environments, for instance, based on pot or tube experiments, which may substantially modify the plant root growth and morphology compared to field conditions.

Therefore the aim of the present research was to compare *in situ* root length and biomass distribution over a vertical profile (3-90 cm) for 5 forage grass species (*Lolium perenne* (Lp), *Festuca arundinacea* (Fa), *Festuca pratensis* (Fp) and two types of *Festulolium* (F11 and F12) and two levels of nitrogen fertilization (300 kg N ha⁻¹ (H) and 190 kg N ha⁻¹(L)).

In October 2014, soil cylinders with a length of 15 cm and a diameter of 10 cm were dug out from 0 cm to 90 cm depth in three year old swards of the species. Roots were washed out to determine root biomass and samples of about 1 g were taken to determine root length and diameter distribution.

All species had higher root biomass in the high nitrogen treatment compared to the low nitrogen treatment. Fa had by far the highest root biomass at all soil depths, which resulted in a total biomass for the whole profile of about 1.7 times the root biomass of Lp and more than twice the root biomass of the other species. Although Zobel (2013) identified several distinct diameter classes for *Lolium perenne* in a pot experiment, this was not noticed in our field-grown plants of the five species. Further research should identify whether the occurrence of these distinct diameter classes could be explained by the limited root growth environment.

Keywords: root phenotyping, image analysis, forage grass, nitrogen, drought



Interactive exhibit

DiaPHEN: field platform to analyze mechanisms of drought tolerance at field level

Magalie Delalande^a, Jean-Luc Regnard^b, Evelyne Costes^b, David Gómez-Candón^c, Pierre Roumet^d

^a **DIAPHEN platform,
INRA domaine de Melgueil, 34130 Mauguio**
www.phenome-fppn.fr/phenome_eng/Facilities/Montpellier-Field

^b **Montpellier SupAgro, UMR AGAP 1334 -
Campus CIRAD TA-A-108/03, Avenue Agropolis F-34398 Montpellier Cedex 5,
France**

^c **Montpellier SupAgro, UMR AGAP 1334, TA-A-108/03,
Av. Agropolis, 34398 Montpellier 9 Cedex 5, France**

^d **Montpellier Supagro, Ge2pop, UMR AGAP 1334, Bat 21,
2 place Pierre Viala, 34060 Montpellier cedex 02**

delalande@supagro.inra.fr; jean-luc.regnard@supagro.fr ;
evelyne.costes@supagro.inra.fr; pierre.roumet@supagro.inra.fr;
davidgomezcondon@gmail.com

Designing varieties able to cope with cropping limitations associated with climate change is a priority objective. The deal consists in identifying, in thousands of accessions, allelic variants showing a favorable plant behavior under dry environments. This consists in evaluating these numerous genotypes under a panel of contrasting environmental conditions.

Accurate phenotyping has become the major bottleneck in programs aiming at building genotypes that can maintain / increase crop performance under climate change and reduced inputs.

Diaphen is a field research facility that gives to scientists the opportunity of studying how main crop species (wheat, maize, sorghum, apple tree, vineyards, etc.) cope with water and/or thermic stress under Mediterranean conditions, and to what extent the crop yield is affected under dry environments.

Diaphen is part of the French Plant Phenotyping Platform (PHENOME) that will provide France with an up-to-date, versatile, high-throughput infrastructure and suite of methods allowing characterization of large genotypic panels of different species under scenarios associated with climate changes.

It is equipped with the most modern tools that allow high throughput non-invasive measurements and make it possible to retrieve relevant variables to characterize structural and functional traits of thousands of varieties while accurately monitoring the environmental conditions in real time. Establishing relationships between plant and soil water status is one of the targets of the platform



Methodologies are under development to obtain thermal, visible, near infra-red, or multispectral images as previous steps to image-based assessment of response to water stress on various crops - maize, sorghum or wheat, apple tree, through main spectral indices.

This poster will present questions that are currently addressed by Diaphen, and first results obtained thanks to some selected approaches: hyperspectral images, high-resolution thermal and multispectral UAV imagery, NIRS or chlorophyll fluorescence.

Keywords: water stress; drought tolerance; phenotyping; Mediterranean conditions



Interactive exhibit

Tools for wheat drought tolerance evaluation and breeding in France

Jean-Charles Deswarte^a, Katia Beauchene^b, Guillaume Arjaure^c, Stéphane Jezequel^d, Guillaume Meloux^d, Julien Landrieaux^c, Alain Boutier^c, Samuel Thomas^e, Benoit Desolan^e, David Gouache^f, Eric Ober^g, Volker Lein^h, Camille Bedardⁱ, Laure Duchalais^j, Jérémy Derory^k, Céline Zimmerli^l, Valérie Laurent^m, Clément Debitonⁿ, Guillaume Tcherkez^o, Frédéric Baret^p

ARVALIS, Institut du vegetal (a Villiers-le-bâcle, France ; b : Ouzouer-le-marché, France ; c : Le Magneraud, France ; d : Gréoux-les-bains, France f : Boigneville, France)

e : ARVALIS, Institut du vegetal/UMT CAPTE ; Avignon, France ; g : NIAB ; Cambridge, UK

h : Saaten Union Recherche SAS ; Estrées-Saint-Denis, France

i : Secobra Recherches ; Maule, France

j : RAGT 2n ; Louville-la-Chenard, France

k : Limagrain Europe ; Chappes, France

l : BAYER SAS ; Milly-la-Forêt, France

m : Florimond Desprez Veuve et Fils ; Cappelle-en-Péville, France

n : UNISIGMA ; Froissy, France

o : Institut de Biologie des Plantes ; Orsay, France

p : INRA – UMR 1114 – EMMAH ; Montfavet, France

jc.deswarte@arvalisinstitutduvegetal.fr

Drought is a limiting factor in several areas of France. However, water stress experienced by French wheat crop is mild compared to other production areas, and inconsistent from one cropping season to another; thus, water-stress tolerance strategies must be designed to fit such levels and scenarios of water-stress. Favorable traits have to be identified, and adequate screening method tested. We present an on-going research strategy aimed at addressing trait identification for improved drought tolerance in Western Europe.

We rely on a network of 3 types of trials:

- Genetic diversity trials (1 site, several years, > 200 modern cultivars) for drought stressed yield and traits of interest. We developed a microplot scale soil characterization and an automated phenotyping system: the PhenoMobile.
- Multilocal trials performed across years and sites, representing the range of water-stress experienced in France, to capture GxE interactions. Soil characterization allows crop water balance to be computed.
- Specific trials performed under rain-out shelters, with 9 cultivars, in order to assess the contribution of targets traits to yield with/without irrigation.
- We focus on yield and its components, isotope (C and O) discrimination in grain, LAI dynamics, biomass partitioning and water use.



We also run climatological analysis using a water balance model, in order to characterize water-stress scenarios, and quantify the representativeness of our trials.

The project is on-going; however, we gathered preliminary results:

- Microplot-scale soil characterization allows for highly significant gains in precision and heritability in droughted treatments
- A clustering of the diversity of drought stress intensity and timing across French producing areas is presented.
- Portable, low-costs technologies as well as automated systems for phenotyping are tested
- Genetic diversity in commercial wheat cultivars for traits of interest has been evaluated

Keywords: *Wheat, drought, phenotyping, water-stress scenario, traits*

Part of this work rely on FSOV (Fonds de Soutien à l'Obtention Végétale) funding (project FSOV 2012-K)



Interactive exhibit

Potential of High Resolution Thermal Imaging System to Evaluate Stomatal Conductance in the Field

A. Dockx¹, L. Bertrand¹, Ph-F. Faux¹, N. Wuyts² & X. Draye¹

¹ Université catholique de Louvain - Earth and Life Institute – Agronomy
Contact: ² Vlaams Instituut voor Biotechnologie - Department of Plant Systems Biology – UGent

adrien.dockx@uclouvain.be

Stomatal conductance and transpiration are critical variables for the assessment of drought tolerance of crops, but are barely used in genetic improvement programs for practical difficulties. Our project evaluates the potential of high resolution thermal imaging systems which provide accurate measurements of leaf temperature, from which stomatal conductance and transpiration can be computed. Because such systems may require several hours for the acquisition of an entire evaluation trial, we have specifically investigated the amplitude of the temporal variation of leaf temperature in the field during the establishment of drought and for a small number of genotypes. Our results reveal that the amplitude of variation of maize leaf transpiration proxies during the day for a given genotype, induced by variation of stomatal conductance and environmental variables, is considerably larger than the genotypic variation of leaf temperature measured at any time. We have then used a statistical approach to model the daily evolution of leaf temperature in order to allow the inference on genotypes that are measured at different time. Interestingly, we have found that the temporal pattern of leaf temperature changes considerably with the position in the field and with the time during the establishment of drought, and that these variations were genotype-specific. This suggests that the interpretation of leaf temperature also requires a careful examination of soil conditions.

Keywords: *Thermal Imaging, Stomatal Conductance, Drought Tolerance, Phenotyping Methods, Maize*



Interactive exhibit

Root and tuber visualization using state of the art x-ray computed tomography

Stefan Gerth^a, Anja Eggert^b, Uwe Sonnewald^c, Norman Uhlmann^d

^{a b d} Fraunhofer Institute for Integrated Circuits IIS, Development Center X-Ray Technology EZRT, Flugplatzstr. 75, 90768 Fuerth, Germany

^c University of Erlangen-Nuremberg, Department of Biologie – Biochemistry

Stefan.gerth@iis.fraunhofer.de

During the last years, x-ray computed tomography (CT) has been applied to study below ground growth of potato tubers (Ferreira et al., 2010) or bean roots (Metzner et. al, 2015). With x-ray CT the volume information of objects can be reconstructed in 3D out of x-ray projections of the object from different aspects.

Using axial 3D-CT, projections of the object are taken under different viewing angles, rotating the object perpendicular to the central x-ray beam. The reconstructed volume data set consists of grey levels which represent information about the x-ray attenuation depending on the mass attenuation coefficient, the density distribution of the material and the spectral distribution of the x-ray source. The calculation of tuber and root volumes of potted plants embedded in soil requires the segmentation from other materials in the x-ray CT volume data. To address the quality of the segmentation additional comparison measurements between Magnetic Resonance Imaging (MRI) and CT were conducted on bean roots (Metzner et. al, 2015).

Adapting this technique for the visualization and analysis of growth processes of potato tubers in soil under controlled external stress conditions enables new phenotyping options. As an example the analysis for heat and drought stressed potato tubers is shown in this presentation. Time resolved measurements are conducted for four different treated batches starting directly after tuber initiation: a) Control Condition without any external stress, b) Drought stress c) Heat stress and d) Heat and drought stress combined. The stress was applied using two A1000-PG growth chambers from Conviron. It is possible to correlate the effect of the external stress to the volume and growth rate of the individual tuber itself. Additional manual segmented bean root systems at three different time stages are shown.

Keywords: Computed tomography, potato tuber, bean roots, growth kinetic, drought stress



Interactive exhibit

Water limitation in four wheat varieties during grain fill

Matthew Hayes, Adam Dimech, Delphine Vincent, Katrina Hill, Heather Anderson, Simone Rochfort, John Mason and German Spangenberg.

**Biosciences Research, Department of Economic Development,
5 Ring Road Bundoora, Victoria, Australia**

Matthew.hayes@ecodev.vic.gov.au

Four commercial Australian wheat varieties, AC Barrie, Bobwhite, Westonia and Wyalkatchem, were subjected to a period of water limitation that coincided with grain fill, and a fully-watered reference population also maintained. This controlled environment study used a gravimetric approach to track soil water, with gas exchange and SPAD measurements to track plant responses to the water limitation. At maturity, dry plant biomass, grain yield parameters and grain protein and metabolite content were also determined.

Grain mass per plant declined by more than 50% in three of the four varieties relative to fully-watered plants, while the relatively rapid cycling variety Westonia avoided the majority of the period of water limitation with grain mass reduced by 26%. The drought treatment had no impact on grain number or dry plant biomass, while grain protein and metabolite content displayed varied responses. The results are discussed in terms of method development for rapid and accurate determination of the impact of drought on grain quality, the translation of controlled environment studies to field trials and extrapolation of findings through modelling.

Keywords: wheat, drought, controlled environment, grain quality.



Interactive exhibit

The Field Imaging Platform (FIP) at ETH Zurich: Evaluation of crop development throughout the season by means of multiple sensors

Andreas Hund^a, Norbert Kirchgessner^a, Christoph Grieder^b, Kang Yu^a, Frank Liebisch^a, Achim Walter^a

^a ETH Zurich

**Institute of Agricultural Science, Universitaetstrasse 2, CH-8092 Zurich
Switzerland**

^b **Agroscope, Institut für Nachhaltigkeitswissenschaften INH
Reckenholzstrasse 191, CH-8046 Zurich, Switzerland**

andreas.hund@usys.ethz.ch

Plant phenotyping is gaining increasing importance in modern breeding. We developed a Field Imaging Platform (FIP) enabling the monitoring of different plant traits throughout the growing seasons. The platform holds visible, near infrared and thermal cameras, two spectrometers and a terrestrial laser scanner. These sensors are positioned using a cable-suspended camera positioning system from Spidercam® with a maximum payload of 12 kg. The unit holding the sensors, includes a pan and tilt drive which allows for arbitrary observation directions of the sensors. It can be freely positioned in 3D over a square field of 1 ha area. The system can be utilized for multiple purposes. One goal is to measure crop development in regular intervals (at least every three days) to identify genotypes deviating in their development (or gene loci leading to such deviation). These responses will be related to fluctuations in environmental conditions. We term this concept “opportunistic phenotyping” as the overall aim is not to expose different genotypes to a fixed stress factor but rather take advantage of fluctuating environmental conditions throughout the growing season. The FIP area currently harbors two GWAS panels, i.e. GABI-Wheat (Ganal et al. 2001) and a perennial ryegrass population, as well as variety tests of soybean, maize and buckwheat. In a prove- of-concept study with wheat, we could show that the system is capable to measure genetic variation in growth-response to temperature (Grieder et al. 2014). In the next step, we aim to map quantitative trait loci for the response of non-invasively determined canopy cover and stem elongation to climatic factors. Likewise, response to dry periods will be monitored using thermal imaging and overall senescence will be monitored using crop indices derived from hyperspectral point sensors. Here, we will present the concept of the opportunistic phenotyping approach including first result.



Interactive exhibit

ANR BacterBlé: a project to study rhizobacterial benefits for adaptation of wheat to nitrogen limitation and drought

Shram Karim^a, Noëlle Guix^a, Stéphane Sauvat^a, Jacques Le Gouis^b, Christine Girousse^b, Nicole Allard^b, Séverine Rougeol^b, Stéphane Lafarge^c, Jean-Philippe Pichon^c, Sébastien Praud^c, Claire Prigent-Combaret^d, Florence Wisniewski-Dyé^d, Daniel Muller^d, Yvan Moenne-Loccoz^d

^aVetAgro Sup

89 avenue de l'Europe - BP 35 - 63370 Lempdes, France

**^bUMR Génétique Diversité et Ecophysiologie des Céréales
INRA - UBP, UMR 1095 - Clermont-Ferrand, France**

^cBiogemma

Centre de Recherche de Chappes - Route d'Ennezat - 63720 Chappes, France

**^dUMR CRS 5557 Ecologie Microbienne
Université Lyon 1 – 69622 Villeurbanne, France**

noelle.guix@vetagro-sup.fr

Global change is a new challenge for sustainable agriculture. Thanks to ANR BacterBlé (2015-2018), we aim at understanding the usefulness of plant growth-promoting rhizobacteria (PGPR) to maintain wheat yield despite reduction of nitrogen fertilisers and irrigation. Several modes of action of PGPR may enhance plant acquisition of N or water, including modulation of the plant hormonal balance that stimulates root ramification and growth. The rationale is that indigenous PGPR populations occur in most temperate wheat soils, but (i) wheat accessions differ in the ability to benefit from PGPR and (ii) past breeding for high-input conditions has overlooked these beneficial interactions. The objectives of the project are to (i) screen a large panel of wheat diversity based on successful interaction with two *Azospirillum* and *Pseudomonas* PGPR strains under controlled conditions, (ii) determine wheat chromosomal regions involved in the interactions between roots and these PGPR strains using an association genetics approach, (iii) validate these genetic determinants and PGPR benefits in controlled environments using a small set of selected lines and (iv) assess their significance under combined abiotic constraints (nitrogen and water limitations) in field experiments. This will facilitate the breeding of genitor varieties with a successful interaction with PGPR by providing molecular markers linked to chromosomal regions associated to this interaction.

Keywords: Association genetics, Drought tolerance, Nitrogen deficiency, PGPR, Root interactions



Interactive exhibit

Osmotic stress and seedlings performances of maize genotypes from drought tolerant mini-core collection

Natalija Kravic, Violeta Andjelkovic, Vojka Babic, Jelena Vancetovic

Maize Research Institute "Zemun Polje"

Slobodana Bajića 1, 11185 Belgrade, Serbia

nkravic@mrizp.rs

Drought is one of the most important environmental stresses and the major limitation to plant growth, development and yield. Osmotic stress caused by drought may lead to oxidative stress, due to enhanced generation of reactive oxygen species in plants. This investigation was conducted on 41 genotypes from Maize Research Institute Zemun Polje gene bank drought tolerant mini-core collection of maize (15 introduced inbred lines, 13 local and 13 introduced landraces), by studying roots and shoots parameters of growth and free proline content at early seedling stage under optimal and water stress condition imposed by polyethylene glycol (PEG). High variability was determined among the investigated genotypes. Osmotic stress caused by PEG treatment led to reduction in length, fresh and dry weight of both roots and shoots in all the genotypes, being slightly pronounced in seedlings roots. Compared to control plants (optimal water condition), growth reduction in PEG-treated plants was followed by proline content increase, being more pronounced in seedling roots and particularly exhibited in inbred lines. Principal Component Analysis (PCA) for morpho-physiological parameters of investigated drought tolerant maize genotypes revealed that length and fresh weight of seedlings roots and shoots contributed to the first axes (PCA1 for control and PCA2 for treatment), which explained 55.402%, i.e., 67.800% of the total variability, respectively. The second axes, which explained 20.592%, i.e., 13.211% of the variation, respectively, were defined with dry weight and free proline content of seedlings roots and shoots. Due to almost similar distribution of the genotypes in both of the investigated environments, the results obtained indicated seedlings characteristics as relevant early indicators of drought tolerance in adult plants.

Keywords: genetic resources, roots, shoots, water deficit, *Zea mays* L.



Interactive exhibit

OïO-Tech Project: Developing new phenotyping tools adapted for plant research

Lacube Sébastien^a, Oury Vincent^b

**^{a,b} INRA, UMR 759, LEPSE
2 Place Pierre Viala, Montpellier 34060, FRANCE
lacube@supagro.inra.fr
*oury@supagro.inra.fr***

The OïO project comes from the observation that agronomics research lack of tools to precisely characterise plant morphology and development, in contrast with the increasing possibilities offered by the rapid development of new technologies (smaller sensors and controllers, wireless acquisition systems, more powerful processors for analysis ...). Moreover, while automatons are getting more and more complex, researchers are given less freedom to adapt data acquisition to their specific needs. For that purpose, OïO-Tech projects aims at developing new phenotyping systems to measure variables for both plant environment, and its morphological and physiological characteristics, while leaving intact the ability of researchers to transform and adapt both hardware and software depending on their requirements. For development, OïO-Tech is working in collaboration with the LEPSE (INRA-MONTPELLIER) to develop, test and adapt new prototypes, benefitting from the expertise and structures of a renowned research unit.

Our first product has been developed in an effort to precisely measure grain abortion linked to water stress on maize plants. After harvest, maize ears are placed into our "MaGeek Box" where the automaton automatically takes photos of the ear and analyses them to determine the number of grain and the characteristics of those grains (surface, volume, type : aborted or not). Simultaneously, OïO-Tech is developing a planimeter for destructive leaf area measurements. This prototype is designed to be highly adaptable to a big diversity of plants and includes software to treat the data and precisely calculate green leaf area. While prototyping, OïO-Tech makes it an important issue to develop both hardware and software based on open-source systems such as Linux or Raspberry Pi so that users still have the possibility to change and adapt codes and data analysis to their needs.

Keywords: OïO-Tech, automatons, phenotyping, grain abortion, leaf area



Interactive exhibit

Effects of water deficit on growth, nodulation and nitrogen fixation of peanut (*Arachis hypogea* L.)

Mohamed Lazali^a, Samira Brahimi^b, Jean Jacques Drevon^c

^aUniversité Djilali Bounaama Khemis Miliana, Faculté des Sciences Faculté des Sciences de la Nature et de la Vie & des Sciences de la Terre 44225 Khemis-Miliana, Algérie.

^bUniversité Djilali Bounaama Khemis Miliana, Faculté des Sciences Faculté des Sciences de la Nature et de la Vie & des Sciences de la Terre 44225 Khemis-Miliana, Algérie.

^cInstitut National de le Recherche Agronomique (INRA), UMR 1222 Eco&Sols, Ecologie Fonctionnelle & Biogéochimie des Sols et Agroécosystèmes, INRA-IRD-CIRAD-SupAgro. Place Pierre Viala, 34060 Montpellier, France.

m.lazali@yahoo.fr

Biological N₂ fixation represents the major source of nitrogen (N) input in agricultural soils including those in arid regions (Zahran, 1999). The major N₂ fixing systems are the symbiotic systems, which can play a significant role in improving the fertility and productivity of low-N soils (Herridge *et al.*, 2008). The rhizobia-legume symbioses have received most attention and have been examined extensively. The behavior of some N₂ fixing systems under severe environmental conditions such as salt stress, water deficit, nutrient deficiency, heavy metals, and pesticides is reviewed (Graham and Vance, 2003). The aim of this work was to evaluate growth and nodulation as well as some physiological and biochemical stress indicators in response to water deficit. In this study, three peanut genotypes (Berrihane, Oum Tboul, Timimoun) were inoculated separately with two local strains of the El Kala region of Algeria (K1 and K2). Nodulated plants were grown under glasshouse conditions with sufficient or deficient water and analyzed for their water deficit responses at the flowering stage. Our results showed that plant growth, nodulation and N₂ fixation were significantly affected by water deficit for all genotypes. In contrast, under the same conditions, root dry weight increased significantly reaching a major exploratory surface. This constraint increased the soluble sugar and proline concentrations especially for the genotypes Berrihane and Oum Tboul inoculated with K1. Additionally, the increased of water-use efficiency under water deficit was associated to an increase in efficiency in use of the rhizobial symbiosis that was positively correlated to an increase in leaf stomatal resistance. These results may contribute to identify useful physiological traits for breeding programs concerning drought adaptation in legumes.

Keywords: peanut, rhizobia, nodule, water deficit, N₂ fixation.



Interactive exhibit

Tolerance of maize to drought: a matter of aquaporins?

Linda Jeanguenin ^{1,a}, Llorenç Cabrera-Bosquet ^{2,b}, Claude Welcker ^{3,b}, François Tardieu ^{4,b}, François Chaumont ^{5,a}

^a Institut des Sciences de la Vie, Université catholique de Louvain, Croix du sud
4-L7.07.14, 1348 Louvain-la-Neuve, Belgium

^b INRA-LEPSE, 2 place Viala, 34060 Montpellier, France

linda.jeanguenin@uclouvain.be

Plant aquaporins play key roles in the cellular water permeability by enhancing the transport of water molecules across lipophilic membranes. In maize, four aquaporin subfamilies were identified, among them were found the PIPs standing for plasma membrane intrinsic proteins. Despite the fact that PIP aquaporins are water channels, their function in the plant response to water deficit is not well characterized (Chaumont and Tyerman, 2014). Gene candidate approaches based on the overexpression of one specific *PIP* gene can lead to either deleterious or beneficial effects for plants under water shortage. Microarray global expression studies on five *Arabidopsis thaliana* accessions showed a decreased transcription of most *PIP* genes under progressive drought (Alexandersson et al., 2010). In addition, physiological and pharmacological approaches conducted among several crops showed that aquaporins are involved in both leaf elongation and transpiration rates in response to atmospheric water deficit (Sadok and Sinclair, 2010; Caldeira et al., 2014). Altogether these data indicate that aquaporins are involved in the plant response to water limitation. Under the frame of the European DROPS project, the expression of 12 *PIP* isoforms was investigated by quantitative PCR in 30 maize lines grown under two contrasted water regimes in the PhenoArch phenotyping platform (LEPSE, Montpellier) where biomass, water use efficiency and transpiration were measured in parallel. Under water limitation, the mRNA level of *PIPs* belonging to the PIP1 group was weakly regulated while it was down-regulated for most *PIP2s*, in both leaf elongation and mature zones. *PIP* expression pattern to water deficit also relied upon the plant life cycle. Furthermore, principal component analysis revealed that expression of most *PIPs* contributed to the first component while biomass and hydraulic parameters contributed to the second component in well-watered conditions. Under water deficit, this distribution changed indicating that aquaporin expression adjustment to water limitation is involved in the regulation of these physiological parameters.

Keywords: Aquaporins, Leaf, Maize (*Zea mays*), Plasma membrane intrinsic protein (PIP), Water deficit



Interactive exhibit

Investigating the physiological roles of the plasma membrane aquaporin ZmPIP2;5 in maize: a transgenic approach

Thomas Milhiet ^a, Mieke Van Lijsebettens ^b, François Chaumont ^c

^a Institut des Sciences de la Vie, Université catholique de Louvain
Croix du sud 4-L7.07.14, 1348 Louvain-la-Neuve, Belgium

^b Department of Plant Systems Biology, VIB-Ghent University
Technologiepark 927, 9052 Gent, Belgium

^c Institut des Sciences de la Vie, Université catholique de Louvain
Croix du sud 4-L7.07.14, 1348 Louvain-la-Neuve, Belgium

thomas.milhiet@uclouvain.be

Aquaporins are highly regulated water channels controlling the water flow across cell membranes (Chaumont and Tyerman, 2014). In plants, they play roles in long-distance water transport and cell osmotic adjustment and thus control the plant water status under fluctuating environmental conditions. Our laboratory previously quantified the expression of plasma membrane aquaporins (PIPs, plasma membrane intrinsic proteins) in maize roots, leaves, stomatal complexes and in reproductive organs at both RNA and protein levels and showed that the expression was dependent on the organ developmental stage and environmental conditions (Hachez *et al.*, 2006, 2008, 2012; Heinen *et al.*, 2014). In general a good correlation was observed between the expression and the cell membrane water permeability. While the determination of PIP expression patterns in maize gives clues about their physiological roles, demonstrating their involvement in plant physiology requires the development of new genetic materials.

In the frame of this project, we generated maize lines overexpressing selected PIP aquaporin isoforms known to be highly and/or specifically expressed in some tissues. For instance, ZmPIP2;5 is the most highly expressed aquaporin in roots. Its association with the presence of apoplastic barriers suggests a role for ZmPIP2;5 in the regulation of radial water movement. Growth and development of transgenic ZmPIP2;5 overexpressing plants are currently analyzed in phenotyping platforms. Hydraulic parameters of both roots and leaves, such as whole root system, single cell hydraulic conductivity and stomatal conductance are under investigation. Finally, the effect of aquaporin overexpression on the growth potential and drought resistance/tolerance of these plants submitted to water deficit will be addressed.

Keywords: Aquaporin – Maize (*Zea mays*) – Plasma membrane intrinsic protein (PIP) – Water movement – Drought tolerance



Interactive exhibit

Diversity of mesophyll conductance to CO₂ in wheat affecting leaf photosynthesis and WUE under drought in reproductive growth stage

Katarina Olsovska^a, Marian Brestic^a, Marek Zivcak^a, Pavol Slamka^a, Pavol Hauptvogel^b

^a Faculty of agrobiolgy and food resources, Slovak University of agriculture in Nitra, Slovak Republic,

^b National Agricultural and Food Center - Research Center of plant production in Piešťany, Piešťany, Slovak Republic

katarina.olsovska@uniag.sk

The contribution of mesophyll versus stomatal factors to leaf photosynthesis limitation and its causality in bread wheat under drought in reproductive growth stage has not been sufficiently studied yet. Also a shift of mesophyll conductance to CO₂ diffusion within a dehydrated photosynthesizing leaf to higher values in modern hexaploid comparing to di- and tetraploid wheat genotypes allowed to improve this characteristics during evolution of ploidy and enhanced wheat photosynthesis and productivity. In a pot vegetation experiment with wheat genotypes and species of different level of ploidy plants were exposed to a progressive dehydration at the beginning of ear formation. During graduating water stress basic photosynthetic characteristics of flag leaves related to leaf water status were derived from gas exchange measurements and intrinsic water use efficiency was calculated on leaf base. Quantifications of non-stomatal limits to leaf photosynthesis were based on A/c_i curve measurements and analyses according to Sharkey et al. (2007). Proportion of mesophyll (L_m) and stomatal (L_s) limitations to total A_{CO₂} limitation was evaluated in relation to genotype- and species-based variability. The results show that in modern wheat genotypes the mesophyll (g_m) rather than stomatal (g_s) conductance has an effect on A_{CO₂} variation under drought and is determined mostly by biochemical (V_{c_{max}}) and anatomical (SLA) limits. However, their contribution in *T. monococcum* and *T. dicoccum* was equal. Genotype Biscay reached the highest g_m allowing the highest CO₂ assimilation during whole period of dehydration comparing to the lowest g_m and A_{CO₂} in *T. monococcum*. "

Keywords: drought, genotypes, mesophyll conductance, water use efficiency

Supported by grant APVV-0197-10 and EU project no 26220220180: Building of AgroBioTech Research Centre



Interactive exhibit

Positive effect of putrescine pre-treatment against drought stress in wheat

M. Pál, G. Szalai, É. Darkó, T. Janda

Agricultural Institute, Centre for Agricultural Research, Hungarian Academy of Sciences,

H-2462 Martonvásár, Hungary

pal.magda@agrar.mta.hu

Polyamines are aliphatic amines found in all living cells. The most abundant polyamines in plants are putrescine (PUT), spermidine, and spermine. Polyamines were presumed to be just direct protective compounds. Besides their direct protective role, they also regulate various fundamental cellular processes as signalling molecules. It has been increasingly shown that the role of polyamines in signalling processes rather than their accumulation chiefly influences abiotic stress tolerance. Application of exogenous polyamine treatments under normal growth and stress conditions can show which other compounds or processes may be influenced. Present study focuses on this aspect of the mode of action of polyamines.

7-day-old wheat plants were treated with 0.5 mM PUT in hydroponic solution for 7d. After 7 days of PUT pre-treatment half of the plants were moved to control conditions ("recovery"), other half of them were exposed to PEG-induced drought stress (15% PEG 6000 for 5 days). PUT pre-treatment increased the root endogenous PUT level, and slightly influence the salicylic acid (SA) content and antioxidant enzyme activities. If 7d PUT treatment was followed by 7d recovery, PUT pre-treated plants have higher biomass compared to the control, but differences in the PUT and SA contents, and antioxidant enzyme activities were disappeared. The beneficial effect of 0.5 mM PUT pre-treatments against drought stress have been proved by photosynthetic parameters (P_n and g_s), prolin content and lipid peroxidation in PEG+PUT-treated wheat plant. Results suggest that PUT could be promising compound for the reduction of abiotic stress sensitivity in plants. It has been revealed that polyamine signalling is involved in direct interactions with other metabolic routes and hormonal cross-talks, but the precise mechanism by which polyamines, as PUT control plant responses are largely unknown.

Keywords: drought stress, putrescine, protective compounds, wheat

This work was funded by OTKA K108811. We would like to thanks also for DROPS project.



Interactive exhibit

Study of the drought tolerance in bread wheat by ear phenotyping.

N. Baillot^a, S. Schoettel^a and A. Piquet^{ab}

^aVetAgroSup, campus agronomique, 89 avenue de l'Europe, 63370 Lempdes

^bINRA, UMR GDEC, 5 chemin de Beaulieu 63039 Clermont-Ferrand Cedex 2

Drought affects wheat component yield particularly the Number of Grains per square Meter (NG/m²) during tillering and stem elongation stages by water stress and the Thousand Weight Grains (TWG) during grain filling by heat stress (Brisson et al., 2010). In a context of research for varietal tolerance under real climatic conditions, the aim of the project proposes to develop fine phenotyping of wheat spike in relation with the crop physiology to understand the process of cereal reproduction under drought stress and to characterize the most tolerant varieties.

A conventional experimental site (INRA Clermont-Ferrand-63) was conducted in 2014 with four different bread wheat varieties: VRC (referent in conventional system), VRB (referent in organic system), V1 and V2 (new varieties recommended in organic crop). After driving a crop diagnosis, grain distribution within 16 spikes for each variety was studied to characterize the climate impact on ear phenotype during 2014.

A drastic decrease (fifty percent) of average rainfall compared to the normal values was observed in May and June of 2014. On the other hand the average temperatures remained lower than the critical temperatures. The results show that VRC has a higher yield than the others during this year (VRC = 67.7 q/ha; V1 = 61q/ha; V2 = 58.8 q/ha; VRB = 49.4q/ha). NG/m² is the yield component affected. Ear phenotyping indicates that spikelet number per spike and grain number per spikelet both explain NG/m² decrease. VRC has the highest levels for these two subcomponents and appears as the more efficient variety for maintaining the highest level of flower fertility.

The results of ear phenotyping show that the drought tolerant ideotype should present a precocity in the development of flowers and their fertility to avoid stress hydric marked from May even those of heat.

Keywords: wheat; ear; phenotyping; drought; yield



Interactive exhibit

Parameters derived from fluorescence induction curves are powerful tools for characterizing plants adaptive strategies to water deficit according to genotype and developmental stage

Julie Ripoll a, Nadia Bertin b, Laurent Urban c

a PhD looking for job opportunities

**258 boulevard Romain Rolland, Résidence la Pauline, Bat. 12 Porte C, 13009
Marseille, France**

b Plantes et Systèmes de Culture Horticoles (UR1115)

**INRA PACA, Domaine St Paul Site Agroparc, CS 40 509 - 84914 Avignon Cedex
9, France**

c Laboratoire de Physiologie des Fruits et Légumes (EA4279)

**Université d'Avignon et des Pays du Vaucluse, Pôle Agrosociétés - Campus
Agroparc, 301 rue Baruch de Spinoza, BP 21239, 84916 AVIGNON Cedex 9,
France**

julie.ripoll87@gmail.com

Climate change has significant and increasing impact on water resources. Breeders will need tools easy to use and non-destructive, to assess the sensitivity of different genotypes to stress conditions. In this study, tomato plant responses were studied during a complete soil drying at the vegetative and reproductive stages and during repeated cycles of water deficit (WD) and recovery periods at the reproductive stage. Four tomato genotypes selected for their strong allelic differences were investigated. Leaf stomatal conductance (g_s), chlorophyll content and chlorophyll *a* fluorescence were measured and the parameters derived from OJIP transients were calculated. Specific and common responses to soil drying were found according to genotypes and developmental stages. Genotypes differed mainly by the way they dissipate energy in processes other than trapping (JODI). Strong decreases in the turnover number (N) and the normalized area (S_m) were observed only at the vegetative stage. Both vegetative and reproductive plants during the soil drying were characterized by low g_s , high chlorophyll content, a decrease in the Performance Index for energy conservation from photons absorbed by PSII antenna until the reduction of PSI acceptors (PIABSTOT) as well as JORE1/JABS (the quantum yield of the electron transport flux until the PSI acceptors). Reproductive plants of the repeated cycle treatment have offset the decrease in JORE1/JABS. We suggest that the cyclic electron flow which was described as an adaptive process to drought or heat stresses was at the origin of the decrease in the electron flux until PSI acceptors. Taken together our observations suggest that parameters derived from OJIP transients are pertinent indicators to analyse and distinguish specific strategies among tomato plants submitted to different WD and that they could be useful for breeders.

Keywords: Chlorophyll fluorescence, Plant developmental stage, Water deficit, OJIP transients, *S. lycopersicum* L.



Interactive exhibit

“CHN”, a crop model using in addition to high performance phenotyping platforms for estimate genetic traits on maize like RUE or WUE

X. Le Bris^a, B. Soenen^{b*}, B. Piquemal^c, D. Gouache^d

^a ARVALIS - Institut du végétal La Jaillière (44), ^b ARVALIS - Institut du végétal Baziège (31), ^c ARVALIS - Institut du végétal Boigneville (91), ^e ARVALIS - Institut du végétal Paris (75) – France

b.soenen@arvalisinstitutduvegetal.fr

“CHN” is a mechanistic crop model with a system soil-plant-atmosphere. It estimates daily flows of carbon (C), water (H) and nitrogen (N) between the different compartments of system. Soil compartment is connected to a database, which regroups different soils per French region, and use pedotransfert functions for estimating useful characteristics of soil. Stocks of water, carbon (stable and labile pools) and nitrogen (urea, ammoniac, nitrate and organic pools) are daily modeling per horizons of 1 cm deep. Atmosphere compartment is connected to a database, with multiannual weather data throughout France. Plant compartment is based on Monteith approach (Monteith, 1997): leaf growth is modeled and leaf area intercepts radiation, which is converted on biomass. Roots growth is modeled too and permits to determinate nitrogen and water available for the plant. Growth is affected by nitrogen and water deficiency, according to functions of stress response developed by Sinclair (Sinclair, 1986). Modeling physiology of crop development stage is necessary and models of ARVALIS - Institut du végétal are used. This compartment is actually running on winter wheat and maize.

This crop model can be used to manage nitrogen and water, or even to characterize growth conditions of phenotypic trials in order to improve the understanding of genotype – environment interactions. Moreover another application is possible in addition to high performance phenotyping platforms: it is possible to estimate genetic traits on maize, which are parameters of “CHN” model, like Radiation Use Efficiency (RUE) or Water Use Efficiency (WUE). Indeed a deviation of a model with generic parameters could be explained by a genetic variability.

Keywords: crop model, genetic variability, phenotyping



Interactive exhibit

Different strategies of seedlings of two *Sorghum bicolor* lines to deal with drought stress

SUTKA Moira R.^a, VITALI Victoria A., AMODEO Gabriela, MANZUR Milena E.

Instituto de Biodiversidad y Biología Experimental y Departamento de Biodiversidad y Biología Experimental, Facultad de Ciencias Exactas y Naturales, Universidad de Buenos Aires y Consejo Nacional de Investigaciones Científicas y Técnicas, Buenos Aires, Argentina. Piso 4 Pabellon II Ciudad Universitaria Int. Güiraldes 2160 C1428EGA Buenos Aires | ARGENTINA
Tel. (54 11) 4576 3300 int. 201. Fax: 4787-2706.

moirasutka@bg.fcen.uba.ar

Sorghum [*Sorghum bicolor* (L.) Moench.] is an ancient drought tolerant crop with potential to replace other cereals not capable to sustain high yields in low or erratic precipitation conditions, a feature on the rise due to climate changes. Understanding the performance of this species in early phenological stages could be a useful tool for future yield improvement programs. The aim of this work was to study the response of sorghum seedlings under drought conditions in two genotypes employed as parental lines in our country: RedLandB2 and IS9530. We characterized morphological, anatomical and physiological parameters at the whole plant level under control and drought conditions in order to perform an integrated study. We found that both lines developed different physiological strategies when were exposed to water restriction. Although both lines were able to change biomass allocation to roots under drought, they showed different root architecture between them. Interestingly, both sorghum lines were able to adjust their plant resistances to water loss at different level: RedLandB2 regulates stomatal resistance (isohydric strategy), while IS9530 controls root resistance (anisohydric strategy). The latter genotype differentially adjusts root hydraulic conductance, where the cellular pathway could be more relevant in such process, involving water channel activity. Moreover, only in IS9530 root hydraulic conductance was restricted in the presence of HgCl₂, in agreement with aquaporins activity. This performed approach adds new information for sorghum species that can be used to evaluate phenotypic plasticity for changing environments. Our result provides also new insight in terms of anisohydric and isohydric strategies that can be developed by plants in relation to water management. However, it is still necessary a thorough study to address the physiological/molecular mechanisms triggered in response to drought, including in this scenario the role of aquaporins.

Keywords: aquaporins, drought, hydraulic conductance, Sorghum, stress tolerance.



Interactive exhibit

Impact of green leaf area dynamics on stem sugar production in sorghum: sowing date and post-flowering water status influence

Thierry Klanvi TOVIGNAN ^{a*}, Daniel FONCEKA^a, Ibrahima NDOYE^b, Ndiaga CISSE^a, Delphine LUQUET^c

^a Centre d'Etudes Régional pour l'Amélioration de l'Adaptation à la Sécheresse (CERAAS), BP 3320, Route de Khombole, Thiès, Sénégal

^b Département de Biologie Végétale, Université Cheikh Anta Diop de Dakar, BP 5005, Dakar, Sénégal

^c CIRAD, UMR AGAP, F-34398 Montpellier, France

thierryt525@gmail.com

Sorghum offers the opportunity to combine grain and stem sugar production in West-African drought prone environments. This study investigated to which extent plant green leaf area dynamics and its regulation by sowing date and post-flowering water availability, influences sugar accumulation in sweet sorghum stem. A field trial was conducted at CNRA of Bambey (Senegal). Twelve photoperiod-sensitive genotypes with contrasted morphology but similar phenology were grown during the rainy season 2013 using two sowing dates (July and August) and two post-flowering water regimes (dry-down and well-watered). Leaf appearance, area and senescence were weekly measured on the main stem as tillering was negligible. Panicle, stem dry weight and stem sugar content were measured at anthesis and maturity.

August sowing shortened the vegetative phase and accordingly the number of appeared leaves, with various extents depending on the genotype. It increased leaf appearance rate but did not modify individual leaf area. Accordingly, plant green leaf area was almost doubled at flowering with July sowing. It was significantly correlated with stem biomass and sugar content (both $R^2=0.5$) at anthesis and with panicle dry weight at maturity. Grain dry weight per panicle was significantly affected by sowing date and water treatment. Stem sugar content at maturity was significantly higher and less affected by water stress in July compared to August sowing. Only genotypes with large plant green leaf area at anthesis, and maintaining about 50% of green leaves until dough grain stage, maintained sugar content under stressed condition.

The benefits of early sowing and large green leaf area to minimize water stress effect and combine sugar and grain production is highlighted.

Keywords: Sweet sorghum, multipurpose, photoperiod-sensitivity, stem sugar production, stay-green, post-flowering drought



Interactive exhibit

Genotypic variation for water-deficit tolerance in *Gossypium hirsutum* L.

Waqas Shafqat Chattha¹, Rana Muhammad Atif^{1, 2}, Zaigham Shahzad³, Farrukh Azeem⁴, Amir Shakeel¹

¹Department of Plant Breeding and Genetics, University of Agriculture Faisalabad, Pakistan,

²Pakistan center for Advanced Studies in Food Security-Agriculture, University of Agriculture Faisalabad, Pakistan,

³Biochimie et Physiologie Moléculaire des Plantes, UMR 5004 Montpellier, SupAgro/CNRS/INRA/Univ, France,

⁴Department of Bioinformatics and Biotechnology, GC University Faisalabad.

waqas1518@gmail.com

Aggravating scarcity of water for irrigation is a major constrain to sustainable cotton production in Pakistan. One of the ways is to develop drought-tolerant varieties and the other one is screening of existing germplasm for drought tolerance. Physiological and biochemical parameters along with agronomic traits provide a much useful indication for water-deficit tolerance. To find out genotypes having better drought tolerance, 45 genotypes of *Gossypium hirsutum* were studied under two moisture levels i.e. well watered (28 acre inches) and water deficit (16 acre inches) conditions. An additional moisture of 9.6 acre inches was received in the form of precipitation. The experiment was planted employing RCBD with split plot arrangement. Data for different physiological, biochemical and agronomic traits were recorded and analyzed using bi-plot analysis technique. Water stress affected all parameters adversely and genotypes responded differently under normal and stress conditions. Eventually, genotypes, CRS-2009, FH-155, FH-207, FH-322, IR-6, NS-131 and S-15 performed better in water-deficit condition with higher stability index of photosynthetic efficiency, water potential, osmotic potential, relative water content, bolls per plant, boll weight, and seed cotton yield; whereas these genotypes accumulated more proline and protein content and comparatively low canopy temperature. It is concluded that CRS-2009, FH-155, FH-207, FH-322, IR-6, NS-131 and S-15 are best suited for cultivation under water deficit conditions.

Keywords: Water deficit, Precipitation, Stability index, Drought tolerance



Interactive exhibit

PHENODYN: a high throughput platform for measurement of organ elongation rate and plant transpiration with high temporal resolution

S. Berthézène¹, N. Brichet¹, V. Nègre¹, B. Parent¹, B. Suard¹, A. Tireau², O. Turc¹, F. Tardieu¹, C. Welcker¹

INRA, LEPSE¹ or MISTEA² Place P. Viala. 34060 Montpellier. France

Leaf elongation rate (LER) is the first trait affected by water deficit or high evaporative demand, with typical time constants of 30 min for change in LER upon rapid changes in soil water content or air vapour pressure deficit (VPD). The same applies to other organs such as maize silks. Phenodyn (<https://www6.montpellier.inra.fr/lepse/M3P/plateforme-PHENODYN>) measures organ elongation rate and transpiration rate of hundreds of plants with a temporal resolution of 3 min (or more if required) in order to follow the changes in LER and transpiration in fluctuating conditions of soil water content, evaporative demand and temperature. Phenodyn imposes known soil water potentials to each plant via independent automatic irrigation. Climatic conditions are either imposed in the growth chamber or left to naturally fluctuate in the greenhouse. Elongation rate is measured with 500 rotational displacement transducers with a precision of 0.2 mm. Transpiration and soil water content are measured with scales; changes in weight are attributed to changes in soil water content after correction for the increase in plant biomass. A set of sensors measures meristem temperature, incident light, air temperature and VPD every minute. Phenodyn is associated to an information system for real time monitoring of experiments, post-analysis of large datasets (around 700.000 data points are generated in each experiment) and identification of genotypic parameters such as rates or time constants. It has been used (i) for analyzing the response of LER to soil water potential and to VPD in mapping populations, diversity panel for association genetics or insertion lines, (ii) for establishing response curves to temperature in different species and genotypes, (iii) for following jointly changes in transpiration and in elongation rates of leaves or silks together with hydraulic variables. It has been used in maize, rice, wheat, sorghum, millet, apple tree and vine. Phenodyn is part of the M3P facility (<https://www6.montpellier.inra.fr/lepse/M3P>). It is accessible to public or private scientists via the website of the national project Phenome-FPPN (<https://www.phenome-fppn.fr/>).



Interactive exhibit

PHENOARCH, a multiscale phenotyping platform for plant architecture, growth rate, water use efficiency and radiation use efficiency

L. Cabrera Bosquet¹, N. Brichet¹, C. Fournier¹, A. Grau¹, J. Mineau¹, V. Nègre¹, P. Neveu², B. Suard¹, A. Tireau², C. Welcker¹, F. Tardieu¹

INRA, LEPSE¹ or MISTEA² Place P. Viala. 34060 Montpellier. France

PHENOARCH (<https://www6.montpellier.inra.fr/lepse/M3P/plateforme-PHENOARCH>) measures traits associated to the plant adaptation to climate change with a throughput of 1650 plants. Typical measured variables are the timing of the plant cycle (phyllochron, duration of phenological phases), plant growth rate in terms of area and biovolume, plant architecture in terms of ramification and angles, light interception, radiation use efficiency and water use efficiency. Soil water potential is controlled individually for each plant via scales; changes in weight are attributed to changes in soil water content after correction for the increase in plant biomass. Microclimatic data fluctuate naturally within a range fixed by users. A set of sensors measures meristem temperature, incident light, air temperature and VPD every minute. A 3D model of the greenhouse allows inferring the environmental conditions sensed by each individual plant by calculating spatial gradients in the greenhouse each day of the year. Plants are imaged every day with 12 side views and one top view, which allow reconstructing a digital 'avatar' of each plant of the platform. Calculations related to plant architecture and to individual organ size are carried out on these virtual plants. Light interception by each plant in the platform is calculated via a virtual scene consisting of the 1650 3D virtual plants in their real positions. The measured timecourses of biomass and of intercepted light, combined with local measurements of light intensity, allow estimation of radiation use efficiency. Responses to water deficit and evaporative demand can be analysed by combining time courses of leaf area or biovolume with environmental data. PhenoArch is associated to an information system for real time monitoring of experiments, post-analysis of large datasets and identification of genotypic parameters such rates, architectural parameters or sensitivities. It has been used for (i) association genetics in panels of genotypes (diversity, MAGIC or biparental crosses), (ii) in-depth analyses of smaller panels such as panels of genetic progress or introgression lines, for morphological or physiological traits, (iii) estimation of parameters of crop models that are then tested and used in the field. PhenoArch has been used with maize, rice, sorghum, wheat, apple tree and vine. It is part of the M3P facility (<https://www6.montpellier.inra.fr/lepse/M3P>) and is accessible to public or private scientists via the website of the national project Phenome-FPPN (<https://www.phenome-fppn.fr/>). Accesses have also been provided via the infrastructure EU project EPPN.



Interactive exhibit

PHENOPSIS: from a phenotyping platform to a whole pipeline of analyses.

M. Dauzat, A. Bédiée, C. Balsera, G. Rolland, D. Vile, B. Muller, V. Nègre, C. Granier

INRA-SUPAGRO, LEPSE- Place P. Viala. 34060 Montpellier. France

A major goal of the life sciences is to understand and model how molecular processes control phenotypes and their alteration in response to biotic or abiotic stresses. The study of *Arabidopsis thaliana* genomics is providing new insights into the understanding of these processes. The functional analysis of genes associated with these responses is made possible by the phenotypic analyses of mutants or natural genetic variants, high-throughput genetic mapping and large-scale analyses of gene expression. Ten years ago, an important bottleneck was the phenotypic analysis of the genetic variability, which requires simultaneous analysis of hundreds to thousands of plants. The PHENOPSIS platform provide since 2002 large quantities of micro-meteorological data, images and phenotypical data for the study of genotype x environment interaction effects on different plant processes in *A. thaliana*. Protocols have been standardised to allow reproducibility between experiments and facilitate meta-analyses. Phenopsis is part of the M3P facility (<https://www6.montpellier.inra.fr/lepse/M3P>). It is accessible to public or private scientists via the website of the national project Phenome-FPPN (<https://www.phenome-fppn.fr/>). Database, ontologies, image analyses and statistical tools ensure that the data produced by specific groups can benefit other groups in analyses of which the purposes extend beyond the ones that have been published.



Interactive exhibit

Development of a fully automated PHENOMOBILE for field phenotyping

B. de Solan¹, F. Baret², S. Thomas¹, K. Beauchene³, A. Comar^{2,4}, A. Fournier³

¹*Arvalis institut du végétal, UMT CAPTE Avignon, France*

²*INRA, EMMAH, UMT CAPTE¹ Avignon, France*

³*Arvalis institut du végétal, Ouzouer le Marché, France*

⁴*HIPHEN, Avignon, France*

The capacity for detailed high throughput phenotyping in field conditions is mandatory to better describe structural and functional traits over large collections of micro-plots. An Unmanned Ground Vehicle called PHENOMOBILE-V1 was developed for this purpose within the framework of the PHENOBLE and PHENOME projects. The vehicle moves automatically over the micro-plots following predefined trajectories within a centimeter accuracy using GPS-RTK positioning. It is made of 4 driving and steering wheels. The PHENOMOBILE-V1 spans over the micro-plots with an adjustable width. All the systems are powered by electricity produced by an electrogen group. A platform with automatically adjustable height is equipped with several sensors. They include RGB cameras for organ counting and green fraction measurement, spectroradiometer working in the visible and near infrared domain for canopy biochemical composition estimation, and LIDARs for 3D description of the canopy architecture. All these measurements are performed from nadir and inclined directions to acquire more information on canopy structure. The sensors are running in active mode (flash) to be make the measurement fully independent from the natural illumination conditions. All the sensors are triggered automatically according to predefined acquisition scenarios.

The system is currently providing a throughput around 150 micro-plots per hour, allowing to sample around 1000 micro-plots within 8 hours. The system may also run during the night. A dedicated processing chain was developed to transform the row data into higher level products while significantly reducing the data volume.

The poster presents the main characteristics of the PHEOMOBILE-V1 as well as the first results obtained over a wheat experiment that includes the dynamics over the whole growth cycle of canopy height, green fraction, FIPAR (Fraction of Intercepted Photosynthetically Active Radiation) and GAI (Green Area Index).



Interactive exhibit

PHENOME: French Plant Phenomic Center

F. Tardieu¹, J LeGouis², P. Lucas³, F Baret⁴, P. Neveu⁵, C Pommier⁶, N Hilgert⁵, D Gouache⁷, X Pinochet⁸.

¹INRA LEPSE, Montpellier, ²INRA GDEC, Clermont Ferrand, ³INRA Transfert, ⁴INRA-Arvalis CAPTE, Avignon, ⁵INRA MISTEA, Montpellier, ⁶INRA URGI, Versailles, ⁷Arvalis, ⁸Cetiom

Climate change causes an increased frequency of unfavourable environmental scenarios with abiotic and biotic stresses, requiring the development of novel adapted varieties. Phenotyping is the major limitation for selecting genotypes in this context. *Phenome* (www.phenome-fppn.fr) develops a versatile, high-throughput infrastructure and a suite of methods allowing characterisation of hundreds of genotypes of different species under environmental scenarios of climate changes (e.g. drought, high CO₂ and high temperatures).

The infrastructure consists of (1) two platforms in controlled conditions (capacity of 1700 plants each) for in-depth analysis of leaf or root system architectures and growths under ranges of water deficits, CO₂ concentration and temperature; (2) two field platforms with semi-controlled environments, in particular large rainout-shelters and one free-air carbon enrichment (FACE) system (capacity 800 individual plots each); (3) three field platforms with higher throughputs (capacity 2000 individual plots each) equipped with soil and climate sensors. All platforms can cope with throughputs of 200-300 genotypes with the necessary number of repetitions and manipulate and/or control environmental conditions in order to impose well-characterised scenarios. Platforms are equipped with a consistent set of 3D functional imaging techniques, namely detailed imaging of roots and shoots in controlled conditions, canopy imaging with an autonomous 'phenomobile' that captures functional and 3D images of each plot, and drones that image hundreds of plots jointly. Two supporting platforms centralise metabolomic and structural measurements associated with phenotyping experiments. Platforms are accessible to public and private partners via the project website.

Applications with technological jumps are developed at infrastructure level, with partnerships with French SMEs. They (1) improve our capacity to measure plant traits at different resolutions in field and platforms (eg root and shoot architectures, light interception, transpiration rate) and environmental conditions (novel sensors); (2) organise phenotypic data originating from different platforms, so that they can be saved and analysed for a long period by a wide scientific community; (3) handle very large datasets with applications on data cleaning via artificial intelligence and analyses of time-related data; an interface with plant and crop models is developed. These methods and techniques are widely transferred towards the phenotyping community, academic and industrial. Phenome has already resulted in the development of SMEs aimed at phenotyping and/or precision agriculture (including one spin off, several patents and new activities of already existing SMEs. Networking and training activities are developed towards seed companies, SMEs and the extension system.

Phenome is part of an Infrastructure (I3) European project (EPPN) and is participating to an initiative for a preparatory phase for a European ESFRI infrastructure. It participates to the French national roadmap of Infrastructures with a widened partnership (CEA, CNRS, INRA).



Interactive exhibit

M3P : the "Montpellier Plant Phenotyping Platforms "

Claude Welcker, Llorenç Cabrera, Anthonin Grau, François Tardieu, Vincent Nègre, Nicolas Brichet, Benoît Suard, Jonathan Mineau, Myriam Dausat, Christine Granier, Bertrand Muller

Laboratory of Plant Ecophysiology under Environmental Stresses, INRA-SUPAGRO, Place P. Viala. 34060 Montpellier. France

The research group **LEPSE**, ranked among the top 5% research group in ecophysiology worldwide in 2014 by a panel of experts is developing high throughput phenotyping platforms for more than 15 years. Three complementary platforms, embarking 500 to 1700 plants simultaneously, aim to analyze and model genetic variability of plant responses to environmental stresses and climate change (mainly drought and elevated temperature). These platforms host large collections of genotypes of the same species, evaluate their tolerance and obtain relevant parameters that will be injected into predicting models allowing the selection and the breeding of future, tolerant and more efficient varieties.

These platforms are gathered into "**Montpellier Plant Phenotyping Platforms**" (M3P), that is a full member of the "Investment for the future" initiative PHENOME. The platforms hosts ~ 50% of external access in the frame of national and international projects on a variety of species (maize, wheat, grapevine, apple tree, sorghum, millet, rice, *A. Thaliana*).



Session 4: Dealing with Genotype x Environment interaction

Keynote speaker

Analysis of GxE in maize by multi-environment GWAS and genomic prediction

Fred van Eeuwijk & Willem Kruijer
Wageningen Universiteit

willem.kruijer@wur.nl, fred.vaneeuwijk@wur.nl

To analyse the performance of a maize diversity panel under varying intensities of drought stress, we developed a modelling framework for multi-environment GWAS and genomic prediction. In our mixed model framework, the GxE matrix of genetic effects is structured as a (Kronecker) product of a genetic and environmental relationship matrix. For the environmental relations various structure options exist, but factor analytic models appeared to be the most suitable ones. For the estimation of the environmental relationship matrix we compared the common average information algorithm with a new EM based algorithm. We illustrate the methodology for various traits in EU-DROPS.



Keynote speaker

Investigating the unstability of yield-related QTL in wheat

Delphine Fleury¹, Boris Parent^{1,2}, Fahimeh Shahinnia^{1,3}, Pauline Thomelin¹, Julian Taylor⁴, Peter Langridge^{1,5}

1 Australian Centre for Plant Functional Genomics (ACPGF), The University of Adelaide, PMB 1, Glen Osmond, SA 5064, Australia.

2 INRA, Unité Mixte de Recherche 759 Laboratoire d'Ecophysiologie des Plantes sous Stress Environnementaux, 34060 Montpellier, France.

3 Leibniz Institute of Plant Genetics and Crop Plant Research (IPK), 06466 Gatersleben, Germany

4 Biometry Hub, The University of Adelaide, PMB 1, Glen Osmond, SA 5064, Australia.

5 School of Agriculture, Food and Wine, The University of Adelaide, PMB 1, Glen Osmond, SA 5064, Australia.

In Australian dryland agriculture, grain crop yields are approximately 50% of their potential and are highly unpredictable. During the 1990's, the rate of productivity increase in Australian broad acre cropping improved by 3.4% annually but has since slowed and declined by -1.4% in drought years. Although many Quantitative Trait Loci (QTL) have been identified in cereals for yield in dry environments, using these QTL in marker assisted selection is still difficult. Genomic resources have tremendously increased in the last years, which help making progress in fine mapping QTL. However many of these QTL are "unstable" across environment. Over ten years program, the ACPFG has cumulated QTL information on three genetic populations for yield, agronomical and morphological traits in various locations in Australia, India and Mexico. Multi-environment analysis showed that the positive allele at chromosome 3B QTL significantly increased yield in deep soils, but less so in shallow soils. By measuring accurately the environmental variables and using ecophysiological models, we can dissect the response to the environment into elementary and simpler traits and identify the conditions where a QTL is specifically expressed. Such detailed information is crucial for breeding application.



Selected talk

Genetic variability of the sensitivity of grain number to drought and high temperature in maize

Millet Emilie^a, Negro Sandra^b, Kruijer Willem^c, Nicolas Stéphane^b, Van Eeuwijk Fred^c, Charcosset Alain^b, Welcker Claude^a, Tardieu François^a

^a INRA - Laboratoire d'Ecophysiologie des Plantes sous Stress Environnementaux

Batiment 7, 2, place VIALA 34060 Montpellier Cedex 02, France

emilie.millet@supagro.inra.fr, claude.welcker@supagro.inra.fr,

françois.tardieu@supagro.inra.fr

**^b INRA - Génétique Quantitative et Evolution - le Moulon
Ferme du Moulon, 91190 Gif-sur-Yvette, France**

ssnegro@versailles.inra.fr, snicolas@moulon.inra.fr, alain.charcosset@moulon.inra.fr

**^c WU Plant Sciences – Mathematical and Statistical Methods
Droevendaalsesteeg 1, 6708PB Wageningen, Nederlands**

willem.kruijer@wur.nl, fred.vaneeuwijk@wur.nl

With climate changes, crops will be subjected to more frequent episodes of drought and high temperature. Plant breeders attempt to maintain or increase grain yield in spite of these conditions. We have considered the possibility that data originating from a network of field experiments may serve for estimating the genetic variability of the sensitivity of yield to temperature and water deficit, provided that they are combined with data originating from a phenotyping platform and with detailed environmental characterization of each field. Here, we have developed a method for deriving the sensitivity of each genotype to temperature and soil water deficit by performing a joint analysis of phenotypic and environmental data. We have analyzed a population of maize hybrids generated by crossing a common flint parent with 250 dent lines. Lines were genotyped with 650K SNPs. Hybrids were phenotyped for grain yield and components in 27 combinations of site x year x treatment involving contrasted water regimes in Europe. Phenology and growth traits of the same hybrids were also measured in the PhenoArch platform. The growth cycle of each hybrid was divided into time intervals from plant emergence to maturity, based on leaf number and ear morphogenesis whose relations with thermal time were established in the phenotyping platform for each hybrid. We have then established the response curves of yield to mean temperature or soil water potential in each time interval for each hybrid. Sensitivities to temperature and water potential were estimated as the slope of these response curves, and analyzed via genome wide association mapping. This study will allow better understanding of mechanisms involved in tolerance to drought and high temperature. It may give way to novels indicators of GxE interactions that might be used in breeding programs to improve the tolerances to conditions associated with climate changes.

Keywords: Maize (*Zea mays*), yield, association mapping, drought, temperature



Selected talk

Genetic and ecophysiological dissection of tolerance to drought and heat stress in bread wheat: from environmental characterization to QTL detection

Bruno Bouffier^a, Jacques Le Gouis^b, Jeremy Derory^a, Matthew Reynolds^c, Alain Murigneux^a

^a**Limagrain Europe, Native Trait, Genetic resources and Pre-breeding
Site de La Garenne, CS 3011, 63720 Chappes, France**
brunobouffier@yahoo.fr, jeremy.derory@limagrain.com, alain.murigneux@limagrain.com

^b**UMR Génétique Diversité et Ecophysiologie des Céréales
INRA - UBP, UMR 1095 - Clermont-Ferrand, France**
Jacques.legouis@clermont.inra.fr

^c**CIMMYT Int.
Apdo. Postal 6-641, 06600 Mexico, DF, Mexico**
m.reynolds@cgiar.org

Wheat is the most widely cultivated crop worldwide and experiences a range of stresses including drought and high temperature. Identifying traits and chromosomal regions linked to such stress is of paramount importance for breeding. The aims of this work were to characterize the stresses occurring in the experimental network, to dissect the genotype x environment interaction, and to identify QTL involved in tolerance to these stress and quantify there interaction with the environment.

Three bread wheat recombinant inbred lines populations resulting from crosses of elite lines combining complementary tolerance to drought and high temperature stresses were grown over three years under irrigated and drought winter sowings, and heat-irrigated spring sowing in the north-western Mexican desert of Sonora. This constituted a 15-trial network within which agronomic and physiological traits were scored.

An environmental characterization was first performed leading to the identification of six environmental scenarios within the network. A representative and informative covariate was selected to represent each of them. A factorial regression using these covariates was then performed. This highlighted differential stress sensitivity of the germplasm studied and revealed a larger interaction with the environment of physiological traits (e.g. canopy temperature) than agronomical traits (e.g. yield). Finally, a multi-environmental QTL detection resulted in the discovery of several genomic regions involved in the control of both physiological and agronomical traits and the sensitivity of QTL effect to specific environmental conditions.

This study enabled the evaluation of the performance of all genotypes in a range of environments and the dissection of the tolerance mechanisms involved. It also permitted the identification of genomic regions involved in the control of tolerance to drought and heat stress in bread wheat. After validation through fine mapping, these regions could be used to improve wheat drought and heat tolerance by pyramiding interesting QTL.

Keywords: Breeding, Factorial regression, GxE, QTLxE, *Triticum aestivum*



Keynote Speaker

Modelling G x E x M with explicit genotypic information

**Graeme Hammer^a, Greg McLean^b, Scott Chapman^c, Bangyou Zheng^c, Al Doherty^a,
Matthew Harrison^d, Erik van Oosterom^a, David Jordan^e, Charlie Messina^f**

^a **The University of Queensland, Queensland Alliance for Agriculture and Food Innovation, Brisbane, QLD 4072, Australia. Email g.hammer@uq.edu.a**

^b **Department of Agriculture and Forestry, Toowoomba, QLD 4350, Australia.**

^c **CSIRO Agriculture, Queensland Biosciences Precinct, 306 Carmody Rd, St Lucia, QLD 4067, Australia**

^d **Tasmanian Institute of Agriculture Research, Burnie, TAS 7320, Australia**

^e **The University of Queensland, Queensland Alliance for Agriculture and Food Innovation, Hermitage Research Station, Warwick, QLD 4370, Australia.**

^f **DuPont-Pioneer, 7250 NW 62nd Avenue, PO Box 552, Johnston, IA 50131, USA
Affiliation**

Climatic variability in dryland production environments (E) generates crop production risks. Optimal combinations of genotype (G) and management (M) depend strongly on E and thus vary among sites and seasons. Traditional crop improvement approaches seek genotypes adapted broadly to give best average performance under a standard management regime across the entire production region, with some subsequent manipulation of management regionally in response to average local environmental conditions. They do not search the full spectrum of potential G*M*E combinations forming the adaptation landscape. Here we examine the potential value of exploiting specific adaptation arising from G*M*E. We present in silico analyses for drought adaptation traits in sorghum and maize to explore the value of specific genotypic information in the range of drought environment types that characterise target production regions. The estimated phenotypic value of traits and links to trait genetic architecture can be used to inform studies on trait physiology, phenotyping, and genomic prediction.

Keywords: crop improvement, crop modelling, plant breeding, trait simulation



Selected talk

Precision agriculture for SAT – near future or unrealistic effort?

Jana Kholová^a, Vincent Vadez^b, Graeme Hammer^c, Greg McLean^d, Santosh Deshpande^e, C. Thomas Hash^f, Michael Blümmel^g

^a **Scientist, International Crops Research Institute for the Semi-Arid Tropics, Patancheru, Telangana 502 324, India, j.kholova@cgiar.org**

^b **Principal scientist, International Crops Research Institute for the Semi-Arid Tropics, Patancheru, Andhra Pradesh 502 324, India, v.vadez@cgiar.org**

^c **Professor, The University of Queensland, Queensland Alliance for Agriculture and Food Innovation, Brisbane, Qld 4072, Australia, g.hammer@uq.edu.au**

^d **Senior Scientist, Agri-Science Queensland, Department of Agriculture, Forestry and Fisheries, Toowoomba, Qld 4350, Australia, Greg.McLean@daf.qld.gov.au**

^e **Scientist, International Crops Research Institute for the Semi-Arid Tropics, Patancheru, Telangana 502 324, India, S.DESHPANDE@CGIAR.ORG**

^f **Principal Scientist, International Crops Research Institute for the Semi-Arid Tropics, Niamey, Niger, c.hash@icrisatne.ne**

^g **Principal Scientist, International Livestock Research Institute, Patancheru, Telangana 502 324, India, m.blummel@CGIAR.ORG**

Enhancement of agricultural production in semi-arid tropics requires multi-disciplinarity. We aim to integrate the knowledge of drought adaptive mechanisms with in-silico prediction of their economic value in target agro-ecologies and develop HT-phenotyping methods enabling their phenotyping towards precision-breeding (i.e. crop ideotypes targeted to specific agro-ecologies). Such approach is being tested and will be presented with example from post-rainy dual purpose sorghum cultivation in India;

Using APSIM model, we characterized the water stress scenarios across the major post-rainy sorghum production area in India and divided the area into "homogenous response units" (Kholova et al. 2013). Consequently, using a set of stay-green QTL isolines, the variability in potential drought adaptive mechanisms was dissected, among which canopy size and conductance, dynamics of canopy development and rate of soil water extraction were all traits leading to a stay-green phenotype. Observed genetic variability in these mechanisms due to stay-green QTL introgression was reproduced by APSIM and plant types conferring quantitative grain&stover production improvement considering standard management in target agro-ecologies were identified (Kholova et al. 2014). To utilize the existing genetic variability in drought adaptive traits (canopy size, development, and conductance) in precision-breeding, a platform enabling their HT-assessment in large populations has been established (Vadez et al., under review).

Next steps towards the technology impact would require analysis of the most lucrative management options for each plant type × environment combination. A large proportion of post-rainy sorghum grain and stover value is determined by its quality. Since there are significant stover&grain quality×E×M interactions, our current aim is to understand what in the mechanistics of stay-green QTL effects on crop production also beneficiates quality in order to select the most economically viable G×E×M options for target agro-ecologies.

Keywords: drought, sorghum, phenotyping, modelling, G×E×M



Poster Session 5: QTL, functional genomics, allelic diversity and breeding application

Interactive exhibit

Screening of wheat germplasm for drought tolerance on the bases of physiological tests

*Habib Ahmad*¹, Israr Ahmad¹ and Inamullah¹*

Department of Genetics, Hazara University Mansehra, KP, Pakistan

drhahmad@gmail.com

The major constraint to wheat production around the world is drought stress and is most serious problem to agriculture of Pakistan. Drought is the main environmental problem that causes high negative effect on cereals crops particularly wheat. Drought could shake morphophysiological features of plant growth, anatomy, morphology, physiology, biochemistry and finally the yield of crop. It is a great challenge for crop breeders to produce cultivars having good potential of survival in drought stress environment. Drought tolerance breeding has been effective way of crop improvement if marker assisted selection based molecular linkage maps for crop species are available.

This paper communicates the results obtained from one hundred wheat accessions evaluated for drought stress. The same genotypes were also evaluated for physiological tests including RWCN, RWCS, WLRN, WLRS and WUE under both normal and drought stress regimes. The Analysis of Variance of the data concluded that highly significant differences among the genotypes in both normal and drought stress. The genotype Margalla-99 recorded the highest RWC in normal while NIAB-83 recorded the highest RWC in drought stress conditions. Faisalabad-83 and Iqbal-2000 ranked first on the basis of WLRN and WLRS while NIAB-83 was ranked first in WUE test. These genotypes can be recommended for commercial cultivation in irrigated and rainfed areas of Pakistan.



Short talk

Association mapping of root traits for drought tolerance in bread wheat

Israr Ahmad^{*1}, *Habib Ahmad*¹ and *Inamullah*¹

Department of Genetics, Hazara University Mansehra, KP, Pakistan

iabotany32@gmail.com

Triticum aestivum (Bread wheat $2n=6x=42$) belongs to family *Poaceae* having hexaploid genome (AABBDD) of 17 Gb. Wheat is the staple food of Pakistan and covers 37% of the cultivable land and contributes 80% of the grains for human consumption while shares 70% grains for food production. The major constraint to wheat production around the world is drought stress and is most serious problem to agriculture of Pakistan. Drought is the main environmental problem that causes high negative effect on cereals crops particularly wheat. Drought could shake morphophysiological features of plant growth, anatomy, morphology, physiology, biochemistry and finally the yield of crop.

It is a great challenge for crop breeders to produce cultivars having good potential of survival in drought stress environment. Drought tolerance breeding may be effective if the marker assisted selection based molecular linkage maps for crop species are available.

The hundred wheat genotypes were screened with 102 SSR markers. Most of the markers were showed high level of polymorphism. Total of 271 polymorphic alleles generated. The alleles per locus was ranged from 1-3 and an average of 2.63 per locus. Polymorphic information content (PIC) values of the markers was calculated in the range of 0.03–0.59. The association analysis revealed that one hundred genotypes having different genetic background were classified into thirteen distinct groups. Total of 12 MTAs were recorded for root traits in GLM and MLM models. The genetic information obtained in the present study in the form of MTAs/QTLs could be utilized for breeding programs to improve drought stress tolerance.

Furthermore, the genome wide association mapping (GWAS) are strongly depend on choice of material, population size and number of markers to be used. Large population and large number of molecular markers are needed to investigate genetic diversity.

Keywords: Association mapping, Drought, GLM, MLM, QTL, Wheat.



Short talk

Screening open-pollinated maize populations for drought tolerance at germination

Álvarez-Iglesias L^a, Malvar R^b, Pedrol N^a, Ordás A^b, Djemel A^c, López-Malvar A^b, Revilla P^b

^a Department of Plant Biology and Soil Science
University of Vigo, Spain
lorena.alvarez@uvigo.es; pedrol@uvigo.es

^b Misión Biológica de Galicia (CSIC)
Pontevedra, Spain
previlla@mbg.csic.es; aordas@mbg.csic.es, rmalvar@mbg.csic.es,
alopezmalvar@gmail.com

^c École Nationale Supérieure Agronomique, Alger, Algeria
djemeldahmane@yahoo.fr

Drought is one of the most limiting stresses for maize worldwide and is becoming more important in Europe as desertification reaches higher latitudes. In order to face this challenge, we need to search sources of drought tolerance primarily within the collections of adapted germplasm. In order to do so, we have screened 50 open-pollinated maize populations from the germplasm collection conserved in the Misión Biológica de Galicia (Spanish National Research Council). We followed a simple and sensitive protocol using solutions of polyethylene glycol 6000 (PEG 6000) to simulate the effects of water stress under controlled and uniform conditions (Álvarez-Iglesias *et al.*, 2013). Up to five replications of each population were evaluated in Petri dishes, and four levels of drought stress were established. The 50 populations belonged to seven germplasm groups, namely Northern and Southern Spain, Canary Islands, USA, popcorn from Spain and from USA, and checks. Germination under stress was highest for popcorn, followed by the American populations, while the Spanish populations had the worst germination. Coleoptile and root growth under stress were highest for American maize and lowest for popcorn but the ranks were not consistent across stress levels and the performance of the other groups was not identical when compared for coleoptile or root growth. Therefore, none of the germplasm groups had an outstanding and consistent drought tolerance at germination and seedling development together, although the American populations showed the best compromise between germination and seedling growth under drought stress. The populations with higher drought tolerance at germination were Longfellow and AS-A, followed by Rustler, BS17, and AS-3(HT)C3, while the three checks, namely the commercial hybrid Anjou387 and the two synthetics EPS5 and EPS9, had the highest drought tolerance for coleoptile and root growth. We need to search more complete sources of drought tolerance in other germplasm pools.

Keywords: Maize; germplasm; stress; drought; germination



Interactive exhibit

Natural and mutagenesis induced variation in drought tolerance candidate genes in maize (*Zea mays* L.)

Borislav Assenov^a, V. Andjelkovic^b (avioleta@mrizp.rs), J. Vancetovic^b, D. Ignatovic-Micic^b, A. Nikolic^b, N. K. Christov^a, E. Todorovska^a

¹**AgroBioInstitute,
8 Dragan Tsankov, 1164 Sofia, Bulgaria,
www.abi.bg**

²**Maize Research Institute "Zemun Polje",
Slobodana Bajica 1, 11185 Zemun Polje, Belgrade, Serbia,
www.mrizp.rs**

As one of the most important agricultural crops, maize is a staple diet for a large portion of the continuously growing world's human population. Among environmental stresses with strong adverse affects on maize production, drought is the most prominent. The mechanism of drought stress response in maize is quite complex and involves numerous signaling networks that include transcription factors (TFs), kinases, late embryogenesis abundant proteins, oxidative enzymes, etc. Large number of candidate genes for drought tolerance has been proposed by QTL and association mapping studies in maize. However, only few of them have been validated in diverse germplasm consisting of local populations and mutant inbreds. In this study, specifically designed primers as well as publicly available STS markers (<http://www.panzea.org/>) were used to determine the natural and mutagenesis induced variability of few drought tolerance candidate genes (**MYBE1**, **MYB8**, **IDP**, **SDG110a**, **PSFII**) of 27 tolerant and sensitive maize inbred lines from the gene banks of Maize Research Institute "Zemun Polje", Serbia and Maize Research Institute, Kneja, Bulgaria by PCR amplification and direct sequencing. Multiple alignment of the sequenced fragments to the drought sensitive US maize inbred B73 and other inbred lines, representing the functional diversity of maize, from the Panzea database was performed. Polymorphisms (SNPs and indels) were identified in both susceptible and tolerant inbred lines. Some of them were unique for the studied here drought tolerant Serbian genotypes and were not found either in the rest of studied lines, or Panzea database. The largest number of SNPs was observed in **MYBE1** gene. Nucleotide diversity varied from 0.1427 to 0.4186 while polymorphism information content (PIC) values ranged from 0.1277 (**MYB8**) to 0.3391 (**MYBE1**). Haplotype blocks distinguishing several groups of tolerant and susceptible inbreds were defined. The application of the SNPs reported here in MAS programs for improved drought tolerance will be discussed.

Keywords: haplotype blocks, functional diversity, maize, SNPs.



Interactive exhibit

Interoperability and Interpretation of Phenotyping Data: Use of Plant Ontologies

Arnaud E¹, Ansell P.², Sirault X.², Cooper L.³, Jaiswal P.³, Pommier C.⁴, Larmande P.⁵, Ruiz M.⁶

¹**Bioversity International,
Parc Scientifique Agropolis II, 34397 Montpellier cedex 5, France**

²**CSIRO Agriculture Flagship/High Resolution Plant Phenomics Centre,
Cnr Clunies Ross St and Barry Dr Canberra ACT 2601, Australia**

³**Dept. of Botany and Plant Pathology, Oregon State University,
Corvallis, OR 97330 - 541-737-1000 USA**

⁴**Institut National de la Recherche Agronomique
RD10 -Route de St Cyr, Building 18, 78026 Versailles Cedex, France**

⁵**Institut de Recherche pour le Développement
911 Avenue Agropolis, 34394 Montpellier, France**

⁶**CIRAD
TA A-108/03, Avenue Agropolis, 34398 Montpellier Cedex 5, France**

*manuel.ruiz@cirad.fr, xavier.sirault@csiro.au, ansell.peter@gmail.com,
jaiswalp@science.oregonstate.edu, cooperl@science.oregonstate.edu,
cyril.pommier@versailles.inra.fr, pierre.larmande@ird.fr, e.arnaud@cgjar.org*

The objective of plant phenotyping is to advance plant science for breeding and crop management. Phenotyping platforms automate the measurements of traits from the cell to the whole plant by using novel sensors and methods in both controlled environment and in the field. Big data are produced in the form of alphanumeric matrices, images, statistical or 3D models that must all properly be annotated with metadata, thus enabling meta-analyses and linkage to the genotypes. However, comparison and interpretation of trait data across phenotyping sites and platforms is impeded by the heterogeneity of variables' names and methods of measurement. Therefore, Plant modelers cannot exchange data produced by models constructed with phenotyping data. To address this problem, an extended use of ontologies is proposed Reference Plant Ontologies (e.g. Plant Ontology, Phenotypic Quality Ontology) are being developed within the NSF-awarded Planteome Project (www.planteome.org), in collaboration with the Crop Ontology, to increase the interoperability of the phenotyping data. Crop Ontology was developed in the framework of the Generation Challenges Programme, which aimed at identifying promising material for drought-resistance, and is used by the Integrated Breeding Platform (www.integratedbreeding.net). The Crop Ontology (www.cropontology.org) provides harmonized breeders' trait names, measurement methods and scales for currently 18 crops aside terms for describing trials environmental and experimental conditions and will include management practices. As an example, the Australian Plant Phenomics Facility manages phenomics experiments with the Phenomics Ontology Driven Database (PODD). PODD stores versioned ontologies in the Web Ontology Language (OWL) alongside experimental layouts, data references, and analysed results to provide semantic querying across a range of heterogeneous experiments.

Keywords: Phenotyping Data; Plant Ontologies; Data Access; Data Interoperability; Data Analysis



Interactive exhibit

Abiotic stress response of durum wheat near isogenic lines

J. Bányai, M. Pál, K. Mészáros, K. Balla, V. Tóth, M. Mayer, T. Spítkó, L. Láng and I. Karsai

**Agricultural Institute, Centre For Agricultural Research, Hungarian Academy of Sciences,
H-2462 Martonvásár, Hungary**

judit.banyai@agrar.mta.hu

Accurate phenotyping is essential to establish the most adequate target trait for selecting grain yield under stress condition. To realise these phenomena we used a rain-out shelter experimental place of the Agricultural Institute at Martonvásár. The effect of drought on the physiological parameters and yield components was examined for eight near isogenic lines (NILs) originated from the crosses of Kofa x Svevo durum wheats. An additional aim was to reveal relationship between the degree of drought tolerance and protective compounds.

In the case of dry condition there was significant correlation between the chlorophyll content of flag leaf and grain weight of the main spike ($r=0.68^*$) at booting stage (ZDS45), while at dough stage (ZDS85) it has a significant correlation with number of tillers ($r=0.64^*$) and the grain weight of tillers ($r=0.62^*$). The higher chlorophyll content of NIL1++ and NIL 3++ lines indicated the longer photosynthetic activity of these lines, resulted higher seed number and seed weight.

The polyamine contents of the leaves, especially of free forms of putrescine and spermidine were higher in all the drought stressed lines compared to the irrigated ones. The activity of antioxidant enzymes showed different changes, the ascorbate peroxidase activity was similar or lower, while that of guaiacol peroxidase was higher in the leaves of plants grown under drought conditions.

In conclusion, considerable variation was detected among the eight NILs in their response to drought stress measured via phenology and yield component traits. The stress tolerance of the NIL1++ and NIL3++ isogenic lines were better than the experimental average therefore the yield components of these lines were over the other studied NIL lines. Although close correlation exists between the putrescine content and guaiacol peroxidase activity, relationship between the amount and the activity of these protective compounds and the level of drought tolerance could not be detected.

Keywords: drought stress, durum wheat near isogenic lines, yield components, protective compounds

The research leading to these results has been conducted as part of the DROPS project which received funding from the European Community's Seventh Framework Programme (FP7/ 2007-2013) under the grant agreement no 244374. The EU BONUS 12-1-2012-0017 and OTKA 108811 projects are also gratefully acknowledged.



Interactive exhibit

Diversity seek (divseek): an international partnership to harness the genetic potential of crop diversity

Wenzl P^a, Bastow R^b, Manzella D^c, Powell W^d, McCouch S^e

^a **Global Crop Diversity Trust, Bonn, Germany (peter.wenzl@divseek.org)**

^b **Global Plant Council, London, UK (ruth.bastow@divseek.org)**

^c **Secretariat of the International Treaty on Plant Genetic Resources for Food and Agriculture, Rome, Italy (daniele.manzella@divseek.org)**

^d **CGIAR Consortium Office, Montpellier, France (w.powell@cgiar.org)**

^d **Cornell University, Ithaca, USA (srm4@cornell.edu)**

More than 1,700 genebanks globally conserve approximately seven million accessions of crop species and their wild relatives. In addition, farmers conserve and adapt germplasm to social, economic and ecological conditions across diverse farming systems. The genetic diversity encapsulated in all these materials underpins and drives crop improvement. Yet efforts to identify and mobilize beneficial genetic variation into breeding programs have been limited, compared to the size of this global resource. Game-changing 'omics' and 'big data' platforms now enable a more effective and broad-based approach to harnessing crop diversity. The recently launched Diversity Seek initiative (DivSeek; <http://www.divseek.org>) aims to capture this opportunity to accelerate the development of climate-ready, high-yielding and nutritious varieties for a growing global population. DivSeek provides a platform to generate synergies and add value to like-minded, but otherwise autonomous efforts by genebanks, breeders, geneticists, and database and computational experts to make crop diversity more readily accessible and usable. It is a community-driven initiative based on voluntary membership, which focuses on common challenges encountered by individual projects. Priority areas of work will include (i) the establishment of a 'cross-crop meeting platform' to share experiences and rapidly spread innovative research approaches and technology platforms, (ii) the development and advocacy of common data standards and interoperable data sets/repositories, (iii) a broadly accepted framework for 'rights management' that helps individual projects comply with data-sharing principles, and (iv) capacity-building efforts in these areas. We welcome colleagues and organizations interested in mining crop diversity for food security to join the growing group of the 60-some institutions that have come together to establish DivSeek.

Keywords: Genetic Diversity, Germplasm, Data Standards, Data Sharing



Interactive exhibit

Associative approach of physiological and biochemical characters implicated in the response to water stress with some candidate genes for resistance to abiotic stress in barley

N. Benkherbache^a, A. Djekoune^b, A.Tondelli^c, E. Francia^d & N. Pecchioni^e.

^a : Departement of Agronomy. University Mohamed Boudiaf - M'sila, Algeria - BP 166 Echbilia 28 M'sila , nbenkher@yahoo.fr

^b : Departement of Biology, University of Constantine- Algeria

^c instituto IEG Italie

^d : University of Reggio Emilia, Italia

e. Cereal Research Centre (CRA-CER -Fugia)

The ability to quantitatively evaluate the performance of crop water-stressed is very important to improve production in semi-arid region. Stress responses involve a set of molecular regulation systems which result phenotype.

This study aims to compare the behavior of eight barley genotypes submitted to water stress, by studying some physiological and biochemical parameters. The phenotypical results obtained are associated to molecular characters to extract the best correlated traits that affect the resistance to water stress by using non-parametric test of Kruskal-Wallis and t- test.

The phenotypic response to water stress shows that high osmotic adjustment capacity is noted for the best local genotypes Fouara and Tichedrett. Proline rate does not seem sufficiently involved in the stress response. Moreover, soluble sugars are directly involved in the phenomenon by their high rates. The membrane stability index showed a decrease in stress.

The combination of the variables of the response to water stress with candidate genes for resistance to drought suggests the existence of significant associations ($P \leq 0.05$) only for membrane stability index with HvBM8 markers HvZCCT -H, and HvBM5A HvLOS2. The Student t test did shows significant associations ($P \leq 0.05$) only with HvBM5A and the index of membrane stability.

Keywords: barley, water stress, osmotic adjustment, markers



Interactive exhibit

Drought tolerance and photochemical reactions in case of some reciprocal crossing type maize hybrids

T.Berzy,(1) –T.Janda,(1) - S.Záborszky,(2)-P.Varga,(3)-J.Pintér(1)

**(1)Maize Breeding Department, Centre for Agricultural Research, Hungarian Academy of Sciences, Martonvásár 2462 Hungary ,
berzy.tamas@agrar.mta.hu**

(2)Department of Plant Production and Soil Science, University of Pannonia, Keszthely 8360 Hungary, zs.georgikon.pate.hu

(3)Department of Meteorology and Water Management, University of Pannonia, Keszthely 8360 Hungary, vpelek@freemail.hu

In 2012 year Hungary had a taste of unfavourable consequences of global warming. The present work investigated the global warming factors most important for agriculture and particularly for hybrid maize. Drought tolerance is thus a key factor as reproductive processes require a moist environment. Plants that survive unfavourable conditions in the initial stage of development (Vujakovic et al. 2000) still require a satisfactory moisture content in the flowering phenophase. The stress sensitive inbred lines have varying levels of vigour (Berzy et al.2007). The present experiments aimed to investigate, how the moisture potential of the canopy varied to different extents of water withholding in plant stands developing from seed originating from direct or reciprocal crosses..

Crosses made on female plants classified as chilling sensitive on the basis of seed analysis all proved to be drought sensitive when water was withheld for more than six days. The poorer seed vigour when hybrids were developed on stress sensitive female partner was evident in the plant height (Limasil,Kámasil,Mv 290) – while inbred line LJH was noted for its poorer physiological seed vigour and for the rapid decrease in leaf water potential (Galgacorn) when the line was used as female crossing partner.

A response to drought stress there was generally a slight reduction in the maximum quantum efficiency.(Fv/Fm) and a greater decline in the effective quantum yield ,and photochemical quenching(qP). While the non-photochemical quenching (qN) increased. These changes were dependent on the genotype. Judging from the quantum efficiency parameters, only the direct and reciprocal combinations of Maraton hybrid give an unambiguous response to water withholding. For both parameters the control plants significantly surpassed the stressed plants.

Strong correlations were observed between the number of seedlings with high seed vigour and field emergence, -while only weak correlations found between the mass and length of the seedlings and field emergence. High values of seed vigour were translated into good yield parameters in the case of hybrids using stress tolerant inbred line H 05 as maternal parent in both experimental year.

Keywords : water withholding, seed vigour



Short talk

Rice (*Oryza sativa*) defense against rice blast disease (*Magnaporthe oryzae*) under drought stress

Przemyslaw Bidzinski^{a, b}, Corinne Michel^a, Morel Jean-Benoit^a

^a UMR BGPI INRA/CIRAD/SupAgro, Campus International de Baillarguet, TA A 54/K, 34398 Montpellier, France email : przemyslaw.bidzinski@supagro.inra.fr
<http://umr-bgpi.cirad.fr/equipes/equipe4-uk.htm>

^b present address: INRA - UMR B&PMP Bât. 7, 2 place Pierre Viala, 34060 Montpellier cedex 2, France
<http://www1.montpellier.inra.fr/ibip/bpmp/english/teams/canaux.htm>

Plants with increased tolerance to drought, almost always display increased susceptibility to pathogens. This suggests negative cross-talk in response to those two biological processes. (Mittler, 2006). Stress signalling networks converge on multiple levels *i.e.* hormones, signalling pathways and transcription factors involved those processes (Fujita *et al.* 2006). So far, plant defence against pathogens under drought stress is not well understood (Prasch and Sonnewald 2013). Moreover, no report exist describing molecular strategies pathogens adopt when infecting already-stressed plants. In this study we are using well characterized model of plant-pathogen interaction between rice and *Magnaporthe* to characterize how drought is impacting on plant/pathogen interaction. The aim of this work is to better understand the genes involved in resistance of the (receptors, signalling, defence arsenal...) and aggressiveness of the pathogen (developmental regulators, nutrition, effectors...). In a long term perspective, this will help for breeding of pathogen resistant plants with sustained yield under drought. Our laboratory established a drought protocol that does not significantly modify plant development but strongly affects its susceptibility (fungal biomass measured increases 2-fold). Cytological analysis showed similar fungal progression on the leaf surfaces of control and drought-stressed plants within first two days after inoculation. However, three and four days after penetration into the plant cells, the fungal growth was much higher in stressed-plants than in un-stressed plants. This increase in fungal growth could be attributed to either reduced resistance of the stressed-plants or increased aggressiveness of the fungus, or both. Preliminary data suggest that the observed increased susceptibility of the plants is due to reduced activation of the defence system. RNAseq data are being produced to further explore this hypothesis.

Keywords: drought, rice blast, rice, defense, yield penalty



Interactive exhibit

Diallel cross among maize drought tolerant populations - principal component analysis for the most important agronomic traits

Sofija Bozinovic^a, Vojka Babic, Dragana Ignjatovic Micic, Zoran Camdzija, Milos Crevar, Jelena Vancetovic

*Maize Research Institute Zemun Polje
Slobodana Bajica 1, 11185, Belgrade, Serbia*

www.mrizp.rs, sbozinovic@mrizp.rs

A total of six drought tolerant maize landraces from MRI Zemun Polje gene bank have been crossed to form complete diallel without reciprocals. These populations have good combining ability with three major heterotic groups in Serbia (BSSS, Lancaster and Iodent). Field trials were conducted in 2012 year, when the most severe drought occurred since meteorological data measurement in Serbia, and 2013 that was optimal for maize growth. Following traits were recorded: anthesis silking interval (ASI), plant (PH) and ear height (EH), barrenness (BAR), root (RL) and stalk lodging (SL), grain yield (GY), ear number per plant (ENP), moisture at harvest (MH), ear length (EL), kernel row number (KRN), kernel number per row (KNR) and hundred kernels mass (HKM). The goal was to determine relationship and importance of these traits for the assessment of drought tolerant population crosses.

Principal component analysis yielded four principal components (PC) that explained 80% of total variance and revealed different relationships among the traits in two years. In 2012 BAR, HKM, KRN and KNR had the highest loadings in PC1 while ENP, MH and GY had the highest loadings in PC2 explaining 25% and 21% of variance, respectively. In optimal 2013 PH, EH and ENP loaded highest in PC1, while EL, KNR and ASI loaded highest in PC2, explaining 24% and 22% of variance, respectively. The most important traits for discriminating the crosses in 2012 were those related to grain yield. Optimal growing conditions in 2013 allowed for all the crosses to develop their full genetic potential. Therefore, genotypic differences for GY between the population crosses were not the most discriminative. Scatter plot for the first three PC scores in 2012 clearly separated Iranian dent POP. N-425 x Argentinean flint ARZM 06-020 cross that showed the highest grain yield and heterosis value in both years.

Keywords: diallel, drought tolerant populations, gene bank, maize, principal component analysis



Short talk

Drought Related Gene-region introgression to a European Elite Cultivar

Reyyan Bulut^a, Hikmet Budak^a

^a Sabanci University, Molecular Biology, Genetics and Bioengineering Program
Tuzla, Istanbul

budak@sabanciuniv.edu; <http://myweb.sabanciuniv.edu/budak/>

Since drought tolerance is a quantitative trait with a complex phenotype, one of the major focus of related research is the identification of drought related loci with QTL mapping to utilize them in developing tolerant genotypes. In this study, we introgressed a drought related genomic region identified in a South Australian cultivar, Kukri into a European elite cultivar, Bolal. In order to limit the loss of good yield characteristics from the elite cultivar, backcrossing was performed until BC3F2. We confirmed and selected the successful introgression of the drought related key region until BC3F2 plants. We will discuss the expression analysis of the introgressed region including extensive characterization of the obtained plants for their yield components and water use efficiency under rainfed conditions. With this research, we aim to develop bread wheat cultivars with high field performance in drought prone environments.

Keywords : drought tolerance, *T. aestivum*, introgression, QTL, wheat improvement



Interactive exhibit

Root Transcriptomics of Durum and Wild Emmer Wheat Under Drought Stress

Burcu Alptekin ^a, Reyhan Bulut ^a, Bala Ani Akpınar ^a, and Hikmet Budak ^a,

**^a Sabanci University, Molecular Biology, Genetics and Bioengineering Program
Tuzla, Istanbul**

budak@sabanciuniv.edu

<http://myweb.sabanciuniv.edu/budak/>

Drought is a major environmental abiotic stress condition that causes a drastic decrease in global wheat yields. Domestication of wheat has improved production at the expense of losing genetic diversity and in this process, several genes; including those involved in stress responses have been eradicated. Therefore, it is crucial to understand wheat drought response mechanisms and adaptation pathways with the ultimate goal of developing wheat cultivars and thus, investigation of naturally occurring, drought-tolerant wheat relatives, as well as modern varieties, holds critical importance in order to understand cellular and molecular mechanism related with drought tolerance.

Wild emmer (*Triticum turgidum* ssp. *dicoccoides*) and Durum wheat (*Triticum turgidum* ssp. *durum*), tetraploid relatives of cultivated wheat, are a valuable source of resistance to several biotic and abiotic stress conditions and carry an important potential for identification of novel stress adaptation pathways. In this study, the root transcriptomes of *Triticum turgidum* ssp. *durum* variety Kızıltan and two *Triticum turgidum* ssp. *dicoccoides* genotypes which are TR39477 and TTD-22 are sequenced via Illumina HiSeq2000 under control and drought conditions. RNA-seq data was assembled in order to be used for the identification of differentially expressed genes under drought stress and results improved our knowledge to understand the function of specific genes in root tissues of two different wild emmer wheat cultivars to overcome drought stress. We identified unique gene(s) differentially expressed in both species.

Keywords: Drought, tetraploid wheat, root, RNA-seq, wild emmer wheat



Interactive exhibit

Defining the role of florigen genes in Maize developmental reprogramming under contrasting watering scenarios

Sara Castelletti^a, Llorenç Cabrera-Bosquet^b, Alain Charcosset^c, Claude Welcker^b, Chiara Tonelli^a, François Tardieu^b, Lucio Conti^a

^a **Department of Biosciences, Università degli studi di Milano, Milano, Italy**
Sara.Castelletti@unimi.it, Chiara.Tonelli@unimi.it, Lucio.Conti@unimi.it,

^b **Supagro INRA, Montpellier, France**
francois.tardieu@supagro.inra.fr, welcker@supagro.inra.fr, cabrera@supagro.inra.fr

^c **UMR de Génétique Végétale, Le Moulon, France**
charcos@moulon.inra.fr

A hallmark of flowering time regulation in photoperiod-sensitive species is the pattern of accumulation of the florigen genes. In short day plants, namely tropical maize lines, the florigen gene *ZCN8* is upregulated under short days but not under long days. Conversely, in temperate maize, *ZCN8* displays diurnal variations, largely independent of photoperiod. Besides photoperiod, florigen genes are transcriptionally regulated in response to several external signals namely temperature and drought. As florigen genes control different aspects of plant vegetative development, including growth regulation and guard cell movements/transpiration, variations in florigen accumulation could account for the diverse modes of developmental reprogramming under drought stress observed in plants. Our goal is to comprehensively relate different developmental adaptations (e.g. growth or the duration of the vegetative phase) to patterns of *ZCN8* accumulation in maize germplasm. We are performing a high-throughput/high-content phenotyping screen on 350 maize lines grown under different watering regimes. By measuring *ZCN8* transcript levels we will be able to relate variations in *ZCN8* abundance to flowering and growth traits in individual lines grown under different watering scenario. This knowledge will also offer the possibility to define individual *ZCN8* eQTLs, and link *ZCN8* eQTLs to physiological QTLs. We will present data illustrating our efforts to capture variability in *ZCN8* transcript accumulation within our panel and relate it to the phenology observed, initially under standard watering conditions. These data should help understand the mode and adaptive significance of florigen genes as major drivers in plant development, thus providing insights into the mechanisms that enable plants to adapt to changing environments.

Keywords: Flowering time, Florigen, transcriptional regulation, growth



Interactive exhibit

Genetic and genomic control of response to water deficit in tomato

ELISE ALBERT^a, YOLANDE CARRETERO^a, JUSTINE GRICOURT^a, ESTHER PELPOIR^a, ROMAIN NOVARETTI^a, CLAIRE DUFFES^a, JULIEN BONNEFOI^b, MATHILDE CAUSSE^a

^a **INRA, UR588, AGPF, CS 40001 Ardon, F-45075 Orléans Cedex 2, France**

^b **GAUTIER Semences, F-13630 Eyragues, France**

In the next decade water will be increasingly limiting crop production, in particular in Mediterranean region. Improving plant water use efficiency (WUE) by studying genotype x water regime (G x WR) interactions is of main interest to improve plant adaptation to lower water availability. At different degrees, plants can change their phenotypes (molecular, morphological and physiological levels) in response to environmental changes. These modifications relate to phenotypic plasticity. In Tomato (*Solanum lycopersicum* L.), extensively grown in Mediterranean region, the first studies have shown genetic variability in the response to water deficit, but very few genes/QTLs have been identified and mostly in wild relative species. Studying water deficit in this fleshy fruit is of particular interest since a well mastered water deficit can stimulate secondary metabolism production, increasing plant defenses and concentration of compounds involved in tomato fruit quality at the same time. In our laboratory, we have analyzed 119 recombinant inbred lines (RIL population) and 142 unrelated cherry tomato (*Solanum lycopersicum* L. cerasiforme) accessions (GWA population), grown in greenhouse under two watering regimes (WR), in two locations (Morocco and France). Plants were phenotyped for plant phenology, plant vigor and fruit quality traits. We assessed genetic variability and G x WR interactions, for the above traits in the two populations. QTL and GWA analysis were conducted to identify QTL x watering regime (QTL x WR) interactions. The presentation will present the first results of our research project. The possible use of water deficit to improve tomato fruit quality in future breeding programs will be discussed.

Keywords: Genotype x Environment interaction, QTL, GWAS, water deficit, tomato



Interactive exhibit

Transcriptomic analysis in banana cultivars during early drought-stress

Cenci A.^a, Zorrilla-Fontanesi J.^b, Kissel E.^b, Hueber Y.^a, Dubois E.^c, Parrinello H.^c, Swennen R.^{a,b,d}, Roux N.^a, Rouard M.^a, Carpentier S.^b

^a **Biodiversity International, Parc Scientifique Agropolis II, 34397 Montpellier Cedex 5, France.**

^b **Laboratory of Tropical Crop Improvement, Division of Crop Biotechnics, KU Leuven, B-3001 Leuven, Belgium**

^c **MGX-Montpellier GenomiX, Montpellier Genomics and Bioinformatics Facility, Montpellier F-34396, France**

^d **IITA, P.O. Box 10, Duluji, Arusha, Tanzania**

Bananas are a major staple food crop for hundreds of millions of people in developing countries. Banana needs high amounts of water which is one of the most limiting abiotic stress factors in its production. Climatic changes as well as expansion of banana cultivation in less humid areas drives the search for better understanding of drought tolerance at the molecular and physiological level. Most cultivated banana varieties are triploids with an AAA, AAB, or ABB genome constitution, with A and B genomes contributed by *Musa acuminata* and *M. balbisiana*, respectively. Higher levels of drought tolerance have been correlated to the presence of B genome.

To explore the transcriptome global response to drought stress in bananas and detect cultivar specific strategies to counteract low water availability, three cultivars (one allo-triploid (ABB) and two auto-triploid (AAA)) with contrasting degrees of drought tolerance were sampled for RNAseq analysis under different water availability conditions. We focused on roots, as these are the first plant parts perceiving stress. Several enzymes involved in the energy production became up-regulated. Analysis of responsive genes was conducted taking into account the paleo-polyploid nature of the *Musa* genome that often implies the presence of two or more paralogous genes with different patterns of gene expression. Variability in differential expression was observed among the three triploid cultivars, in particular involving the homeoalleles contributed from the B genome. The fine tuning of an automated workflow to mine for differences in response to drought stress of the A and B derived homeoalleles is in progress.

Keywords: Banana, differential expression, drought tolerance, polyploidy, transcriptome



Interactive exhibit

WHEALBI:Wheat and Barley Legacy for Breeding Improvement; A EU-FP7 project to link genomics and agronomy.

Gilles Charmet¹, Nils Stein², Joanne Russel³, Robbie Waugh³, Luigi Cattivelli⁴, Marco Bink⁵, Beat Keller⁶, Jacob Lage⁷, Nathan Morris⁸, Sébastien Crépieux⁹, Emmanuelle Lagendijck¹⁰, Ronan Pendu¹⁰

¹ INRA-Université Clermont II, UMR GDEC, Clermont-Ferrand, France, ² Leibniz – Institut für Pflanzengenetik und Kulturpflanzenforschung (IPK) Gatersleben, Germany, ³The James Hutton Institute (JHI), Dundee, Scotland, United Kingdom, ⁴Consiglio per la ricerca e sperimentazione in agricoltura (CRA) Fiorenzuola d'Arda PC, Italy; ⁵Stichting dienst landbouwkundig onderzoek (DLO), Wageningen, Netherlands; ⁶Universität Zurich, Zurich, Switzerland; ⁷KWS-UK, Thriplow near Cambridge, United Kingdom; ⁸National Institute of Agricultural Botany (NIAB), Cambridge, United Kingdom; ⁹ARCADIA International, Bressels, Belgium; ¹⁰INRA-transfert SA, Paris, France

WHEALBI is granted 5 M€ by EU-FP7 for 5 years starting January, 2014. It involves 18 partners (8 academics, 7 industry /SME) in 9 countries and aims at improving European wheat and barley production in competitive and sustainable cropping systems. Germplasm will be selected and characterised by next-generation-sequencing. Adaptive traits will be evaluated in both transnational field experiments and precision phenotyping platforms. Germplasm will be stored in a bio-repository and associated data in knowledge bases that will represent a valuable legacy to the community. Whole genome association scans will be conducted for several traits, signatures of adaptive selection will be explored, and allele mining of candidate genes will reveal new variation associated with specific phenotypes. Pre-breeding tools will be developed to optimize the efficiency of allele transfer from unadapted germplasm into elite breeding lines. New methodologies will explore how to optimally exploit the large amount of new genotypic and phenotypic data available. Ideotypes with improved yield stability and tolerance to biotic and climatic stresses will be designed and provide proof of concept of the efficiency of genome and phenome assisted selection. Ideotypes and reference varieties will be evaluated in innovative cropping systems, particularly organic farming and no-till agriculture, and an economic evaluation will be conducted. Results will be disseminated to a broad user community, highlighting the benefits and issues associated with the adoption of sustainable wheat and barley crop production. WHEALBI aims to help the EU remain a major actor in world small grain cereal production while addressing the pressing global priorities of improving food quality and reducing environmental impact.

www.whealbi.eu

Keywords: *exome sequence, allele mining, drought, disease, genomic selection*



Interactive exhibit

Combining a dual-omics approach and biochemical analysis of bulked recombinant maize inbred lines to identify candidate genes underlying plant growth responses to water deficit

Laëtitia Virlouvét ^a, Claude Welcker ^b, Valérie Méchin ^c, Marie-Pierre Jacquemot ^d, Hélène Corti ^e, Sébastien Mongrand ^f, Adrien Puppo ^g, Chantal Arar ^h, Jean-Philippe Pichon ⁱ, Matthieu Falque ^j, Benoît Valot ^k, François Tardieu ^l, Michel Zivy ^m, Sylvie Coursol ⁿ

^a Univ Paris-Sud -UMR Génétique Végétale, Gif-sur-Yvette, France,

^b INRA - Laboratoire d'Ecophysiologie des Plantes sous Stress Environnementaux, Montpellier, France, ^c INRA - Institut Jean-Pierre Bourgin, Saclay Plant Sciences, Versailles, France, ^d INRA - Institut Jean-Pierre Bourgin, Saclay Plant Sciences, Versailles, France, ^e INRA - UMR Génétique Végétale, Gif-sur-Yvette, France, ^f CNRS - Laboratoire de Biogenèse membranaire, Bordeaux, France, ^g Univ Paris-Sud - UMR Génétique Végétale, Gif-sur-Yvette, France, ^h Biogemma, F-63720 Chappes, France, ⁱ Biogemma, F-63720 Chappes, France, ^j INRA - UMR Génétique Végétale, Gif-sur-Yvette, France, ^k INRA - PAPPSO, UMR Génétique Végétale, Gif-sur-Yvette, France, ^l INRA, Laboratoire d'Ecophysiologie des Plantes sous Stress Environnementaux, Montpellier, France, ^m CNRS - PAPPSO, UMR Génétique Végétale, F-91190 Gif-sur-Yvette, France, ⁿ INRA - Institut Jean-Pierre Bourgin, Saclay Plant Sciences, Versailles, France

laetitia.virlouvet@versailles.inra.fr, claud.welcker@supagro.inra.fr, valerie.mechin@versailles.inra.fr, marie-pierre.jacquemot@versailles.inra.fr, corti@moulon.inra.fr, sebastien.mongrand@biomemb.u-bordeaux2.fr, adrienpuppo@yahoo.fr, chantal.arar@free.fr, jean-philippe.pichon@biogemma.com, falque@moulon.inra.fr, benoit.valot@univ-fcomte.fr, francois.tardieu@supagro.inra.fr, zivy@moulon.inra.fr, Sylvie.coursol@versailles.inra.fr

Maize is an essential dual-used food and energy crop. However, maize has a large ecological footprint because it is one of the major recipients of irrigation water. Improvement of maize for drought tolerance is therefore essential in the context of recurrent increased risks of water stress. Here, we used a strategy based on bulked segregant analysis to gain further insights into the underlying mechanisms and genes associated with a promising genomic region exhibiting two QTLs for growth responses to water deficit (Welcker *et al.*, 2007). Recombinant inbred lines (RILs) that were used for QTL mapping were grouped according to their allelic values in the studied QTL region. Each group was then evaluated by transcriptomic and proteomic profiling of the leaf growing zone upon well-watered and water deficit conditions. Seventy transcripts and three proteins showed significant variation between bulked RILs. Using mapping analysis and quantitative RT-PCR experiments as additional criterions, we established a candidate gene list of nine differentially expressed genes colocalizing with the QTL region. Further quantification of specific transcript and metabolite amounts support the idea that the stress-responsive *ZmMYB31* gene encoding a transcriptional repressor of the lignin biosynthetic pathway (Fornalé *et al.*, 2010) might contribute to the growth response of the maize leaf upon water deficit.

This work was supported in part by the Génoplante projects B06 and WaterLess (grant no. ANR-05-GPLA-034-05) and by a Ph.D. research fellowship of the University Paris-Sud to LV.

Keywords: candidate genes, growth responses, maize, ZmMYB31, water deficit



Interactive exhibit

Drought stress tolerance as a complex target of sunflower breeding including selection against several biotic and abiotic stress tolerance factors in Carpathian basin

Tamas Csikasz, Monika Treitz

**Kaposvar University Feed Crops Research Institute
H-7095 Iregszemcse, Napraforgó u. 1., Hungary
csikasz.tamas@ke.hu, treitz.monika@ke.hu**

Carpathian basin has a specific position regarding climate change. Basically, due to basin's character and the global warming the climate has changed to semi-arid type as water deficit and heat shock occur many growing season. But every third or fourth year, the seasons may be extreme wet and cold as we can observe it during the last 10 years. In the same time, the rainfall pattern is unpredictable and inhomogeneous excessively. Total precipitation amount per year were: 2011 - 350mm; 2012 - 377mm; 2013 - 613mm and 2014 - 823mm. The numbers of heat days per year were: 2011 - 10days; 2012 - 25days; 2013 - 15days and 2014 - 4days. It seems clear that the breeding strategy for drought tolerance has to be much more complex one as before. A good sunflower breeding strategy has to include elements against both abiotic and biotic stress factors.

Abiotic stress factors of drought tolerance: Water deficit, Heat, UVB Ray and Salinity. Many times these factors do not cause yield depression separately. During evolution species of *Helianthus* genus have gained several resistance components against drought, so the domesticated sunflower is one of the best crop for relatively dry conditions. However, the joint action of these factors may cause serious biomass and yield depression in a large scale.

Biotic stress factors of drought tolerance: *Macrophomina phaseolina*, *Alternaria ssp.*, *Rhizopus ssp.*, *Puccinia helianthi*. These pathogens are thermophilic organisms and common in Carpathian basin. Infections or epidemics of these pathogens may increase the negative effects of abiotic drought stress factors to yield or biomass production.

Complex tolerance or resistance to abiotic and biotic stress factors can provide the excellent level of yield stability. A new generation of high drought tolerant sunflower hybrids developed with our breeding strategy will be presented.

Keywords: sunflower, abiotic stress, biotic stress, breeding strategy, Carpathian basin



Short talk

Algerian maize from the Saharan oasis: novel sources for drought tolerance

Cherchali F Z^a, Benchikh-Le Hocine M^a, Djemel A^a, Mefti M^a, Malvar RA^b Revilla P^b

^a *École Nationale Supérieure Agronomique, Alger, Algeria*
djemeldahmane@yahoo.fr, mmefti@yahoo.fr, zola.ina@hotmail.com,
ma_benchikh@yahoo.f

^b *Misión Biológica de Galicia (CSIC). Pontevedra, Spain*
previlla@mbg.csic.es, rmalvar@mbg.csic.es

Maize (*Zea mays* L.) is a major crop in the world. Its production and yield stability is greatly affected by drought stress. Therefore, identification of drought tolerant maize germplasm is essential. We evaluated maize populations from the Algerian Saharan oasis along with European varieties and two American hybrids in humid (Algiers) and semiarid (Tessimsilt) Algerian locations under drought and optimum field conditions. At Algiers, plots were well watered from planting to the initiation of drought treatment, which started two weeks before flowering by withdrawing irrigation. At Tessimsilt, drought treatment was applied two weeks before flowering by reducing irrigation to 50% of well-water treatment. For both locations, the irrigation was applied after flowering stage to allow grain filling. Agronomic performance of all genotypes under drought treatment was reduced. Under normal condition, both European and American maize yielded more than the Algerian maize, except for DZ-TGN population. However, under drought treatment, only the northern Spanish variety showed significantly greater yield production, and DZ-ILT, DZ-LOM and DZ-TAO yielded more than the American hybrids and the southern Spanish variety. The agronomic performance of the Algerian populations under stress differed from the European and American varieties; however, these differences were small when compared to the northern Spanish variety. Plant growth was normal with plant height varying between 56 cm and 103 cm for Algerian maize and between 107cm and 93 cm for European and American checks. The Anthesis-Silking interval varied between 7 to 3 days for the Algerian material and, between 8 to 4 days for checks. Kernel weight was higher for European and American than for Algerian varieties. We conclude that there Algerian populations are novel sources of favorable allele for drought tolerance. However, they require improvement of kernel weight and yield.

Keywords: maize; *Zea mays* L.; Algerian germplasm; stress; drought



Short talk

Phenotypic and genetic study of traits associated with maintaining yield under post-anthesis source limitation in bread wheat

Dejan Dodig^a, Vesna Kandić^a, Steve Quarrie^b

^a **Maize Research Institute Zemun Polje, Slobodana Bajića 1, 11185 Belgrade-Zemun, Serbia, ddodig@mrizp.rs; vkandic@mrizp.rs**

^b **Faculty of Biology, University of Belgrade, Studentski trg 1, 11000 Belgrade, Serbia, steve.quarrie@gmail.com**

When environmental stress develops during reproductive phases of growth, wheat plants have to rely increasingly on remobilisation of previously stored assimilates to maintain grain filling. In two-year field trials we studied nearly 30 traits in 96 wheat varieties in plants that were defoliated by cutting off all leaf blades shortly after anthesis. Yield/ear of defoliated plants varied from about 66 to 96% yield/ear of control plants, and both grain number/ear and thousand grain weight significantly contributed to this. Yield maintenance in defoliated plants was highly significantly correlated with peduncle length (flag leaf node to base of the ear), and especially with extruded peduncle length (flag leaf ligule to base of the ear). High capacity to maintain grain filling was also associated with high grain filling rate, and awn length. These wheats were also screened for allele variation at 44 SSR marker loci. Association mapping with one-year data identified four SSR marker loci which were highly significantly associated with capacity to maintain yield and grain size in defoliated plants: *gwm458* (1DC), *gwm484* (2DS), *gwm539* (2DL) and *gwm186* (5AL). Highly significant associations with stem length (to base of the ear), peduncle length and surface area were also associated with these markers. Crosses that we made based on phenotypic and genotypic scores for typical breeding traits in wheat were successful in improving grain weight, at least under moderate stress during grain filling. These traditional traits also benefit yield productivity and grain filling under non-stress environments. However, a number of traits that are expected to be of specific benefit under severe stress conditions probably need to be targeted.

Keywords: wheat, defoliation, post-anthesis stress, yield, QTL



Interactive exhibit

Characterization of Temperate Maize Inbred Lines for Drought Tolerance

Sekip Erdal^a, Zekeriya Akman^b

^a **Bati Akdeniz Agricultural Research Institute
Antalya, Turkey
sekip.erdal@gthb.gov.tr – www.batem.gov.tr**

^b **Suleyman Demirel University, Agricultural Faculty, Field Crops Department
Isparta, Turkey
akmanz@ziraat.edu.tr – www.sdu.edu.tr**

Drought is one of the most important abiotic stress that has adverse effects on maize yield and quality. Since, drought stress has been a priority issue for tropical regions, extensive research was conducted and several populations, hybrids and inbred lines for tropical environments were developed. However, little attention was done for drought tolerance in temperate maize compared to tropical maize.

The objective of the study was to screen a set of nineteen temperate inbreds and a drought tolerant tropical maize inbred line for drought tolerance and determine the genetic distance of the inbred lines by molecular markers. In the study genotypes were evaluated in well-watered and drought stress conditions in 2012 and 2013 in Antalya where located in Mediterranean region of Turkey. Drought stress was achieved at the flowering by withdrawn water approximately 2-3 weeks before flowering. Morphological and agricultural data were taken and genetic similarity of the lines were determined.

According to the results of the study, 5 temperate inbred lines were determined as the most tolerant lines to drought, while 4 inbreds were identified as the sensitive lines in terms of yield. Tolerant promising lines were also had good performance in terms of secondary traits. A wide genetic variation was detected with the molecular characterization of the lines. Unweighted pair group method with arithmetic mean dendrogram revealed four main and eight sub-clusters. It was concluded that the inbreds used in the study were belong to Lancaster, Stiff-Stalk, Tropical and unrelated genetic background. The most promising tolerant inbred line, Ant I-69 formed an unknown single cluster. Also the lines representing Lancaster heterotic group showed better performance than other groups.

In conclusion, it was envisaged that temperate maize germplasm can be assessed for breeding drought tolerance and selected maize inbred lines were proposed for future studies.

Keywords: Maize, temperate, inbred lines, drought tolerance, molecular markers



Short talk

Interaction between drought and floral induction in rice

Francesca Galbiati^a, Remo Chiozzotto^b, Alberto Spada^c, Franca Locatelli^b,
Annamaria Genga^b and Fabio Fornara^a

^a **University of Milan, Department of Biosciences, Via Celoria 26, 20133
Milan, Italy**

^b **CNR, Institute of Agricultural Biology and Biotechnology, via E. Bassini
15, 20133 Milan, Italy**

^c **University of Milan, Department of Agricultural and Environmental
Sciences, Via Celoria 2, 20133 Milan, Italy**

Drought is responsible for severe yield losses in Southern developing countries every year. Plants have adopted different strategies to cope with reduced water availability and some of them involve modulating flowering time in order to avoid the drought period. For example, in *Arabidopsis thaliana* this phenomenon has already been deeply characterized and described as drought escape. Plants adopting this strategy tend to flower earlier when exposed to drought stress. Conversely, drought treatments imposed to rice plants (*Oryza sativa*) before or during panicle development determine a flowering delay. Among the different pathways that control flowering time, the photoperiod pathway plays a prominent role to activate transcription of florigenic genes, including *HEADING DATE 3a (Hd3a)* and *RICE FLOWERING LOCUS T 1 (RFT1)*. The effects of drought treatments imposed during floral transition and its impact on subsequent panicle initiation have not been thoroughly studied. We first set up a protocol to synchronize drought and the floral transition. Plants were grown on soil and exposed to inductive photoperiods while reducing the water content. We reproducibly obtained a delay of flowering upon exposure of plants to a mild drought stress. Global profiling of the leaf transcriptome and quantification of marker genes expression during drought and floral induction showed that both treatments were effective, and that the delay of flowering was determined by suppression of *Hd3a* transcription in leaves. Quantification of gene expression and the use of available mutant lines allowed us to identify *EARLY HEADING DATE 1 (Ehd1)* as integrator of flowering and drought signals. The results of this work will open new perspectives for connecting two important biological processes.

Keywords: rice, drought, floral induction, Ehd1, transcriptome



Short talk

Chlorophyll *a* fluorescence parameters of JIP-test in maize breeding for water-limited environments

Vlatko Galić ^a, Mario Franić ^a, Domagoj Šimić ^a

^a Agricultural Institute Osijek, Južno predgrađe 17, Osijek, Croatia
vlatko.galic@poljinos.hr, www.poljinos.hr

Chlorophyll fluorescence parameters of JIP-test are considered as reliable early indicators of stress in photosynthetic tissues. The JIP-test is particularly useful for crop plants when applied in vivo under field drought stress conditions. Our previous investigations in maize showed that inbred lines B73 and Mo17 remarkably differed for two most important fluorescence parameters (Fv/Fm and Performance Index) under the very dry scenario. Subsequent QTL analysis of the intermated B73xMo17 (IBM) maize population revealed 10 significant QTLs for seven JIP test parameters, of which five were co-localized when combined over the four environments indicating polygenic inheritance. Our results demonstrated that QTL analysis of chlorophyll fluorescence parameters was capable of detecting one pleiotropic locus on chromosome 7, coinciding with the gene *gst23* that may be associated with efficient photosynthesis under the field scenarios differing in water supply. Converging approaches of genomic selection and challenging high-throughput phenotyping for chlorophyll fluorescence parameters in the water-limited field environments could eventually improve breeding in drought tolerant maize.

Keywords: Chlorophyll *a* fluorescence parameters; intermated B73xMo17 recombinant inbred lines; JIP-test; maize; quantitative trait loci



Interactive exhibit

Adaptation to temperate conditions of sub-tropical drought tolerant maize populations

**Brigitte Gouesnard^a, Anne Zanetto^b, Mariangela Arca^c, Stéphane Nicolas^c,
Alain Charcosset^c, Claude Welcker^d**

***a INRA, UMR AGAP, 2 place Viala, 34060 Montpellier Cedex. France.
Brigitte.gouesnard@supagro.inra.fr.***

***b INRA, UE Diascope, domaine de Melgueil, 34130 Mauguio. France.
Anne.zanetto@supagro.inra.fr***

***c INRA, UMR Génétique végétale, Ferme du Moulon, 91190 Gif/Yvette. France
snicas@moulon.inra.fr, alain.charcosset@moulon.inra.fr***

***d INRA, UMR LEPSE, 2 place Viala, 34060 Montpellier cedex. France.
Claude.welcker@supagro.inra.fr***

For temperate areas, sources of drought tolerance can be found in tropical and sub-tropical breeding populations such as those developed by CIMMYT and other institutes in tropical areas. Their use in temperate germplasm needs their adaptation to climatic conditions, either by backcrossing or by selection. In 2008, we introduced 13 drought tolerant maize populations from Zimbabwe (CIMMYT) and Kenya (KARI). Based on a first evaluation of these populations, we chose four populations (DLCI, and Kikamba from KARI; ZM309 and ZM521 from CIMMYT) to be selected by mass selection in Mauguio (Mediterranean area). The mass selection was applied on early flowering date, short anthesis-silking interval, low smut, ear size. The selection intensities were 20% on the first cycle (200 full-sib ears on 1000 plants), and 5% on the second and third cycles (200 half-sib ears on 4000 plants in isolation field under low-irrigated condition). In 2014, the three cycles of selection of populations were evaluated in Mauguio under optimal conditions. The populations of the third cycles were 3.5 to 5.5 days early than populations of the first cycle, and ASI was reduced up to 8.5 days. Two bulked DNA samples of 100 plants of the first and the third cycle of each population were analyzed with the 50K SNP array. Allelic frequencies were estimated using the method developed by A. Charcosset team (Arca et al., in prep). We searched SNP under selection by analysis of variance and by the Fc parameter method (Goldringer and Bataillon, 2004). Around 5% of SNP were under selection. Among them, the four SNP, more frequent over populations, were located on chromosome 10 (bin 10.4) near the QTL of photoperiod found by Ducrocq et al. (2009). Assuming we have not lost drought tolerant alleles, the advanced cycles of populations are available for pre breeding.

Keywords : Zea mays L; adaptation, subtropical, exotic, drought, SNP



Interactive exhibit

Enhancing resource Uptake from Roots under stress in cereal crops (EURoot): an international, multidisciplinary initiative for adapting cereals to climate instability and resource scarcity

Emmanuel Guiderdoni ^a, on behalf of the EURoot consortium*

**^a CIRAD, UMR AGAP
Avenue Agropolis, 34398 Montpellier cedex 5, France
guiderdoni@cirad.fr – www.euroot.eu**

The EURoot consortium gathers 20 partners including SMEs joining their efforts to enhance maize, barley, rice and durum wheat capability to acquire water and nutrients through their roots and maintain growth and performance under stress conditions. From 2012, EURoot has been conducting a suite of experiments integrated into 3 work packages (WPs) designed to better understand and model: i. The genetic and functional bases of root traits involved in soil exploration and resource uptake (WP1), ii. The bio-geochemical properties of the soil, including beneficial association with mycorrhizal fungi, influencing extraction of nutrients and water by the root system (WP2) and iii. The plant signaling processes involved in soil environment sensing and responsible for adaptive root system response enhancing soil exploration and resource acquisition (WP3). In addition, two platform WPs allow the sharing of innovative phenotyping and imaging methods tested for their relevance to field conditions (WP4) and integration of root architecture, resource dynamics in the soil and root uptake through multi scale modeling, to design root ideotypes allowing enhanced resource acquisition under stress (WP5). We will illustrate the consortium progresses accomplished so far in; i. identifying cereal root-related genes through QTL/association mapping and mutant screen; ii. studying maize root development and placement under low/heterogeneous nutrient and topsoil drying in rhizotron and field; iii. investigating molecular and biochemical signals in drought- or nitrogen- stressed maize roots, iv. acquiring data from root phenotyping and imaging platforms that can be used for calibrating model-based analysis of root trajectories and soil-root functional models. EURoot results will be further translated into screening methods, models and tools to guide the challenging improvement for root traits that allow enhanced water and nutrient capture.

Keywords: cereals, drought, nutrients, phenotyping, roots



Interactive exhibit

Screening for drought tolerance and genetic diversity analysis in landraces of lentils

Omar Idrissi^{1,2}, Sripada Udupa³, Ellen De Keyser⁴, Patrick Van Damme^{1,5} and Jan De Riek⁴

1 Department of Plant Production, Faculty of Bioscience Engineering, Ghent University, Coupure links 653, 9000, Ghent, Belgium; 2 Institut National de la Recherche Agronomique du Maroc (INRA) Centre Regional de Settat, B.P 589, Settat, Morocco; 3 International Center for Agricultural Research in the Dry Areas (ICARDA), B.P. 6299, Rabat, Morocco ; 4 Institute for Agricultural and Fisheries Research (ILVO)-Plant Sciences Unit, Applied Genetics and Breeding, Caritasstraat 21, 9090, Melle, Belgium; 5 Faculty of Tropical AgriSciences, Czech University of Life Sciences, Prague, Kamycka 129, 165 21 Prague 6 – Suchdol, Czech Republic.

Drought is one of the most challenging abiotic stresses limiting lentil (*Lens culinaris* Medikus) production in arid and semi-arid areas. Lentil is an annual food legume widely grown under rainfed environments where drought stress episodes occur frequently. Therefore, developing a rapid method for screening drought-tolerant genotypes for breeding programs is of great interest. A collection of 70 lentil landraces from Morocco, Italy, Greece and Turkey was evaluated for its drought characteristics under greenhouse conditions in Ghent, Belgium, using leaf Relative Water Content (RWC), Water Losing Rate (WLR) and Wilting Score (WS). These landraces were also analyzed using 19 simple sequence repeat (SSRs) DNA markers. Non-parametric Kruskal-Wallis Test was used to identify markers associated to the three parameters used to measure the landraces' drought tolerance (RWC, WLR and WS). Significant associations between drought tolerance and SSR markers were observed. Results show that the described method of screening for drought tolerance is time- and resource-effective for food legumes breeding programs targeting drought tolerance.

Key words: lentil landraces, SSRs, screening, drought.



Interactive exhibit

Genetic Analysis of water use efficiency traits and yield under drought stress conditions in Groundnut (*Arachis hypogaea* L.)

K. John^{1*}, P. Raghava Reddy² and K. Raja Reddy

**Regional Agricultural Research Station, Tirupati-517502, Andhra Pradesh, India
Acharya N.G.Ranga Agricultural University, Rajendranagar, Hyderabad-500
0030 (A.P.) India**

¹ **Senior Scientist (Genetics & Plant Breeding), RARS, Tirupati, Andhra Pradesh, India**

² **Former Vice- Chancellor, Acharya N.G. Ranga Agricultural University, Andhra Pradesh, India**

³ **Director of Research, Acharya N.G. Ranga Agricultural University, Andhra Pradesh, India**

johnlekhana@rediffmail.com

Eight groundnut genotypes were crossed in half diallel fashion without reciprocals to study the combining ability, gene action, heterosis, character association and path coefficient analysis in respect of water use efficiency traits and yield. JL-220 and F₁, ICGV-91114 x JL-220 had comparatively higher SCMR and TCGS-584 and JL-220 for low specific leaf area. Significant positive gca effect for SPAD chlorophyll meter reading was registered by K-1375 in both seasons and JL-220 and TCGS-647 during *rabi*, these genotypes were considered to good general combiners. For SPAD chlorophyll meter reading only one cross, K-1375 x TCGS647 during *kharif* and two crosses *viz.*, ICGV-91114 x TCGS-584 and ICGV-91114 x JL-220 were considered to be the good performing hybrids during *rabi*. The estimates of gca effects showed that among the parents K-1375, TIR-25 and TCGS-647 during *kharif* and ICGV-91114 during *rabi* were found to be superior as evident from its highest significant positive general combining ability effects for specific leaf area. The best performing hybrids for specific leaf area were TPT-4 x TCGS-647, ICGV-91114 x TCGS-584, TPT-4 x JL-220, TCGS-584 x TCGS-647, TCGS-584 x K-1375 and ICGV-99029 x TCGS-647 during *kharif*. For water use efficiency only the genotype, TPT-4 (*kharif*) and K-1375 (*rabi*) were the best combiners. Only one hybrid, TPT-4 x TIR-25 (*kharif*) and three hybrids *viz.*, ICGV-91114 x ICGV-99029, TPT-4 x K-1375 and ICGV-91114 x JL-220 (*rabi*) were the specific hybrids for high water use efficiency as evident from its high significant and positive sca effects. ICGV-99029 (*kharif*) and TPT-4 (*rabi*) were considered to the best general combiners for pod yield per plant. The crosses *viz.*, ICGV-91114 x TCGS-647 (both seasons), JL-220 x ICGV-99029, TIR-25 x ICGV-99029, ICGV-91114 x K-1375 and TCGS-584 x ICGV-99029 (*kharif*), TPT-4 x TIR-25 and TCGS-594 x K-1375 (*rabi*) were considered as desirable specific combinations for pod yield per plant. The F₁, K-1375 x TCGS-647 exhibited the highest significant and positive heterosis over mid-parent (8.30%) and standard parent (13.84%) during *kharif* and the same cross performed the maximum heterosis of 16.69% over standard parent during *rabi*. The F₁, ICGV-91114 x TCGS-584 recorded maximum significant positive heterosis over mid-parent (7.55%) and better parent (3.55%) during *rabi*. In F₁ generation during *kharif* moderate heritability and moderate GAM was recorded for specific leaf area showed additive gene effects. Low heritability and moderate GAM was noticed for pod yield per plant indicating the importance of additive gene effects, selection for such characters may be rewarding. In F₁ generation during *rabi*, moderate heritability was exhibited for SCMR and water use efficiency. High GAM was observed for water use efficiency. Moderate heritability and low GAM was observed for SCMR, whereas low heritability and low GAM was recorded for specific leaf area and



pod yield per plant indicating the preponderance of non-additive gene action in inheritance of these characters, hence, selection for these characters is not effective.

The correlation studies revealed that genotypic correlations were higher than phenotypic correlations for most of the characters in parents F_1 's and F_2 's. These indicate that the strong inherent association between the characters governed largely by genetic causes and reduced by environmental forces. The path coefficient analysis revealed that among the parents the maximum positive direct effect on pod yield per plant was contributed by specific leaf area (0.3326) during kharif. SPAD chlorophyll meter reading exerted positive indirect effect through water use efficiency. In F_1 generation, the maximum positive direct contribution to pod yield per plant was from water use efficiency (0.0280) and SPAD chlorophyll meter reading (0.0039). SPAD chlorophyll meter reading exerted positive indirect effect through specific leaf area. During rabi, among the parents, the maximum positive direct contribution to pod yield per plant was from SPAD chlorophyll meter reading (0.4135), The highest direct negative effect to pod yield per plant was from water use efficiency (-0.4460) and specific leaf area (-0.0953). SPAD chlorophyll meter reading exerted positive indirect effect through water use efficiency. In F_1 generation during rabi, the maximum positive direct effect contribution to pod yield per plant was from specific leaf area (0.1057). The negative direct effect to pod yield per plant was from SPAD chlorophyll meter reading (-0.0162). SPAD chlorophyll meter reading exerted positive indirect effect through water use efficiency. In F_2 generation during rabi, the direct effects of specific leaf area (0.0431) with pod yield was found to be positive. The highest negative direct effect to pod yield per plant was from SPAD chlorophyll meter reading (-0.0845) and water use efficiency (-0.0149). SPAD chlorophyll meter reading exerted negative indirect effect was through specific leaf area and water use efficiency.

Keywords: Combining ability, genetic variability, heterosis, character association, path analysis, groundnut



Interactive exhibit

Chickpea yields grown under various priming methods, durations and initial soil moisture levels

Kamithi, K. D. ¹, Kibe, A. M. ² and Wachira, F. ³

¹Department of Agriculture, Laikipia County, Kenya, ²Department of Crops, Horticulture and Soil Sciences, Egerton University, P. O. Box 536, Egerton-Kenya, ³ Department of Biochemistry and Molecular Biology, Egerton University, P. O. Box 536, Egerton-Kenya

kuriakamithi@yahoo.com

Dry lands experience low, unreliable and erratic rainfall that is normally inadequate for optimum crop growth and development. Low soil moisture regimes found in ASALs, particularly during sowing time, causes poor seed germination leading to poor crop stand growth and eventually low crop yields. Therefore, in order to increased grain production, efforts were made to optimize germination and yield of *desi* chickpea, which is adversely affected by initial low soil moisture content at sowing time. A two season field experiment was conducted at Mwea Irrigation Agricultural Development Centre (MIAD) farm in 2012/2013 seasons, Kirinyaga County, Kenya, to evaluate the production potential of ICCV 97105 grain and grain attributes under different priming methods, varying priming methods, i.e., no priming, hydro priming & halo prime at three levels of i.e. 0.1, 0.2 and 0.3 % NaCl₂ concentration; three priming durations (8, 10 and 12 hours) and varying initial soil moisture levels 100% field capacity (FC), 75 % FC, 50 % FC and 25 % FC). The experiment was laid out in a split plot design with the pre sowing irrigation and combined priming method and priming duration allocated in the main, sub-plots, respectively. The control treatment was the pre-sowing irrigation at field capacity (FC). The number of pods/m² were highest (1,631 and 566) in both seasons I (Oct 2012 – Jan 2013) and II (July 2013 – Oct 2013), respectively under pre sowing irrigation of 75% FC. Consequently the highest grains yields of 1177.0 and 513.1 kg/ha were obtained, respectively. In both seasons HCL1T8 (0.1% NaCl₂ for 8 hours), significantly produced higher number of pods/m², i.e., 1615 and 754 in season I and II. Interaction effects of irrigation and priming on grain yield (kg/ha) during both seasons revealed that pre sowing irrigation of 75% FC, halo primed with 0.1% NaCl₂ for 8 hours and 100% FC hydro primed for 8 hours produced 1562.0, 1788.0 kg/ha, respectively in season I and 755.0 and 748.3 kg/ha, respectively in season II. Therefore, for farmers to realize optimal grain yields of *desi* chickpea in Mwea, it's advisable to apply pre sowing irrigation of 75% FC or above before sowing their seeds and halo prime the seeds with either 0.1% NaCl₂ for 8 hours, or 0.2% NaCl₂ for 12 hours or 0.3% NaCl₂ for 10 hours to produce 1562.0, 1604.0 and 1460.0 kg grain/ha, respectively. Farmers not willing to do halo priming can apply pre sowing irrigation of 100% FC and do hydro priming for 8 hours (HyT8). This will yield significantly higher grain yields of up to 1788.0 kg/ha depending on rainfall and management practices

Keywords: Chickpea, priming, initial soil moisture



Interactive exhibit

Adapting the Apsim model for assessing maize cultivars performances through European stressing environments

Lacube Sébastien ^a, Tardieu François ^b, Parent Boris ^c, Hammer Graeme ^d

**^a INRA, UMR 759, LEPSE
2 Place Pierre Viala, Montpellier 34060, FRANCE
lacube@supagro.inra.fr**

**^b INRA, UMR 759, LEPSE
2 Place Pierre Viala, Montpellier 34060, FRANCE
francois.tardieu@supagro.inra.fr**

**^c INRA, UMR 759, LEPSE
2 Place Pierre Viala, Montpellier 34060, FRANCE
boris.parent@supagro.inra.fr**

**^d Queensland Alliance for Agriculture and Food Innovation, University of
Queensland
Brisbane, QLD 4072, AUSTRALIA
g.hammer@uq.edu.au**

Genetic progress will largely depend on the adaptation of new genotypes to the diversity of environments, market requirements and types of agriculture. Most experiments for cultivar evaluation use networks of field experiments to assess the suitability of hundreds of genotypes to environmental conditions. In most cases, most of them run for a few years, thereby taking into account a small fraction of the climatic variability.

The use of crop models for predicting plant performance under different climatic conditions (annual variation and/or different locations) is a feasible alternative, assuming that models have an efficient capacity for simulating genotype by environment interactions (i.e. : response of plant to specific environmental conditions using genotypic parameters). If the designed model is convenient, it can be used to analyse the sensitivity of a given trait to changes in specific environment variables, assisting breeding decisions.

Our first aim is to adapt the current formalisms of the APSIM model to integrate genotypic variability on key development processes affected by environmental stress, with specific parameters for each genotype that can be measured in a phenotyping platform. For that purpose, a new leaf growth module has been implemented in the model, incorporating genotypic variability of phyllochron, number of leaves and sensitivity of leaf growth to water deficit and vapour pressure deficit. All these parameters are measured in the platform PhenoArch, thereby generating a specific vector of parameters for each genotype.

The objective will be to simulate the ranking of different existing genotypes in a grid of locations around Europe and analyse specific traits advantages to define the best suited ideotype for each environmental conditions, under current and future climatic conditions (incorporating climate change scenarios).

Keywords: APSIM, maize, genotypic variability, simulation, leaf growth



Interactive exhibit

Genetics of wheat adaptation to drought in the frame of sustainable agricultural systems and global climate change

BreedWheat Project

Arvalis, Bayer, Biogemma, Caussade, Desprez, INRA, Limagrain, Momont, RAGT, Secobra, Syngenta

Contacts :

Jacques.legouis@clermont.inra.fr

Stephane.lafarge@biogemma.com

BreedWheat aims at strengthening the competitiveness of the French wheat breeding sector as well as to address the societal demand for sustainability, quality, and safety in agricultural production. This pre-competitive project developed over a period of nine years brings together 13 public research units from various INRA sites and Universities across France as well as 10 partners from private companies and cooperatives, 2 technical institutes, and the competitiveness cluster Céréale Vallée.

In this frame, combined approaches are developed to decipher the ecophysiological, genetic and molecular basis of key factors impacting the important agronomic traits that are yield and grain protein composition in the context of sustainable systems and climate change. A set of field trials has been dedicated to drought stress during three years representing six sites (2 each years). A panel of 220 winter European elite varieties was tested on each trial in irrigated/dry conditions. This genetic material was genotyped using a 420k Axiom array (TaBW420k) developed within BreedWheat leading to 92k polymorphic SNPs. Grain yield, yield components and grain protein concentration were measured. Phenotypic and environmental data analysis have been conducted to determine stress impact and to validate the field trials. Among the six sites x season combinations, three were validated as "drought stress field trials" comparing irrigated/dry conditions. Genome wide association analysis is ongoing to identify genomic areas linked to drought tolerance and GxE interactions. Our goal is to have access to informative markers to facilitate selection for drought tolerance and also to select the most promising regions to fine map some of them.

Keywords: Association genetics, Drought tolerance, Wheat



Short talk

Genetic analysis of maize root dynamics using a novel aeroponics platform

Aleksander Ligeza^a Benjamin Lobet^b and Xavier Draye^b

^a Crop physiology and Plant breeding, Earth and Life Institute, Agronomy (ELI-A), Université catholique de Louvain, Croix du Sud 2 - L7.05.11, 1348 Louvain-la-Neuve, Belgium

aleksander.ligeza@gmail.com

^b Crop physiology and Plant breeding, Earth and Life Institute, Agronomy (ELI-A), Université catholique de Louvain, Croix du Sud 2 - L7.05.11, 1348 Louvain-la-Neuve, Belgium

benjamin.lobet@uclouvain.be

^c Crop physiology and Plant breeding, Earth and Life Institute, Agronomy (ELI-A), Université catholique de Louvain, Croix du Sud 2 - L7.05.11, 1348 Louvain-la-Neuve, Belgium

xavier.draye@uclouvain.be

Conventional methods of root phenotyping do not address the dynamics of root system architecture. We have developed a novel high throughput root phenotyping platform based on aeroponics, automation and high resolution imaging. The platform has been successfully used with wheat, rice, barley, maize and tomato populations. In this framework DROPS, the platform has been used to uncover the root dynamics in a maize diversity panel composed of 252 lines. The platform accommodates 990 maize plants simultaneously, that are individually scanned in a backlight configuration every two hours for up to 3 weeks, with three independent biological replicates. Automated image analysis allowed us to estimate parameters for the distribution of root growth, angle of initial root trajectories, gravitropic set points of young lateral roots and branching patterns. Our results reveal a wide amplitude of variation and medium to large heritabilities for most traits. The genome wide association analysis of these datasets is currently underway. Relating these datasets with field data through modeling is also envisioned. The relevance and interest of root growth dynamics to improve plant performance upon water deficit is discussed.

Keywords: Root system architecture, systems dynamics, phenotyping, genetics, aeroponics



Short talk

Designing African Rainfed Cotton Ideotype by Simulation

Romain Loison ^a, Alain Audebert ^b, Philippe Debaeke ^c, Edward Gérarddeaux ^d

^a CIRAD, UR AÏDA
Av. Agropolis 34398 Montpellier, France
romain.loison@cirad.fr

^b CIRAD, UMR AGAP
Av. Agropolis 34398 Montpellier, France
alain.audebert@cirad.fr

^c INRA, AGIR
BP 52627
31326 Castanet-Tolosan, France
philippe.debaeke@toulouse.inra.fr

^d CIRAD, UR AÏDA
Av. Agropolis 34398 Montpellier, France
edward.gerardeaux@cirad.fr

Crop simulation models (CSM) dynamically estimate agricultural production as a function of weather and soil conditions, and crop management. They can be used for evaluating cultivars in actual and future tropical conditions. In Northern Cameroon, cotton (*Gossypium hirsutum* L.) is grown exclusively in rainfed conditions and its yield has been decreasing steadily since the 80s. Therefore our objectives were to evaluate the usefulness of CSM to identify current rainfed cotton ideotypes for two contrasted environments of northern Cameroon. Based on field observations constituting the minimum dataset, phenology, morphology, leaf area index and yield simulated by CROPGRO-Cotton were successfully calibrated and validated in our conditions. Results showed that ideotype should have earlier anthesis date, longer reproductive duration, thicker leaves with higher potential assimilation rate compare to the reference cultivar (L484). In the North region, it seemed that having bigger leaf than L484 should be favorable whereas in the Far North smaller ones are more suitable to local drought-prone conditions. We concluded that morpho-physiological traits could and should be imported into breeding programs in F5 generation where high genetic diversity still exist and plant material start to be considered as a line rather than a single plant. Consequently, we invite breeders to target cultivars with low "emergence to anthesis" to reproductive ratio, thick leaf, high chlorophyll content, and smaller leaf for the conditions with the lowest water availability and bigger ones for the conditions with best water availability.

Keywords: *Gossypium hirsutum* L.; CROPGRO Cotton; Virtual cultivar; Seed cotton yield; Leaf area index.



Interactive exhibit

Halophyte grasses as a source of genes to improve stress tolerance in glycophyte cereals : the Stress Associated Protein gene of *Aeluropus littoralis*

**Donaldo Meynard^a, Walid Ben Rohmdane^b, Rania ben Saad^c, Bastien Cayrol^a,
Thaura Ghneim Herrera^d, Michael Selvaraj^e, Denis Fabre^a, Christophe Périn^a,
Jean-Benoît Morel^f, Abdullah Al Doss^b, Emmanuel Guiderdoni^a, Afif Hassairi^b**

^a CIRAD, UMR AGAP, 34398 Montpellier, France - ^b King Saud University -
Address, Saudi Arabia - ^c Centre de Biotechnologies de Sfax
B.P 1177 Sfax 3018, Tunisia - ^d ICESI, Calle 18 # 122-135, Cali, Colombia -
^e CIAT, Apartado Aéreo 6713 Cali, Colombia - ^f INRA, UMR BGPI, 34398
Montpellier, France

donaldo.meynard@cirad.fr, afif.hassairi@gmail.com, raniabensaad@yahoo.fr,
tghneim@icesi.edu.co, M.Selvaraj@CGIAR.ORG, jbmorel@cirad.fr

Halophyte plants have developed remarkable anatomical, morphological and physiological adaptations to respond to the imposition of multiple, combined, environmental stresses (salinity, drought, heat...). They are therefore valuable genetic resources to identify key adaptive genes that can help improving stress tolerance in glycophyte crops either through genetic engineering or in searching for favorable ortholog alleles in the natural crop diversity. We used an A20/AN1 zinc finger stress associated protein (SAP) gene of the C4 halophyte grass *Aeluropus littoralis* to engineer drought, salt and cold tolerance in the glycophyte crops durum wheat and rice (Ben Saad et al 2012a, 2012b). Higher performance of rice lines under drought imposed at vegetative stage was due to maintenance of photosynthesis and of the integrity of the photosynthetic apparatus (Ben Saad et al 2012b). AISAP Rice lines had 40-90% higher yield following field drought imposed at flowering stage compared to their azygous siblings and varietal checks (Ghneim-Herrera et al, submitted). Transcript profiling of AISAP lines subjected or no to a salt stress revealed that their transcriptome was primed for induction of some stress-related genes under control conditions and had a dramatically alleviated overall response upon salt shock (Ben Rohmdane et al, submitted). Yeast-2-hybrid and co-immunoprecipitation experiments identified key AISAP interactors pointing for a role of AISAP in protein complexes leading to ubiquitination and degradation through the 26S proteasome. The OsSAP9 gene is the most likely ortholog of AISAP in rice and shares 76% amino acid identity. To determine whether AISAP has evolved specific functions, we are currently complementing the *ossap9* rice mutant with AISAP.

Keywords: abiotic stress tolerance, *Aeluropus littoralis*, halophyte, rice



Interactive exhibit

Analysis of maize inbred lines for drought tolerance based on anthesis silk interval, yield performance and microsatellites

Sanja Mikić^a, Dušan Stanisavljević^a, Miroslav Zorić^a, Ljiljana Brbaklić^a, Bojan Mitrović^a, Gordana Šurlan Momirović^b, Ankica Kondić Špika^a

^a Institute of Field and Vegetable Crops
Maksima Gorkog 30, 21000 Novi Sad, Serbia
sanja.mikic@ifvcns.ns.ac.rs

^b University of Belgrade, Faculty of Agriculture
Nemanjina 6, 11080 Zemun, Serbia

Drought is a severe threat to maize yield stability in Serbia occurring occasionally but with significant yield losses. However, breeding programmes for drought tolerant genotypes seem not be emphasized enough. To test the tolerance of newly developed elite maize inbred lines and their hybrids to drought stress, field trials for yield performance and anthesis silk interval (ASI) were set in drought stressed environments in 2011 and 2012. Inbred lines were tested for ASI and yield *per se* in four environments in both years, whereas the hybrid yield performance was analysed in 2012 only. A correlation between days from pollen shedding to silk emergence and yield *per se* of maize inbred lines was moderate -0.54. The hybrids, whose parental lines had short ASI in drought conditions, ranked highly for yield performance in field trails also under drought stress. Three inbred lines, NS62, NS118 and NS732, were selected for their potential drought tolerance and good combining abilities. Association analysis of inbred lines with microsatellite markers indicated significant correlations between ASI and two markers, bnlg238 and bnlg1525, stable in four and two environments, respectively. Two alleles, 161bp and 167bp, of marker bnlg238 influenced shortening of ASI in all environments and had positive effect on yield *per se* in three environments. Alleles 163bp and 174bp of marker bnlg1025 affected shortening of ASI and increasing of yield *per se* in all four environments. Although these preliminary results indicate the possible use of the makers in selecting tolerant genotypes, more detailed studies should be undertaken to validate the findings before it can be applied in our breeding programmes.

Keywords: ASI, drought, inbred lines, maize, yield



Interactive exhibit

Multitraits evaluation of berseem clover (*Trifolium alexandrinum* L.) ecotypes under full-irrigation and water restriction conditions

**M. Mubashar Huassain¹, Saeed Rauf¹, Jakub Paderewski², Ikram UL Haq¹,
Dorota Sienkiewicz-Paderewska³, Philippe Monneveux⁴**

¹*Department of Plant Breeding & Genetics, University College of Agriculture, University of Sargodha, Pakistan, 38000, saeedbreeder@hotmail.com*

²*Department of Experimental Design and Bioinformatics, Warsaw University of Life Sciences, Poland, Nowoursynowska 159, 02-776 Warsaw*

³*Department of Agronomy, Warsaw University of Life Sciences, Poland, Nowoursynowska 159, 02-776*

⁴*International Potato Center (CIP), Avenida La Molina 1895, La Molina, Lima, Peru*

Berseem clover (*Trifolium alexandrinum* L.) is an important forage crop in Mediterranean region. Its yield is however frequently affected by insufficient irrigation due to unavailability of water. In the present study, twenty ecotypes of berseem clover have been evaluated in lysimeters under full irrigation and water restriction conditions. In the full irrigation treatment soil humidity was maintained at field capacity, while in the water restriction treatment water was only supplied after severe wilting and to maintain humidity in the deep profile of the soil. Assessed traits included forage yield, calculated as the sum of the biomass harvested at 70 and 110 DA days after emergence, and morpho-physiological traits. Significant effects of water restriction were noted on yield, leaf gas exchange parameters, canopy temperature and osmotic adjustment. Most morpho-physiological traits had higher broad sense heritability than forage yield, both under full irrigation and water restriction conditions. Water restriction increased genetic and phenotypic variability and heritability of most traits under study. Under these conditions forage yield was positively associated to leaf temperature and recovery rate index and, under full irrigation, to net photosynthetic rate, canopy depression temperature and leaf area. The possible use of these traits as indirect selection criteria in berseem clover breeding programs is discussed. Some ecotypes with favorable traits such as high forage yield potential, good adaptation to water restriction and aptitude to multiple harvesting have also been identified.

Key Words: berseem clover; ecotypes; forage yield; morpho-physiological traits; water restriction.



Interactive exhibit

Comparison of High-Throughput Genotyping Technologies in Maize:

Increase in number of regions detected in association genetics

Negro S.S.¹, Millet E.², Kruijer W.³, Madur D.¹, Le Paslier M-C.⁴, Combes V.¹, Van Eeuwijk F.³, Tardieu F.², Bauland C.¹, Welcker C.², Nicolas S.¹, Charcosset A.¹

¹ **Génétique Quantitative et Evolution - Le Moulon, INRA - Université Paris-Sud - CNRS - AgroParisTech, Ferme du Moulon, F-91190, Gif-sur-Yvette, France**

² **LEPSE, INRA, 2 place Viala, F-34060 Montpellier, France**

³ **Biometris, Applied Statistics, Wageningen University, PO BOX 100, 6700 AC Wageningen, the Netherlands**

⁴ **Etude du Polymorphisme des Génomes Végétaux, INRA, CEA Institut de Génomique, Centre National de Génotypage, 2 rue Gaston Crémieux, F-91057, Evry, France**

Recent progress in genotyping and resequencing technologies can improve our understanding of the mechanisms involved in quantitative trait variation by performing genome-wide association studies on large diversity panels. *Circa* 250 Dent inbred lines with narrow phenology variation were selected within the DROPS project. Hybrids with a flint tester were evaluated for male flowering time and plant height at seven sites in Europe, during two years (2012 and 2013), and for two treatments (watered and drought). We genotyped this panel using 50K Infinium HD Illumina array (~50,000 SNP Ganai et al., 2011), 600K Axiom Affymetrix array (~600,000 SNP Unterseer et al., 2014) and Genotyping By Sequencing approach developed by Cornell university (~600,000 SNP; Elshire et al., 2011; Glaubitz et al., 2014). We studied the impact of increasing the marker density on (i) the estimates of kinship and population structure, (ii) the accuracy of the QTL positions, and (iii) the gain in power (number of significant markers identified). We also addressed the issues of the genotyping reproducibility and the imputation quality for GBS, considering the 50K Illumina array as the reference. Genotyping are highly reproducible (c. 100% for 50K vs 600K and c. 99% for 50K vs GBS) and the imputation quality for the GBS were high (c. 97%). GBS lead to a much higher proportion of rare alleles compared to Illumina and Affymetrix arrays. Increased marker density, using 600K and GBS, leads to the detection of new regions with marker-trait associations and a higher precision of QTL positions. However, each technology leads to detection of associations in specific regions, and thus none of these three technologies seems able to capture all of the genomic regions involved in trait variation. The suggestion is that the density and/or distribution of SNPs genotyped by GBS and 600K is still not sufficient to identify all relevant genomic regions.

Keywords: genome-wide association genetics, association mapping



Short talk

Toward the enhancement of peanut (*Arachis hypogaea* L.) tolerance to drought using beneficial alleles from the wild species

Joël Romaric NGUEPJOP ^{a,b}, Daniel FONCEKA ^{b,c}, Hodo Abalo TOSSIM ^b, Djibril SANE ^a, Jean-François RAMI ^c

^a **Université Cheikh Anta Diop de Dakar (UCAD), Dakar, Sénégal**

nguepjop@gmail.com - www.ucad.edu.sn

^b **Centre d'Etude Régional pour l'Amélioration de l'Adaptation à la Sécheresse (CERAAS), Thiès, Sénégal**

www.ceraas.org

^c **Cirad UMR AGAP, Montpellier, France**

daniel.fonceka@cirad.fr - <http://umr-agap.cirad.fr/>

Cultivated peanut is an allotetraploid (AABB) deriving from a recent hybridization event between two diploid species with A and B genomes. Cultivated peanut has a limited genetic variation at the DNA level that has greatly hampered the application of molecular breeding approaches for tackling the improvement of complex traits such as terminal drought tolerance. Wild relatives of the cultivated peanut have maintained a rich genetic variation that allowed them to grow and reproduce in a broad range of environments. They are potential sources of beneficial alleles that can be tapped to improve the cultivated species. In our study, we developed an advance backcross QTL (AB-QTL) population from the cross between a Senegalese elite cultivar *A. hypogaea* "Fleur11" used as recurrent parent and a synthetic tetraploid "ISATGR278-18" that combines the AA genome of *A. duranensis*, a close wild relative of *A. hypogaea* believed to be one of the most probable ancestor of the cultivated species, and the KK genome of *A. Batizocoi*, a more distant wild relative reported to be compatible with the B genome of the cultivated species. A total of 135 AB-QTL lines (BC₂F₄) have been produced, genotyped with mapped SSR markers and evaluated in an alpha lattice design for 8 morphological, 11 agronomical and 3 physiological traits in well-watered and water-limited conditions during the post rainy season 2014 at Bambey station in Senegal. High variability was observed for several morphological traits within the AB-QTL population. A significant contrast for physiological trait was observed between AB-QTL lines under well-watered and water-limited conditions. In this poster we present the results of the QTL analysis for plant morphology and physiological traits such as SCMR (SPAD Chlorophyll Meter Readings), Leaf temperature and fluorescence. The effects of wild alleles for traits related to the plant morphology and water deficit are discussed.

Keywords: Peanut; drought improvement; wild species; beneficial exotic QTL; AB-QTL analysis.



Interactive exhibit

Selecting of high yielding and wheat drought tolerant variety adapted to Burundi semi arid agro ecological zone.

Nihorimbere G., Nibasumba A., Mbonankira E., Bigirimana.J, Gahungu A., Hezingingo P., Bamiruwabo S.(2015).

*Institut des sciences Agronomiques du Burundi (ISABU)
B.P 795 Bujumbura*

In Burundi, Wheat (*Triticum aestivum*) is mainly grown in high lands regions. These areas include Mugamba and Bututsi agro-ecological zones. Nevertheless, wheat is also adapted to the moderate altitude region which is prone to climate change. Currently, in those regions, the nutrients accumulation of wheat grains is stressed and the grain seems burned while the thousand grains weigh still very low. Therefore, due to the obtained low wheat yield, the farmers avoid growing wheat and local millers rely on foreign wheat importation. In 2002, ISABU wheat program introduced from CIMMYT 50 drought tolerant lines. The preliminary adaptation trials were conducted and three varieties 11th SAWYT 40, 11th SAWYT 19 and 15th SAWSN 1 were selected for further evaluation. The main objective of the study was to identify the more yielding and stability variety between the three ones while conducted under water stress conditions. The evaluation trials were conducted in 2011 and 2012 within the three representatives' semi arid research stations: Mahwa, Karusi and Murongwe of National Agriculture Research Institution (ISABU). The experimental design was split plot where the three performing varieties were randomized within the sub plots and four sowing days: 15 February (early date), 15th March (recommended date) and 15 April (later date) were randomized within the main plots. The mean yield of the variety 15th SAWSN 1 was not influenced by the sowing date (p value=0.55) while other varieties were outperformed when sown early date (p value <0.001). There was no significant difference for the thousand grain weight for 15th SAWSN 1 (p value=0.06) while a significant difference (pvalue=0.02) was observed for others varieties. So far, the variety 15th SAWSN 1 was selected as high yielding and drought wheat tolerant variety adapted within Burundi middleland agro ecological conditions.

Key words: Wheat, drought tolerant lines, agro ecological zone, semi arid, thousand grain weigh



Interactive exhibit

Genetic variability studies of soybean breeding lines for yield and yield attributing traits in different rainfed agro-domains of Nepal

¹R. Darai, ¹S. Subedi ¹R.P.Sah, and ²P. Thakur

¹ Senior Scientist, Scientist, STO, Technical Officer, GLRP, Khajura, Nepalgunj, Banke

³Senior Scientist/Coordinator, ORP, Nawalpur, Sarlahi
rajendra5042@yahoo.co.uk

Soybean (*Glycine max* L. Merrill) is second most important food legume of Nepal, grown either as sole or intercrop with maize or in paddy bund. It alone shares 7.4% in area and 8.19% production out of total legumes. Being a miracle legumes crop that can harbors momentous levels of protein and oil. It has immense potential to increase the area and production due to its yield stability and wider adaptation trait. Its importance increases due to the burgeoning of the poultry and cattle's farming. Low productivity of soybean is due to the susceptibility to the prevalent diseases, extreme temperature, narrow genetic traits, pod blight and flower abortion. In fact, the success of soybean improvement program depends on its genetic variability of yield and yield attributes. Considering the truths, soybean cultivars were collected from IARS and NAGRC and studied in depth. An investigation was carried out in the forms of regeneration and observation screening nursery, coordinated varietal trial and participatory trial to assess the variability traits, yield potential, insect-disease reaction etc at Rampur and Nawalpur over the years 2012 to 2014. Coordinated varietal trial was carried out in RB design with four replications and OBN in rod row while in pre-release varietal trial in none design. Yield and yield contributing traits were analyzed to understand the extent of variability for yield and yield attributing traits. The accessions showed wide variability for traits viz., days to flowering, days to maturity, plant height, 100 seed weight, grain yield, number of seeds per pod, number of pods per plant and number of primary branches. The qualitative traits viz., growth habit (Erect and semi erect), growth type (determinate, semi determinate and indeterminate) have also showed significant variability. Among the traits studied, important traits showed higher heritability and genetic advance. The trait association studies showed that the characters viz., plant height, number of pods per plant, number of seeds per pod could be improved and simultaneous selection would offer scope for yield improvement.

Keywords: Soybean, genotypes, genetic variability, yield, and yield attributes



Interactive exhibit

Effect of drought tolerance, estimation of heterosis, proportional contribution and gene action in maize sown at diverse water regimes

Ijaz Rasool Noorka^a, JS Pat Heslop Harrison^b, Taufiqullah^c and Ihsan khaliq^d

^a *University college of Agriculture, University of Sargodha, Pakistan
ijazphd@yahoo.com*

^b *Department of Biology, University of Leicester, United Kingdom
phh4@leicester.ac.uk*

^c *University college of Agriculture, University of Sargodha, Pakistan
t_ullah66@yahoo.com*

^d *Department of Plant Breeding and Genetics, University of Agriculture,
Faisalabad, Pakistan
ikhaliq63@yahoo.com*

Drought the most important phenomena of the today's agriculture was observed in Maize crop varieties. The study is based on line × tester analysis to estimate heterosis, proportional contribution of lines, testers and their interaction and gene action in cross combinations of different maize genotypes under different water regimes. Total 12 parents comprised of eight lines and four testers; crossed to produce 32 F₁ hybrids. Parents including their hybrids were evaluated in CRD with three water treatments under controlled conditions with three replications in two seasons. Heterosis, percent contribution of lines, testers and line × tester interaction and gene action was studied for the traits i.e. ear leaf area, number of kernel rows per ear, 100 grain weight, biological yield, vegetative dry matter and anthesis-silking interval. Variable heterosis both in magnitude and direction was observed. Both additive and non-additive gene effects have role in the control of anthesis-silking interval; whereas non-additive gene effects were observed for ear leaf area, number of kernel rows per ear, 100 grain weight, biological yield and vegetative dry matter. However 100 seed weight was mainly affected by dominance effects under this study that helped for the selection of parents to be used for the development of synthetics and hybrids durable for different water regimes.

Key words: Additive, Hybrid, Susceptible, Line × tester, Water stress



Interactive exhibit

Vulnerability of Rice Crop to Climate Change in West Nusa Tenggara (NTB) Province, Indonesia

Ratri, D. N^a, Hariadi, M.H.^b

*^{a,b} The Agency for Meteorology, Climatology and Geophysics
of the Republic of Indonesia (BMKG)
Jl. Angkasa I No. 2 Kemayoran, Jakarta Pusat 10720
dianuratri@gmail.com^a, mugni_hadi@yahoo.com^b*

Future agricultural planning is a meaningful strategy for alternative agricultural activities in terms of location that is needed by decision makers. Future challenges for agricultural sectors are climate variability and changes. Less rainfall that leads to drought could be challenge for rice farmers. To look at the projection about land suitability for rice, a study on climate change related to the rice plant vulnerability is needed. The Food and Agriculture Organization (FAO) method was adopted for the purpose of identifying possible changes in land suitable for planting rice (*Oriza sativa*) in West Nusa Tenggara (NTB), Indonesia under future climate change projections. This study utilized climate theme layers and non-climate theme layers, analysis tools, and an overlay technique using the Geographic Information System (GIS). The climate data were simulated by a Regional Climate Model (RCM)—the CSIRO Conformal-Cubic Atmospheric Model (CCAM) driven by two host General Circulation Models (GCMs), ECHAM5/MPI-OM and GFDL CM2.1. Those two climate models offer us climate projection information and we could employ the information for the future agricultural planning, we could produce an optimistic scenario for rice farmers.

Keywords: Land Suitability Analysis, Climate Change, ECHAM5/MPI-OM, GFDL CM2.1, Rainfall variability



Interactive exhibit

Performance of SUSTOR-potato model across contrasting growing conditions

Rubí Raymundo¹, Senthold Asseng¹, Rishi Prasad¹, Ulrich Kleinwechter², Bruno Condori³, Walter Bowen¹⁰, Joost Wolf⁴, Jorgen Olesen⁵, Qiaoxue Dong⁶, Lincoln Zotarelli¹, Manuel Gastelo³, Ashock Alva⁷, Maria Travasso⁸, Vijay Arora⁹, Wendy Graham¹, and Cheryl Porter¹.

¹ **Agriculture and Biological Engineering department, University of Florida, Gainesville, FL, USA**

² **International Institute for Applied Systems Analysis (IIASA), Luxemburg, Austria.**

³ **International Potato Center (CIP), Lima, Peru**

⁴ **Plant Production Systems Group, Wageningen University, Netherlands**

⁵ **Department of Agroecology - Climate and Water, Aarhus University, Denmark**

⁶ **China Agricultural University, Beijing, China**

⁷ **United States Department of Agriculture-Agricultural Research Service (USDA-ARS), USA**

⁸ **Instituto de Clima y Agua (INTA), Los Reseros y Las Cabañas, 1712 Castelar, Argentina**

⁹ **Department of Soil Science, Punjab Agricultural University, Ludhiana, India**

¹⁰ **Agriculture and Food Resources Economics department, University of Florida, Gainesville, FL, USA**

r.raymundo@ufl.edu

Crop models became an important tool in climate change impact assessments, but often lack comprehensive field testing. We tested the SUBSTOR potato model with 87 field experiments including 204 treatments from 19 countries. The field experiments varied in cultivars, N fertilizer and water supply, sowing dates, soil types, temperature environments and atmospheric CO₂ concentrations and included open top chamber (OTC) and Free-Air-CO₂-Enrichment (FACE) experiments. Tuber yields were in general well simulated across a wide range of current growing conditions, for diverse potato species and cultivars, including *Solanum tuberosum*, *Solanum andigenum*, *Solanum juzepczukii* species and modern, traditional, medium and late maturity-type cultivars, with a RMSE of 2.1 Mg ha⁻¹ for tuber dry weight, and 5.3 Mg ha⁻¹ for tuber fresh weight. Tuber yields were less responsive to elevated atmospheric CO₂ and had difficulties in simulating high temperature impacts on crop growth. Single cultivars (cv. Desiree and cv. Atlantic) grown across the globe using constant cultivar parameter sets were well simulated with the model. Other simulated crop variables like leaf area, stem weight, crop N and soil water often differed substantially from measurements; however, some of these variables had also significant measurement errors indicated by large error bars. The SUBSTOR Potato model was found suitable for simulating current growing conditions and crop management options across geographic regions but requires improvements in simulating high temperature and elevated atmospheric CO₂ impacts before being used in climate change impact assessments.

Keywords: Crop model, Potato, Climate change, Heat stress, Carbon dioxide



Interactive exhibit

Screening drought tolerance maize genotypes by using combining ability

Ludvik ROZMAN

**University of Ljubljana, Biotechnical Faculty, Dept. of Agronomy
Jamnikarjeva 101, 1000 Ljubljana, SLOVENIA
ludvik.rozman@bf.uni-lj.si**

The main aim of our study was to evaluate general (GCA) and specific (SCA) combining ability of 50 new Lj- maize hybrids to photosynthetic activity (FA) and to water use efficiency (WUE). The hybrids were developed by using the scheme of incomplete diallel, and involved 15 inbreds (P1–P10 as female parents and P12–P16 as male parents). The material was maintained in the maize gene bank of the Biotechnical Faculty in Ljubljana (Slovenia). The field trial was conducted on the experimental station of the Biotechnical Faculty at Jable near Ljubljana and was based on the randomized complete blocks and 3 replications. The FA we measured with Licor Li6400 machine adjusted at the same parameter: light source 1500 $\mu\text{mol m}^{-2} \text{s}^{-1}$, with reference $\text{CO}_2=380$ ppm, leaf temperature at 23 °C and 40 % moisture. The measuring we made at tasseling on the middle of above ear leaf of 3 plants from 8.30 to 12.00 a.m. The WUE we calculated using relation between FA and evapotranspiration. Statistical analysis and CA were calculated using Microsoft Excel, Statgraphics Centurion and Agrobase Gen II® programs. Weak significant differences we found of GCA (only 2-3 homogenous groups) and of SCA for FA, but higher and significant differences of GCA and SCA for WUE were found. In some cases the inbreds with good GCA confirmed also the good SCA and, on the other hand, our results confirmed the finding of other authors that the inbreds with good SCA not always express the good SCA. However, we found out the some good inbreds regarding to CA, which could be a good source for further successful breeding.

Keywords: maize, photosynthetic activity, water use efficiency, combining ability



Interactive exhibit

Genetic analysis of proline contents a marker of plant survivability under drought

Farghama Khalil^a, Saeed Rauf^b, Zafar Iqbal^c

^a Department of Plant Breeding & Genetics, University College of Agriculture, University of Sargodha, Pakistan

^b Department of Plant Breeding & Genetics, University College of Agriculture, University of Sargodha, Pakistan

^c Department of Plant Pathology, University College of Agriculture, University of Sargodha, Pakistan

Proline is an important marker of osmotic adjustment in plants and its concentration tends to increase under stress condition. It has been vigorously investigated in many crop species and higher concentration has been linked with drought tolerance. However, inheritance of the proline is known to be complex and affected by the environment and genetic backgrounds. Therefore, study was investigated to determine the type of genetic variability associated with proline in large half sib populations and probable environment for the selection of plant progenies with high proline contents. The study also investigated the correlations of proline with key traits such as osmotic adjustment, biomass traits and inorganic salts. The result would help in progress toward breeding crop species for drought tolerance and in particular usefulness of proline contents in practical drought tolerance breeding.

Keywords: genetic variability, additive gene action, heritability, K⁺⁺



Short talk

Exploring the basis of drought tolerance in *Helianthus argophyllus*, *Helianthus annuus* and their crosses

Muhammad Abid^a, Saeed Rauf^b, Muhammad Asam^c

^a Department of Plant Breeding & Genetics, University College of Agriculture, University of Sargodha, Pakistan

^b Department of Plant Breeding & Genetics, University College of Agriculture, University of Sargodha, Pakistan

^c Department of Plant Pathology, University College of Agriculture, University of Sargodha, Pakistan

In order to improve the drought tolerance, wild species has been considered as an important source of tolerance. In sunflower, *Helianthus argophyllus* has been utilized in various breeding program for the introgression of abiotic stress tolerance. On the basis of these ground, a study was designed to evaluate *Helianthus argophyllus* and annuus breeding lines and subsequent interspecific hybrids and female parents against drought stress for various biochemical, physiological and morphological traits. All the plant materials was sown in growth chamber in controlled condition under completely randomized design with three replications. Simulated drought condition was developed by foliar spray or irrigating 8 μ mol of abscisic acid (ABA), and 50 g L⁻¹ polyethylene glycol at regular interval. Sunflower species and their hybrids were compared for plant biomass, leaf gas exchange traits, plant growth regulators, osmotica such as cuticular waxes, leaf silicon contents. The species and their derivatives showed significant differences showing that species were adapted to variable tolerance mechanisms against drought stress. The data may help to understand the drought tolerance mechanism and to adapt strategies for enhancing drought tolerance in sunflower.

Keywords: abscisic acid, net photosynthesis rate, leaf area, mechanism, plant growth



Short talk

High-throughput phenotyping of a maize introgression library under water deficit conditions

Sciara G.^a, Salvi S.^b, Cané M. A.^c, Welcker C.^d, Cabrera L.^e Grau A.^f, Bovina R.^g, Tardieu F.^h Tuberosa R.ⁱ

^{abc} Dipartimento di Scienze Agrarie – Università di Bologna
Viale Fanin 44 Bologna, Italy

giuseppe.sciara2@unibo.it, silvio.salvi@unibo.it, mariaangela.cane@unibo.it

^dLaboratoire d'Ecophysiologie des Plantes Sous Stress Environnementaux
IBIP - Bât. 7 - 2 place Pierre Viala - 34060 Montpellier, France
welcker@supagro.inra.fr

^eLaboratoire d'Ecophysiologie des Plantes Sous Stress Environnementaux
IBIP - Bât. 7 - 2 place Pierre Viala - 34060 Montpellier, France
cabrera@supagro.inra.fr

^fLaboratoire d'Ecophysiologie des Plantes Sous Stress Environnementaux
IBIP - Bât. 7 - 2 place Pierre Viala - 34060 Montpellier, France
antonin.grau@supagro.inra.fr

^g Dipartimento di Scienze Agrarie – Università di Bologna
Viale Fanin 44 Bologna, Italy
riccardo.bovina@studio.unibo.it

^hLaboratoire d'Ecophysiologie des Plantes Sous Stress Environnementaux
IBIP - Bât. 7 - 2 place Pierre Viala - 34060 Montpellier, France
tardieu@supagro.inra.fr

ⁱDipartimento di Scienze Agrarie – Università di Bologna
Viale Fanin 44 Bologna, Italy
roberto.tuberosa@unibo.it

A maize Introgression Library (IL) of 75 lines was derived from the cross between Gaspé Flint (an extremely early Canadian landrace, used as donor parent) and B73, used as recurrent parent (Salvi et al., 2011). The population was formerly shown to segregate for several flowering time QTLs as well as for Seminal Root Architecture (SRA) traits. In this experiment, the IL was characterized using the high-throughput phenotyping platform PhenoArch (INRA, Montpellier), a greenhouse platform equipped for large-scale automated imagery and evapotranspiration measurements. Objective of this investigation was to a) to screen the IL for the presence of growth and water use efficiency (WUE) QTLs under different water regimes and b) to test the effect of previously identified QTLs for flowering time and SRA on the growth and WUE.

The maize IL lines were tested under well-watered and water-deficit conditions (soil water potential > -1 and ~ -4 Bar, respectively). Each pot was weighted at least once per day allowing for the accurate estimation of daily evapotranspiration. By means of image analysis and suitable models (multiple regression and sigmoidal fitting), it was possible to estimate biomass



accumulation and thus WUE. Preliminary results showed statistically significant genetic effect for several traits, including biomass accumulation, leaf emission rate and WUE ($P < 0.05$, Dunnett test).

Based on the collected phenotypic data and highly dense SNP genotyping, several QTLs for biomass accumulation and WUE were mapped on Chr. 1, 2, 3, 5, 8, 9, 10, both in well-watered and water-deficit conditions. Different QTLs for phenology and RSA traits seems to affect differently plant development, biomass accumulation and WUE. A particularly interesting QTL conferring increased WUE in both WW and WD conditions was mapped on chr. 9.

Keywords: Maize, Drought resistance, Water use efficiency, High-throughput phenotyping, phenology



Short talk

Trait capture for drought tolerance in quality protein maize in two agro-ecological zones of Nigeria

SHOWEMIMO, F.A

Department of Plant Breeding & Seed Technology, College of Plant Science and Crop Production, Federal University of Agriculture, Abeokuta. P.M.B. 2240. OGUN STATE, NIGERIA

Drought is the most important abiotic factor contributing to yield losses in in maize in Africa. Identification and measurement of secondary traits associated with grain yield provides a guide to specific mechanisms that contribute to grain yield under drought. Thus water depletion patterns, leaf rolling and canopy temperatures, root length, root-shoot ratio and root hair density are indicative of root importance in trait capture for drought tolerance in maize. 30 maize genotypes were studied in three separate field experiment using Randomized Complete Block Design (RCBD). Experiment 1 was conducted during wet season of 2008, the other two were irrigated (thrice and once a week respectively) dry season of 2009, at the research field of IAR, Samaru, Zaria. Highly significant difference was obtained for yield and yield components among the genotypes and genotypes x environments, Stress Intensity (SI) was highest (30.1%) for one irrigation regime per week. Water stress slows ear growth, due to delayed silk emergence, reduced tassel, widening interval between anthesis and silking (ASI). Yield, under stress at flowering, shows a strong dependency on grain number per plant ($r > 0.6$), barrenness ($r > 0.8$) and ASI ($r = 0.3$ to 0.6). Genetic variance estimate were positive and high for all the traits except for plant height that is low. Heritability estimates for all the traits were moderate to high. Based on Susceptible Stress Index (SSI), Harmonic Mean (HM), and Tolerance Index (TI); QML 806, QML 807 and QML 803 were remarkably drought hardy and high yielding.

Keywords: Traits, genetic variance, drought, tolerance, indices



Interactive exhibit

Monitoring standard deviations of chlorophyll a fluorescence parameter Fv/Fm of JIP-test during increasing water deficit

Jasenka Antunović Dunić^a, Vlatko Galić^b, Mario Franić^b, Hrvoje Lepeduš^c, Vera Cesar^a, Domagoj Šimić^b

^a *Department of Biology, J.J. Strossmayer University, Osijek, Croatia*

^b *Agricultural Institute Osijek, Osijek, Croatia*

^c *Faculty of Philosophy, J.J. Strossmayer University, Osijek, Croatia*

Chlorophyll fluorescence (ChlF) parameters of JIP-test are considered as early indicators of stress in photosynthetic tissues. The JIP-test is particularly useful for crop plants when applied *in vivo* under mild drought stress under control and field conditions. However, due to increasing intrinsic photosynthetic heterogeneity affected by increasing drought stress severity, the usefulness of the classical ChlF parameters is in question. Objective of this study was to monitor changes in values of the maximum efficiency of photosystem II (Fv/Fm) parameter and its corresponding standard deviations during increasing water deficit in barley measured in 25 replications and conducted in three independent pot experiments. After ten days of growing, drought stress was induced by withholding water and monitored for the next ten days. During the 10-days interval, Fv/Fm values decreased from 0.80 to 0.48, 0.53 and 0.54 in three experiments, respectively. However, standard deviations of Fv/Fm values increased successively being from 0.005 on the day 1 to 0.18, 0.19 and 0.26 on the day 10 in the respective three experiments. The consistent sharp increase of the corresponding standard deviation of about 0.02 occurred at the Fv/Fm value of 0.75 indicating considerable increasing of photosynthetic heterogeneity. Therefore, we propose a threshold Fv/Fm level of 0.75 that would reflect a point at which the spatio-temporal heterogeneity of Fv/Fm should be considered since it represents a boundary value for fully functional photosystem II. In our studies in the field environments in maize though, we found that even under moderate drought stress, Fv/Fm values were rarely lower than 0.75 with small standard deviations corroborating the use of classical ChlF parameters.

Keywords: barley; Chlorophyll a fluorescence; Fv/Fm values; JIP-test; maize; standard deviation



Interactive exhibit

Developing algorithms for modelling the dynamics of N balance in maize in a gene-to-phenotype context

Saeid Soufizadeh^a, Erik van Oosterom^b, Greg McLean^c, Graeme L. Hammer^d

^a *Department of Agroecology, Environmental Sciences Research Institute, Shahid Beheshti University, Iran. E-mail: s_soufizadeh@sbu.ac.ir*

^b *Queensland Alliance for Agriculture and Food Innovation, The University of Queensland, Brisbane, QLD 4072, Australia. Email: erik.van.oosterom@uq.edu.au*

^c *Department of Agriculture, Fisheries and Forestry, Australia. E-mail: Greg.McLean@daff.qld.gov.au*

^d *Queensland Alliance for Agriculture and Food Innovation, The University of Queensland, Brisbane, QLD 4072, Australia. E-mail: g.hammer@uq.edu.au*

Current crop models have to be improved in algorithm structure and input parameters to achieve the level of physiological rigour needed for using modelling in a gene-to-phenotype context. This requires a paradigm shift toward modeling causes of physiological processes that dynamically generate their emergent consequences, rather than using approaches that mathematically describe the consequences themselves. The objective of the present study was to revise the APSIM-maize routines to incorporate improved approaches to the modelling of N responses in maize based on underpinning physiological processes to capture genotype and environmental effects in a dynamic manner. The current maize module of Agricultural Production Systems sIMulator (APSIM) that was originally written in FORTRAN, was redesigned and programmed in object-oriented C++. A new algorithm for N dynamics was developed where demand for N by individual organs was based on their size and met in hierarchical fashion, such that N allocation to organs became a function of genotypic differences in organ size and environmental differences in N supply. Parameterization of the model was performed using field experiments conducted at three rates of N in Australia. Model predictions were evaluated using a comprehensive set of field experiments. Parameterization of the model showed that the critical specific leaf nitrogen (SLN) required for maintaining the maximum rate of dry matter accumulation was 1.1 g/m². Results indicated that the new N model based on organ demand, rates of retranslocation, and N uptake could successfully predict maize responses to N with simulations of crop attributes in close agreement with observed values for a range of N conditions (Figure 1). N stress resulted in lower SLN and subsequent reduction in leaf area index and radiation use efficiency (RUE) of the crop. This newly developed model has capacity to examine consequences of key genotypic differences in N dynamics of maize.

Keywords: APSIM; genotypic differences; model development; radiation use efficiency; specific leaf nitrogen.



Interactive exhibit

GnpIS-Maize, an information system for high throughput maize genomic, genetic and phenomic data

***Delphine Steinbach^a, Guillaume Merceron^a, Pommier Cyril^a, Erik Kimmel^a,
Dorothee Charruau^{a*}, Nacer Mohellibi^a, Alaux Michael^a, Stéphane Nicolas^b,
Yannick De Oliveira^b, Johann Joets^b, Alain Charcosset^b, Hadi Quesneville^a***

^a INRA URGI Unité de recherches en génomique info,
delphine.steinbach@versailles.inra.fr, guillaume.merceron@versailles.inra.fr
cyril.pommier@versailles.inra.fr, erik.kimmel@versailles.inra.fr
dorothee.charruau@versailles.inra.fr (*previous
contract*), nacer.mohellibi@versailles.inra.fr, Michael.alaux@versailles.inra.fr
hadi.quesneville@versailles.inra.fr, <http://urgi.versailles.inra.fr/gnpis>

^b INRA UMR GQEM Génétique Quantitative et Evolution- Le Moulon
Ferme du Moulon 91190 Gif sur Yvette
stephane.nicolas@moulon.inra.fr, ydeoliveira@moulon.inra.fr, joets@moulon.inra.fr,
fr,charcos@moulon.inra.fr, <http://moulon.inra.fr>

URGI (Unité de Recherche Génomique-Info) is an INRA bioinformatics research unit. It hosts a bioinformatics facility (URGI platform) labelled and state-approved at institute and national level in the French network (IFB) that proposes services (data integration, software development, training) to INRA scientists and their collaborators. One of its missions is to develop and host a genomic, genetic and phenomic information system called GnpIS, for plants of agronomical interest (wheat, maize, pea, rapeseed, tomato, oak..) and their bioagressors. User needs and data are collected from scientists directly from INRA units or in the frame of projects or consortium. Data are automatically loaded into GnpIS by using ETL (Extract-Transform-Load) tools. GnpIS is referenced in the network of European information system transPLANT and makes its data accessible from EBI transPLANT portal <http://www.transplantdb.eu>, through NoSQL SolR or Elasticsearch technology. We will present here an overview of GnpIS applied to Maize public data, summarizing several deliverables from different projects funded in the last years, by French national Agency (ANR). We will present i) a summary of the data, already on line and public on URGI portal: <http://urgi.versailles.inra.fr/gnpis>. We will present ii) a summary of the software development done and functionalities to query for example on maize markers and on recent genotyping, phenotyping and association data (GWAS). We will present the different ways to submit data to GnpIS by using the excel templates files or by using external tools developed by our partners such as Biomeqator, ThaliaDB or Sniplay. We will present on going perspectives concerning RNASeq data management in GnpIS and user query. We could also present a software demo of GnpIS with an example on the GWAS query form, to select best markers applied to 3 traits of interest, data taken from Publication Bouchet *et al.* 2013.

Keywords:

Database, information system, high throughput, data, maize



Interactive exhibit

Genotype by environment interaction for grain quality in a historical series of Mediterranean durum wheat cultivars

Joan Subira, Fanny Álvaro, Conxita Royo

IRTA (Institute for Food and Agricultural Research and Technology), Field Crops Program, 25198 Lleida, Spain. E-mail: joan.subira@irta.cat; fanny.alvaro@irta.cat; conxita.royo@irta.cat

The quality of durum wheat grain is strongly affected by environmental conditions. In this study we evaluated the effect of breeding activities conducted during the last century on the genotype x environment (GE) interaction for grain and semolina quality traits and identified climatic variables involved in the genotypic response to environmental conditions. Grain protein content, test weight, gluten strength and yellow colour index were determined in a set 24 Mediterranean durum wheat cultivars released in different periods during the 20th century and classified as: old (released before 1945), intermediate (released between 1950 and 1985) and modern (released from 1988 to 2000). Experiments were conducted in five north-eastern Spanish environments differing in meteorological conditions during grain filling. In these environments, grain filling length was positively related to water input and reference evapotranspiration (RE), and negatively to the maximum temperature. ANOVA revealed that grain protein content was the trait most affected by the environment and also the one with the lowest GE interaction. Gluten strength showed the highest GE interaction, while yellow index was mainly under genetic control. The environment effect accounted for most of test weight variation. Quality traits differed in cultivars from different breeding periods. Protein content decreased across time, gluten strength and yellow index increased, and no temporal trend was observed for changes in test weight. Cultivars released in different periods showed contrasting responses to environmental conditions during grain filling. Short grain filling periods had a more detrimental effect in the test weight and gluten strength of modern and intermediate cultivars than in old ones. However, in environments with low RE the protein content of modern and intermediate cultivars was enhanced. The period of release of the cultivars did not explain the GE interaction observed for yellow colour index.

Keywords: durum wheat, quality, GE interaction, historical series, environmental conditions



Interactive exhibit

Genfam: integrative system for gene family analysis, including a method of evolutionary event identification and evidences for an involvement in environmental stress response

Delphine Larivière^{a,b}, Jonathan Lorenzo^a, Stéphanie Sidibe-Bocs^a, Jean-François Dufayard^a, and Dominique This^b

^a CIRAD, UMR AGAP

TA-A 108/03. Ave Agropolis. 34398 Montpellier cedex, France
delphine.lariviere@cirad.fr
jonathan.lorenzo@cirad.fr
stephanie.sidibe-bocs@cirad.fr
jean-francois.dufayard@cirad.fr
<http://umr-agap.cirad.fr/>

^b Montpellier SupAgro, UMR AGAP

TA-A 108/03. Ave Agropolis. 34398 Montpellier cedex, France
dominique.this@supagro.fr – <http://umr-agap.cirad.fr/>

Important research efforts are made to characterize mechanisms of biological interest, such as stress tolerance, through gene family studies. The identification of these families allows the functional annotation of genes, as genes belonging to one family are supposed to have similar or related functions. We have developed an online comparative genomics application, GenFam, allowing the user to build custom gene families based on several data sources, to run analysis workflows, and to gather results into a synthetic visualization. It allows displaying functional evidences and evolutive history information through widely used tools and the new algorithm IDEVEN. This algorithm is complementing phylogenetic analyses by using syntenic block data and synonymous mutation rates (dS). The system contains additional modules oriented towards stress response study, such as (differential) gene expression data, functional annotations (gene ontologies), and the identification of specific stress-related cis elements in the promoter regions. The aim of this work is to facilitate knowledge representation and functional inference for scientists working on gene families, and an easier way to link stress-related evidences within a gene family tree. It can therefore highlight adaptive evolution within gene families in relation to stress-prone environments and identify candidate genes for drought tolerance in non-model crops by translational studies.

Keywords: bioinformatics, gene family, data integration, evolution, functional inference



Interactive exhibit

Addressing via a systematic field layout the spatial heterogeneity owing to breeding at dry conditions. A case study in lentil

Anastasia Kargiotidou^a, Dimitrios Vlachostergios^b, Evaggelia Sinapidou^a, Alexios Polidoros^c, Epameinondas Paplomatas^d, Chrysanthi Foti^b, and Ioannis Tokatlidis^a

^a *Dep. of Agricultural Development, Democritus Un. of Thrace, 68200 Orestiada, Greece,* ^b *Fodder Crops and Pastures Institute 413 35 Larissa, Greece,*

^c *School of Agriculture, Aristotle Univ. of Thessaloniki, Thessaloniki, 54124, Greece,* ^d *Dep. of Crop Science, Agricultural University of Athens, 11855, Greece*
itokatl@agro.duth.gr

Breeding for drought tolerance is imposed to be conducted with limited water. Under dry conditions the problem of spatial heterogeneity in field experimentation worsens preventing objective genotype evaluation. An even and systematic entry arrangement is of the most effective options to tackle the problem. Comparatively to the 'randomized complete block' and 'adjustment to nearest neighbour' models, the hypothesis was tested with the honeycomb model in three lentil (*Lens culinaris* L.) landraces grown at separate trials each including 1000 plants (area of 900m²). Huge spatial heterogeneity was recorded, stemming partially from drought stress, depicted by the extreme CVs for single plant yields were (123-169%). It was hypothesized that the entire heterogeneity would have been controlled whether comparison of a number of simulated entries would not reveal significant residuals from the overall mean yield (*t*-test). Each experiment was analysed assuming that included 4, 7, 9, 12, 13, 16, 19 or 21 simulated entries. In general, the top to bottom gap of means increased with increasing the number of entries but this was not always true. In contrast to 'randomized complete block' and 'adjustment to nearest neighbour' models, in most honeycomb analyses no significant residuals existed. However, the number of the significant residuals did not associated with the number of entries. The conclusion was that the triangular plant arrangement of honeycomb designs that allocates entry evenly across the whole experimental area might be a viable option to sample the environmental heterogeneity; under extreme spatial heterogeneity however, it does not ensure absolute control, while the number of entries involved within an area does not seem crucial.

Keywords: entry allocation, field experimentation, landrace, nearest neighbour, randomized complete block

*This research has been cofinanced by the European Union (European Social Fund – ESF) and Greek national funds through the Operational Program "Education and Lifelong Learning" of the National Strategic Reference Framework (NSRF) / Research Funding Program: **THALES**. Investing in knowledge society through the European Social Fund.*



Interactive exhibit

The importance of density-independent cultivars in maize and wheat for dryland production and adaptation to climate change

Ioannis Tokatlidis

*Democritus University of Thrace, Department of Agricultural Development,
68200, Orestiada, Greece. itokatl@agro.duth.gr*

A Fluctuating condition across locations and seasons is connected with ineffective resource use widening the gap between potential and harvested yield in rainfed maize and wheat. A particular root cause is density-dependence, implying that the optimum density is either very high for some seasons or largely varying across seasons, that threatens crop sustainability and food security. The problem is acute in maize (even irrigated) and it might occur in wheat at the Mediterranean type environments. Extensive review of the available literature reaches the following potential implicative key points. (1) The cultivars differ in optimum density and their comparison at a single-dense stand ends up to wrong cultivar choice. (2) Environmental diversity is followed by enormously varying seasonal yield potential. (3) Variability in yield potential is associated with variability in optimum density alike. (4) Even though they are positively correlated, at sowing the expected yield level cannot be used as an indicator of the target population. (5) For wheat in particular, planting over seeding varies across and within seasons complicating further the issue. (6) A very important element that justifies density-dependence is presumably stagnation in yielding capacity at the single-plant level, i.e. plant yield efficiency. (7) The finally established population is not the most appropriate and farmers sustain yield penalty. (8) The density-independent cultivar that reaches the yield plateau at a wide and of low threshold range of densities is an imperative need to address the issue. (8a) Among the available cultivars the less-dependent should be sought and case studies are supporting that the pursuit is a sound task. (8b) Breeding should prioritize plant yield efficiency targeting density-independence, and relevant research is encouraging that this is a realistic goal. Availability of versatile cultivars, exhibiting plasticity and flexibility to environmental diversity is an urgent mandate to cope with ongoing climate change.

Keywords: climate change, sustainable agriculture,

Work co-financed by EU (ERDF) and Greek funds through the program code 09 SYN-22-604 "SYNERGASIA2009 – Action I. Cooperative small- and mid-scale projects ".



Interactive exhibit

Evaluation of Some Agromorphological Characters in Advanced Lines of Two Lentil (*Lens culinaris* Medik) Cross Combinations

Faruk Toklu^{*,1}, Tolga Karaköy², Hakan Özkan¹

¹Çukurova University, Agricultural Faculty, Department of Field Crops, 01330, Balcalı-Adana-Turkey

²Cumhuriyet University, Vocational School of Sivas, Sivas-Turkey,

*corresponding author email: fapet@cu.edu.tr

Lentil is second commonly grown grain legume crop after the chickpea in Turkey. Biotic and abiotic stress conditions as foliar diseases and drought etc. affecting the lentil production adversely in several years. By this research several agromorphological plant characters evaluated in 127 advanced lines (F_7) of Karacadağ x Silvan and 54 advanced lines (F_7) of Karacadağ x Firat 87 cross combinations. Advanced lentil lines planted at Research Field of Vocational School of Kozan in Adana-Turkey and Sivas-Turkey locations together parents and check varieties during the 2013-14 growing period.

Significant differences observed between advanced lines compared to parental genotypes and check varieties; for days to flowering, plant height, number of branches, biological yield, weight of pods per plant, number of pods per plant, number of seeds per plant, number of nodes per plant, 1000 grain weight and grain yield per plant. The results revealed that improvement for several plant characters having biotic and abiotic stress conditions is possible using true breeding lines.

Keywords: Lentil, advanced lines, drought resistance, agronomic characters



Interactive exhibit

Physiological and proteomic approach to long-term drought of four winter oilseed rapes after vernalization (*Brassica napus* L.)

Urban MO^a *, Vítámvás P^a, Vašek J^b, Klíma M^a, Krtková J^c, Kosová K^a and Prášil IT^a

a Crop Research Institute, Department of Genetics and Plant Breeding, Prague, Czech Republic, www.vurv.cz ; author e-mail: dehydrins@gmail.com

b Czech University of Life Sciences, Department of Genetics, Prague, Czech Republic, www.czu.cz

c University of Washington, Department of Biology, Washington, USA, www.washington.edu

A proteomic response to long-term drought treatment (28 days) has been studied in leaves of a drought-adaptable and “plastic” winter oilseed rapes (cultivars Californium and Navajo) and a drought-sensitive winter oilseed rapes (cultivars Viking and Cadeli). The photosynthetic (GS, Pn, E, Ci, mbRef), the biochemical (chlorophylls content, proline, osmotic potential, etc.), and water content parameters (evapotranspiration changes, dry-weight gravimetric water content, fraction of transpirable soil water related to Pn or E) were measured. Out of the all differentially abundant protein spots just 362 spots were assessed by 2-D DIGE as quantitatively changed at last ± 2 -fold. Of these, 100 representative protein spots have been selected for MALDI-TOF/TOF identification and 79 proteins have been identified. The identified proteins with an increased relative abundance upon drought include proteins involved in amino acid, nitrogen and sulphide metabolism/protein metabolism; ATP interconversion; carbohydrate/energy metabolism; photosynthesis; redox homeostasis, ROS and signalling; stress and defence related; transcription, translation, RNA processing. The search for protein spots revealing large changes in protein relative abundance (more than ± 3 fold; $p \leq 0.05$) has revealed 24 protein spots (e. g. elongation factor EF-G/SCO1, epithiospecifier protein, 2-Cys peroxiredoxin, fibrillin, fructose- 1,6 -bisphosphatase precursor, ribulose- 1,5 -bisphosphate carboxylase / oxygenase activase, glyoxalase I, germin-like protein etc.) matching this criteria for stress/control ratios within one or more each individual genotypes. STRING and BiNGO were subsequently used to upgrade this result. STRING visualizes the functional links of protein-protein interaction and BiNGO visualizes over- or underrepresented categories of biological pathways and molecular functions. The differences between adaptable and sensitive cultivars will be discussed.

These results provide new insights in drought acclimation/adaptation in contrasting winter oilseed rapes and connect data at phenotype (photosynthetic, biochemical, and physiological) and proteome level.

Keywords: 2D-DIGE, drought stress, canola, photosynthetic acclimation, proteomics

Acknowledgement: This work was supported by the Ministry of Agriculture of the Czech Republic (QJ1510172).



Interactive exhibit

Quantitative analysis of proteome extracted from barley crowns grown under different drought conditions

Vítámvás P.^a, Urban M.O.^a, Škodáček, Z.^a, Kosová K.^a, Pitelková I.^a, Vítámvás J.^{a,b}, Renaut J.^c, Prášil I.T.^a

^a*Crop Research Institute, Prague, Czech Republic, www.vurv.cz;
author e-mail: dehydrins@gmail.com*

^b*Faculty of Forestry and Wood Sciences, Czech University of Life Sciences
Prague, Prague, Czech Republic, www.czu.cz*

^c*Luxembourg Institute of Science and Technology, Belvaux, Luxembourg*

Barley cv. Amulet was used to study the quantitative proteome changes during distinct drought conditions by two-dimensional difference gel electrophoresis (2D-DIGE). Plants were cultivated for ten days under two different drought conditions. To obtain control and drought-treated plants, the soil water content (SWC) was held on 65%, 35 % and 30 % of soil water capacity, respectively. Osmotic potential, water saturation deficit, ¹³C discrimination and dehydrin accumulation were monitored during sampling of crowns for proteome analysis. Total proteome was extracted by trichloroacetic acid/ sodium dodecyl sulphate - phenol protein extraction. Analysis of 2D-DIGE gels has revealed 105 differentially abundant spots during experiment. Most of them were differentially abundant between control and drought-treated plants and 25 spots displayed changes between both drought conditions. Seventy protein spots were successfully identified by tandem mass spectrometry. A lot of identified proteins belong to enzymes involved in sugar metabolism (e.g., sucrose synthase), in S-adenosyl methionine cycle (e.g., methionine synthase), amino acid metabolism (e.g., alanine-glyoxylate aminotransferase) and into stress-associated proteins as HSPs and LEA proteins. Two spots revealing a continuous significant increase with a decreasing SWC (UDP-glucose 6-dehydrogenase, and glutathione peroxidase) could be good candidates for testing their protein phenotyping capacity together with proteins that significantly distinguished both drought treatments. Possible role of all proteins in barley response to drought stress is discussed.

Keywords: *Hordeum vulgare*, crown, drought, proteomics, phenotyping candidate



Short talk

Effect of a QTL of maize response to drought on the phosphoproteome of leaf elongation zone: looking for candidate post-translational modifications

Ludovic Bonhomme^a, Benoît Valot^b, François Tardieu^c and Michel Zivy^d

^a UMR INRA/UBP Génétique, Diversité et Écophysiologie des Céréales, Clermont-Ferrand, France, ludovic.bonhomme@clermont.inra.fr

^bUMR 6249 Chrono-Environnement, Besançon, France, benoit.valot@univ-fcomte.fr

^cLaboratoire d'écophysiologie des Plantes sous Stress Environnementaux, Montpellier, France, francois.tardieu@supagro.inra.fr

^d PAPPISO, UMR 0320/8120 Génétique Quantitative et Evolution – Le Moulon Gif-sur-Yvette, France, zivy@moulon.inra.fr

Plant response to drought involve a wide range of physiological and biochemical responses, including at the proteome level. Rapid changes in protein activity, localization, and interactions can be controlled post-translationally. To analyze early responses to water deficit in maize, we assessed the phosphorylation status of proteins in the growing zone of leaves. The effects of different duration of water deficits and of recovery periods of 5 to 60 min were analyzed by using a SCX/IMAC approach combined with stable isotope labelling. As a whole, 3664 phosphorylation sites were identified, 1250 were quantified and 138 showed significant changes, mainly including a number of proteins involved in the regulation of gene expression and cell cycle-dependent processes. Nearly 50% of them recovered to their control level 60 min after rewatering and some of them showed early-responsive patterns in the range of 5-10 min (Bonhomme et al 2012).

Using the same methodology, we then analysed the response to water deficit and recovery in 3 near-isogenic lines that differed in a chromosomal region containing a QTL of drought response. We quantified 1826 phosphorylation sites among which 767 displayed a significant genotype and/or treatment effect. Overall, phosphoproteome changes were detected independently to any transcriptomic variation. Interestingly, about 1/3 (600/1826) of the quantified sites showed a genotype effect, while 1% of the genome varied. Only 5% of them involved proteins encoded in the QTL region. Together these data suggest that the QTL region contains a locus that, directly or indirectly, partially controls the status of numerous phosphorylation sites.

Keywords: proteomics, maize, water deficit, genetics



Session 6: Breeding for drought, strategies, choices

Keynote speaker

Genomics-assisted breeding to enhance drought resistance in cereals

S Salvi, M Maccaferri, E Frascaroli, P Landi, M A Cané, J Soriano, S Millner, A Martinez, R Bovina, R Tuberosa

Department of Agricultural Sciences, University of Bologna, Italy

Improving cereal yield in conditions of drought stress is a daunting undertaking due to the quantitative nature of the adaptive response of plants to water deficit, its low heritability and by phenotyping (Tuberosa 2012, *Frontiers Plant Physiology*). Although conventional breeding has successfully enhanced resistance to abiotic stress through a direct selection for yield, genomics-assisted breeding (GAB) provides novel opportunities to accelerate such gains through marker-assisted selection targeting beneficial alleles at major QTLs (e.g. via marker-assisted selection) and/or genome-wide selection for unmapped QTLs. Additional opportunities through genetic engineering and/or DNA-editing are offered by the cloning of major QTLs controlling the plasticity of morpho-physiological traits (e.g. root architecture) with a key role in cereal adaptation to drought conditions. The first step for deploying locus-specific variability is the identification and characterization of QTLs. Recently, multiparental and association mapping coupled with high-density SNP profiling have streamlined gene/QTL discovery in crops. The availability of a well-annotated sequence will greatly streamline the discovery phase, while opening the way to genome editing. Additionally, greater attention will be devoted to mutant collections that have recently been assembled in cereal crops (e.g. wheat), thus allowing for a more relaxed perception of the true potential of GAB.

Notwithstanding the plethora of QTLs described in the literature, so far only a handful of major QTLs have contributed toward the release of cereal cultivars with enhanced resilience to drought and other abiotic stresses. A critical factor for a more widespread exploitation of locus-specific GAB is the limited availability of major QTLs with consistent effects across different elite genetic backgrounds, environments and management practices (GxExM). While QTL cloning will increasingly shed light on the molecular and functional basis of abiotic stress resistance, phenotyping remains a major limiting factor for more effectively leveraging GAB. The growing interest in yield modeling based on QTL effects for morpho-physiological features provides further opportunities for improving cereal performance under unfavourable conditions. From an applicative standpoint, a successful integration between GAB and conventional breeding requires a multidisciplinary approach and stronger public-private partnerships.



Keynote speaker

Genetics and breeding for rice that uses less water

Adam H Price^a

^a University of Aberdeen

Institute of Environmental and Biological Sciences, Aberdeen, AB24 3UU, UK

<http://www.abdn.ac.uk/sbs/people/profiles/a.price>

Most of the research that I have conducted on rice genetics over nearly 25 years has focused on identifying ways in which understanding root form and function will help grow rice using less water, be it in drought-prone upland systems or lower water input irrigated systems. The research includes biotic interactions in the soil since it can be anticipated that the more rice is grown aerobically, the more interactions with nematodes, mycorrhizal and parasitic weeds will impact on performance.

An earlier highlight was the introduction of root growth QTLs from the cultivar Azucena into the Indian upland cultivar Kalinga III using marker assisted selection in collaboration with Bangor University (Steele et al 2013). More recently, aquaporin genes underlying a drought avoidance QTL on chromosome 7 have been shown to affect root hydraulic conductance while the genes underlying a QTL for rice-*Striga* interactions have been identified in research in a collaboration with Wageningen (Cardoso et al. 2014).

In addition to exploiting conventional genetic mapping, we have been increasingly conducting genome wide association studies to gain finer resolution in QTL position. In this regard we are making a panel of rice accessions specific to Bangladesh and NE India where alternate wetting and drying is being promoted as a water saving technique (Price et al. 2013). The rice diversity panel is being used to assess resistance to nematodes and the colonization with arbuscular mycorrhizal fungi revealing very high variation. A simple technique using a buried herbicide has been developed that allows rooting depth to be determined very cheaply on thousands of plants suitable for genetic studies. These developments will be discussed.

Keywords: rice, water, QTL, candidate gene, breeding



Keynote speaker

Extending the phenotype – crop modeling to estimate the ‘unobservable’

Scott Chapman^a, Graeme Hammer^b, David Jordan^b, Andries Potgieter^b, Robert Furbank^c, Xavier Sirault^d, David Deery^d, Jose Jimenez-Berni^d

***^a CSIRO Agriculture Flagship
Queensland Bioscience Precinct, St. Lucia, QLD, Australia***

***^b Queensland Alliance for Agriculture and Food Innovation
The University of Queensland, St Lucia, QLD, Australia***

***^c Australian National University
Canberra, ACT, Australia***

***^d CSIRO Agriculture Flagship
Black Mountain, Canberra, ACT, Australia***

Crop models approximate plant processes in order to compute phenotypes of interest. Some of these phenotypes, seasonal water use for example, are difficult to observe directly over the season. However, proximal sensing of crop canopy and root characteristics and their response to the environment start to provide information to 'correct' the model and allow prediction, or fixed, ground and aerial sensors provides information that can be extended by models. Different levels of models may be developed for short/long time frames and incorporating greater or lesser mechanistic detail. A key point to consider is that models and the informing of them can come from multiple types of experiments, including plant phenotyping in glasshouses and still be used to contribute to 'disentangling' the phenotypes of economic interest.

Automated data collection and new sensing technologies are accelerating the knowledge around crop physiology. Computation of relevant phenotypes for selection and/or evaluation of stress responses can also be assisted by simulation modelling tools. These capabilities start to contribute to the acceleration of plant breeding and delivery of new cultivars.

Keywords: models, proximal sensing, data-model fusion



Keynote speaker

Breeding for drought: Outputs and lessons Learnt from the GCP Experience

GCP team and collaborators

CGIAR Generation Challenge Programme (GCP)

c/o CIMMYT, km45 Carretera Mexio-Veracruz, El Batan, Estado de Mexico, Mexico

j.ribaut@cgiar.org – www.generationcp.org

The Generation Challenge Programme (GCP) was a 10-year (2004-2014) and \$170M CGIAR initiative, focusing on crop improvement in developing countries with an emphasis on drought tolerance. Building heavily on translational research, its mission was to use genetic diversity and advanced crop science to improve crops by adding value to conventional breeding for drought-prone and harsh environments. This was achieved through a true partnership of more than 200 partners drawn from regional and national research programs, the CGIAR and academia. Drought tolerance was the main target trait of the GCP, and genomics-assisted breeding for better crop production under water-limited conditions was at the heart of the research in its second phase (2009–2014), with a focus on 9 crops: bean, cassava, chickpea, cowpea, maize, rice, sorghum and wheat. This effort resulted in a number of research outputs specific to drought tolerance including: genetic and genomic resources, genes and QTL and ultimately improved germplasm (Success stories at: www.generationcp.org/sunsetblog/). The overall lessons learned from that 10 year adventure include: the importance of empowering national programs for effective collaboration and impact on the ground; the need for a flexible approach to research management, including a combined approach of competitive and commissioned projects; the indispensable need for capacity building embedded in research activities; and, the importance of having a product deployment strategy.



Selected talk

100 years of wheat selection in Switzerland decreased rooting depth but increased plasticity in response to drought

Cordula Friedli^a, Samuel Abiven^b, Achim Walter^a, Andreas Hund^a

^a ETH Zurich

Institute of Agricultural Science, Universitätstrasse 2, CH-8092 Zurich
Switzerland

cordula.friedli@usys.ethz.ch – www.kp.ethz.ch

^b, University of Zurich

Soil Science and Biogeochemistry Address, Winterthurerstr. 190, CH-8057
Zurich, Switzerland

samuel.abiven@geo.uzh.ch – www.geo.uzh.ch

Improving root architecture is an important aim to adapt plants to reduced water and nutrient availability. Specifically, deep rooting is discussed as a promising strategy to improve water uptake under drought (e.g. Manschadi et al. 2008, Wasson et al. 2012). However wheat breeders have dramatically reduced plant height by introducing dwarfing genes leading to reduced lodging under high fertilizer input and an increased harvest index.

There is limited information about how rooting depth and root biomass was affected by breeders (e.g. Waines & Ehdaie 2007). Knowing about the trends in root biomass and root distribution of these varieties may enhance our understanding of historic and future trends of the most important crops.

Our objective was to elucidate if and how root architecture of winter wheat and its response to drought changed due to breeding. We evaluated the “Swiss Era Wheats” being most widely grown in Switzerland between 1910 and 2010 including promising new Swiss bread wheat varieties. All 14 wheat varieties were grown in our Deep Root Observation Platform (DROP) at ETH Zurich consisting of 1.6 m tall growth columns. Two water stress treatments were established: early water stressed until flowering and late water stressed from flowering until maturity. Both water stress treatments were established starting at complete field capacity. Thus, water stress in the root zones developed gradually starting from the upper part of the soil column with most intensive rooting. Plants were harvested at flowering and maturity, and root biomass distribution in the columns was determined in 250 mm intervals.

Our preliminary results indicate that reduction in plant height led to a severe reduction in rooting depth under well watered conditions. However, under early water stress, short, modern varieties could cope with their tall, old ancestors indicating the ability to respond to low water availability.

Keywords: wheat, breeding history, drought, rooting depth, green revolution



Sessio n 3: List of posters

N°	Name		Poster title	type of poster
1	ABDELGAWAD	Hamada	Growth and genome-wide transcriptional analysis reveal that elevated CO2 mitigates the impact of drought stress in <i>Arabidopsis thaliana</i>	interactive exhibit
2	ALVAREZ PRADO	Santiago	Genotypic variability of maize growth and developmental traits under semi-controlled conditions	1-min presentation
3	AVRAMOVA	Viktoriya	Identification of stress response and recovery mechanisms by a multi-scale analysis of the effect of drought in the growth zone of maize leaves	interactive exhibit
4	BEAUCHENE	Katia	PhénoField®, a high-throughput phenotyping , PHENOME (FPPN) platform	1-min presentation
5	BELLO	Abdulrazaq Abolore	Influence of soil moisture stress on vegetative growth and root yield of some selected cassava genotypes under greenhouse condition	interactive exhibit
6	BENNANI	Sahar	Implication of root parameters in drought tolerance at the early germination stage for bread wheat	interactive exhibit
7	BODNER	Gernot	Hyperspectral imaging for phenotyping plant root systems	interactive exhibit
8	BRESTIC	Marian	Photosynthetic parameters in screening of wheat genotypes for tolerance to drought and high temperature	interactive exhibit
9	CHAPUIS	Romain	How to estimate maize sensitivity to water deficit in field? A method consistent with the estimators measured in a phenotyping platform	interactive exhibit
10	CONTRERAS-MOREIRA	Bruno	Transcriptomic analysis of drought responses of elite barley cultivar Scarlett and Spain landrace SBCC073	interactive exhibit
11	CONXITA	Royo	Mediterranean durum wheat landraces as potential donors for early vigor improvement	interactive exhibit
12	COUPEL LEDRU	Aude	Genetic architecture of water use efficiency in grapevine: a key role for night transpiration	1-min presentation
13	DE LEON	Nathalia	Image-Based Precision Phenotyping of Maize Ear Morphology and Kernel Size	1-min presentation
14	DE SWAEF	Tom	Forage grass species root distribution in long term field trials	interactive exhibit
15	DELALANDE	Magalie	DiaPHEN: field platform to analyze mechanisms of drought tolerance at field level	interactive exhibit
16	DOCKX	Andrien	Potential of High Resolution Thermal Imaging System to Evaluate Stomatal Conductance in the Field	interactive exhibit
17	DESWARTE	Jean-Charles	Tools for wheat drought tolerance evaluation and breeding in France	interactive exhibit
18	FROIS CALDEIRA	Cecilio	Insights in water loss and uptake in coffee plants	1-min presentation



N°	Name		Poster title	Type of poster
19	GERTH	Stefan	Highlands of Ethiopia	interactive exhibit
20	HAYES	Matthew	Water limitation in four wheat varieties during grain fill	interactive exhibit
21	HUND	Andreas	The Field Imaging Platform (FIP) at ETH Zurich: Evaluation of crop development throughout the season by means of multiple sensors	interactive exhibit
22	KARIM	Shram	ANR BacterBlé: a project to study rhizobacterial benefits for adaptation of wheat to nitrogen limitation and drought	interactive exhibit
23	KONATE	Abdourasmane	Evaluation of a high throughput phenotyping method for drought tolerance in rainfed lowland rice based on infrared thermography	1-min presentation
24	Kravic	Natalija	Osmotic stress and seedlings performances of maize genotypes from drought tolerant mini-core collection	interactive exhibit
25	LACUBE	Sébastien	OïO-Tech Project: Developing new phenotyping tools adapted for plant research	interactive exhibit
26	LAZALI	Mohamed	Effects of water deficit on growth, nodulation and nitrogen fixation of peanut (<i>Arachis hypogea</i> L.)	interactive exhibit
27	Jeanquenin	LINDA	Tolerance of maize to drought: a matter of aquaporins?	interactive exhibit
28	MAHMOOD	Yadgar	Identifying physiological traits for drought tolerance in adapted and ancestral wheat germplasm	1-min presentation
29	MEUNIER	Félicien	Optimizing root system hydraulic architectures for water uptake	1-min presentation
30	MILHIET	Thomas	Investigating the physiological roles of the plasma membrane aquaporin ZmPIP2;5 in maize: a transgenic approach	interactive exhibit
31	MORENO	Beatriz	Lateral root growth: a framework to analyse the variability among elongation patterns and the impact of auxin and sugar signals	1-min presentation
32	MUTEZ	Ahmed	Optimizing transpiration by rhizosphere management	1-min presentation
33	NAYARA	Cristina de Melo	Addressing drought tolerance in sugarcane varieties through leaf physiological traits	1-min presentation
34	Olsovská	Katarina	Diversity of mesophyll conductance to CO ₂ in wheat affecting leaf photosynthesis and WUE under drought in reproductive growth stage	interactive exhibit
35	PAL	Magda	Genotype by environment interaction for grain quality in a historical series of Mediterranean durum wheat cultivars	interactive exhibit
36	PANDEY	Madhav	Growth angle of seminal roots in wheat correlates with drought responsive physiological traits and grain yield evaluated in fields with contrasting soil moisture regimes	1-min presentation



N°	Name		Poster title	Type of poster
37	PERRIER	Lisa	Using rapid fluorescence for phenotyping C source regulation by drought and its relation with growth regulation in contrasted biomass sorghum genotypes	1-min presentation
38	PIQUET	Agnes	Study of the drought tolerance in bread wheat by ear phenotyping.	interactive exhibit
39	RIPOLL	Julie	Parameters derived from fluorescence induction curves are powerful tools for characterizing plants adaptive strategies to water deficit according to genotype and developmental stage	interactive exhibit
40	SOENEN	Baptiste	"CHN", a crop model using in addition to high performance phenotyping platforms for estimate genetic traits on maize like RUE or WUE	interactive exhibit
41	SPITKO	Tamas	Effect of water shortage on yield and yield components of maize	1-min presentation
42	SUTKA	Moira	Different strategies of seedlings of two Sorghum Bicolor lines to deal with drought stress	interactive exhibit
43	TOVIGNAN	Thierry Klanvi	Impact of leaf area development on stem sugar production in sorghum: sowing date and post-flowering water status influence	interactive exhibit
44	WAQAS	Shafqat	Genotypic variation for water-deficit tolerance in Gossypium hirsutum l.	interactive exhibit
45	ZAMAN ALLAH	Mainassara	Using Field-based aerial imaging platform to improve selection efficiency in breeding for drought tolerance in Maize	1-min presentation
46	BARET	Frédéric	Monitoring phenotyping platforms using UAV borne sensors: PHENODRONE	interactive exhibit
47	BERTHEZENE	Stéphane	PHENODYN: a high throughput platform for measurement of organ elongation rate and plant transpiration with high temporal resolution	interactive exhibit
48	CABRERA	Llorenç	PHENOARCH, a multiscale phenotyping platform for plant architecture, growth rate, water use efficiency and radiation use efficiency	interactive exhibit
49	DAUZAT	Myriam	PHENOPSIS: from a phenotyping platform to a whole pipeline of analyses	interactive exhibit
50	De SOLAN	Benoît	Development of a fully automated PHENOMOBILE for field phenotyping	interactive exhibit
51	TARDIEU	François	PHENOME: French Plant Phenomic Center	interactive exhibit
52	WELCKER	Claude	M3P: the "Montpellier Plant Phenotyping Platforms	interactive exhibit



Session 5: List of posters

N°	Name		Poster title	Type of poster
53	AHMAD	Habib	Screening of wheat germplasm for drought tolerance on the bases of physiological tests	interactive exhibit
54	AHMAD	Israr	Association mapping of root traits for drought tolerance in bread wheat	1-min presentation
55	ALVAREZ-IGLESIAS	Lorena	Screening open-pollinated maize populations for drought tolerance at germination	1-min presentation
56	ANDJELKOVIC	Violeta	Natural and mutagenesis induced variation in drought tolerance candidate genes in maize (<i>Zea mays</i> L.)	interactive exhibit
57	ARNAUD	Elizabeth	Interoperability and Interpretation of Phenotyping Data: Use of Plant Ontologies	interactive exhibit
58	BANYAI	Judith	Abiotic stress response of durum wheat near isogenic lines	interactive exhibit
59	BASTOW	Ruth	Diversity seek (divseek): an international partnership to harness the genetic potential of crop diversity	interactive exhibit
60	BENKHERBACHE	Nadjat	Associative approach of physiological and biochemical characters implicated in the response to water stress with some candidate genes for resistance to abiotic stress in barley	interactive exhibit
61	BERZY	Tamas	Drought tolerance and photochemical reactions in case of some reciprocal crossing type maize hybrids	interactive exhibit
62	BIDZINSKI	Przemyslaw	Rice (<i>Oryza sativa</i>) defense against rice blast disease (<i>Magnaporthe oryzae</i>) under drought stress	1-min presentation
63	BOZINOVIC	Sofija	Diallel cross among maize drought tolerant populations - principal component analysis for the most important agronomic traits	interactive exhibit
64	BULUT	Reyyan	Drought Related Gene-region introgression to a European Elite Cultivar	1-min presentation
65	BURCU	Alptekin	Root Transcriptomics of Durum and Wild Emmer Wheat Under Drought Stress	interactive exhibit
66	CASTELLETTI	Sara	Defining the role of florigen genes in Maize developmental reprogramming under contrasting watering scenarios	interactive exhibit
67	CAUSSE	Mathilde	Genetic and genomic control of response to water deficit in tomato	interactive exhibit
68	CENCI	Alberto	Transcriptomic analysis in banana cultivars during early drought-stress	interactive exhibit
69	CHARMET	Gilles	WHEALBI: Wheat and Barley Legacy for Breeding Improvement; A EU-FP7 project to link genomics and agronomy	interactive exhibit
70	COURSOL	Sylvie	Combining a dual-omics approach and biochemical analysis of bulked recombinant maize inbred lines to identify candidate genes underlying plant growth responses to water deficit	interactive exhibit



	Name		Poster title	Type of poster
71	CSIKASZ	Tamas	Drought stress tolerance as a complex target of sunflower breeding including selection against several biotic and abiotic stress tolerance factors in Carpathian basin	interactive exhibit
72	DAHMANE	Djemel	Algerian maize from the Saharan oasis: novel sources for drought tolerance	1-min presentation
73	DODIG	Dejan	Phenotypic and genetic study of traits associated with maintaining yield under post-anthesis source limitation in bread wheat	1-min presentation
74	ERDAL	Sekip	Characterization of temperate maize inbred lines for drought tolerance	interactive exhibit
75	GALBIATI	Francesca	Interaction between drought and floral induction in rice	1-min presentation
76	GALIC	Valtko	Chlorophyll a fluorescence parameters of JIP-test in maize breeding for water-limited environments	1-min presentation
77	GOUESNARD	Brigitte	Adaptation to temperate conditions of sub-tropical drought tolerant maize populations	interactive exhibit
78	GUIDERDONI	Emmanuel	Enhancing resource Uptake from Roots under stress in cereal crops (EURoot): an international, multidisciplinary initiative for adapting cereals to climate instability and resource scarcity	interactive exhibit
79	IDRISSI	Omar	Screening for drought tolerance and genetic diversity analysis in landraces of lentils	interactive exhibit
80	JOHN	K.	Genetic Analysis of water use efficiency traits & yield under drought stress conditions in Groundnut (<i>Arachis hypogaea</i> L.)	interactive exhibit
81	KAMITHI	K.D.	Chickpea yields grown under various priming methods, durations and initial soil moisture levels	interactive exhibit
82	LACUBE	Sébastien	Adapting the apsim model for assessing maize cultivars performances through European stressing environments	interactive exhibit
83	LAFARGE	Stephane	Genetics of wheat adaptation to drought in the frame of sustainable agricultural systems and global climate change	interactive exhibit
84	LIGEZA	Aleksander	Genetic analysis of maize root dynamics using a novel aeroponics platform	1-min presentation
85	LOISON	Romain	Designing African Rainfed Cotton Ideotype by Simulation	1-min presentation
86	MEYNARD	Donaldo	Halophyte grasses as a source of genes to improve stress tolerance in glycophyte cereals : the Stress Associated Protein gene of <i>Aeluropus littoralis</i>	interactive exhibit
87	MIKIC	Sanja	Analysis of maize inbred lines for drought tolerance based on anthesis silk interval, yield performance and microsatellites	interactive exhibit
88	MUBASSHAR - IKRAM UL HAQ	Hussain	Multitraits evaluation of berseem clover (<i>Trifolium alexandrinum</i> L.) ecotypes under full-irrigation and water restriction conditions	interactive exhibit
89	NEGRO	Sandra	Comparison of High-Throughput Genotyping Technologies in Maize: Increase in number of regions detected in association genetics	interactive exhibit



N°	Name		Poster title	Type of poster
90	NGUEJOP	Joel Romaric	Toward the enhancement of peanut (<i>Arachis hypogaea</i> L.) tolerance to drought using beneficial alleles from the wild species	1-min presentation
91	NIHORIMBERE	Gaspard	Selecting of high yielding and wheat drought tolerant variety adapted to Burundi semi arid agro ecological zone	interactive exhibit
92	RAJENDRA	Darai	Genetic variability studies of soybean breeding lines for yield and yield attributing traits in different rainfed agro-domains of Nepal	interactive exhibit
93	RASOOL NOORKA	Ijaz	Effect of drought tolerance, estimation of heterosis, proportional contribution and gene action in maize sown at diverse water regimes	interactive exhibit
94	RATRI	Dian Mugni	Vulnerability of Rice Crop to Climate Change in West Nusa Tenggara (NTB) Province, Indonesia	interactive exhibit
95	RAYMUNDO	Rubi	Performance of SUSTOR-potato model across contrasting growing conditions	interactive exhibit
96	ROZMAN	Ludvik	Screening drought tolerance maize genotypes by using combining ability	interactive exhibit
97	SAEED	Rauf	Genetic analysis of proline contents a marker of plant survivability under drought	interactive exhibit
98	SAEED	Rauf	Exploring the basis of drought tolerance in <i>Helianthus argophyllus</i> , <i>Helianthus annuus</i> and their crosses	1-min presentation
99	SCIARA	Giuseppe	High-throughput phenotyping of a maize introgression library under water deficit conditions	1-min presentation
100	SHOWEMIMO	Francis	Trait capture for drought tolerance in quality protein maize in two agro-ecological zones of Nigeria	1-min presentation
101	SIMIC	Domagoj	Monitoring standard deviations of chlorophyll a fluorescence parameter Fv/Fm of JIP-test during increasing water deficit	interactive exhibit
102	SOUFIZADEHA	Saeid	Developing algorithms for modelling the dynamics of N balance in maize in a gene-to-phenotype context	interactive exhibit
103	STEINBACH	Delphine	GnpIS-Maize, an information system for high throughput maize genomic, genetic and phenomic data	interactive exhibit
104	SUBIRA	Joan	Genotype by environment interaction for grain quality in a historical series of Mediterranean durum wheat cultivars	interactive exhibit
105	THIS	Dominique	Genfam: integrative system for gene family analysis, including a method of evolutionary event identification and evidences for an involvement in environmental stress response	interactive exhibit
106	TOKATLIDIS	Ioannis	Addressing via a systematic field layout the spatial heterogeneity owing to breeding at dry conditions. A case study in lentil	interactive exhibit
107	TOKATLIDIS	Ioannis	The importance of density-independent cultivars in maize and wheat for dryland production and adaptation to climate change	interactive exhibit
108	TOKLU	Faruk	Evaluation of Some Agromorphological Characters in Advanced Lines of Two Lentil (<i>Lens culinaris</i> Medik) Cross Combinations	interactive exhibit
109	URBAN	Milan	Physiological and proteomic approach to long-term drought of four winter oilseed rapes after vernalization (<i>Brassica napus</i> L.)	interactive exhibit
110	URBAN	Milan	Quantitative analysis of proteome extracted from barley crowns grown under different drought conditions	interactive exhibit
111	ZYVI	Michel	Effect of a QTL of maize response to drought on the phosphoproteome of leaf elongation zone: looking for candidate post-translational modifications	1-min presentation



Technical session: phenotyping for the responses to environmental conditions
European Plant Phenotyping Network (EPPN)

12 June 2015, Montpellier INRA – SupAgro campus

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

Designing varieties able to cope with climatic conditions associated with climate change is an urgent objective. It consists in identifying, in the thousands of varieties and natural accessions existing in genebanks, allelic variants allowing a favorable plant behavior. This needs to evaluate hundreds of genotypes under a variety of environmental conditions. The session aims at (i) presenting main concepts associated with the characterization of environmental conditions, (ii) presenting sensors of wide use, (iii) discussing recent progress in imaging at individual levels, in phenotyping platforms, and at canopy level with sensors carried by ground vectors and UAV. This session will complete presentations on Phenotype-to-gene approaches during the workshops on drought (Recent progress in drought tolerance: from genetics to modelling, 8-9 June) and on maize and sorghum genetics (Genomics and phenomics for model-based maize and sorghum breeding, 10-11 June) held at Montpellier (Le Corum).

The program includes presentations (F. Tardieu, S. Chapman) and a visit of the platforms of the M3P facility (<http://www6.montpellier.inra.fr/lepse/M3P>), including the presentation of sensors and imaging systems in the platforms and of UAV born imaging systems.

F Tardieu & C Welcker, INRA Montpellier - France



Programme

08:30	Welcome	<i>Venue: Amphi 208, SupAgro campus</i>
09:00	Introduction of the technical session	
	<i>C. Welcker, B. Muller</i>	
09:10	Phenotyping for the responses to environmental conditions	
	<i>F. Tardieu</i>	
09:45	UAV Field	
	<i>S. Chapman</i>	
10:00	Coffee Break	
10:30 - 13:00	Visit of the Montpellier Plant Phenotyping Platform	
	Phenotyping in field	
	<i>B. De Solan, B. Adam, B. Suard</i>	
	PhenoPsis	
	<i>C. Granier, D. Vile, B. Muller, A. Bedie, M. Dauzat</i>	
	PhenoDyn	
	<i>C. Welcker, B. Parent, R. Chapuis, S. Berthezene, V. Nègre</i>	
	PhenoArch	
	<i>F. Tardieu, L. Cabrera, A. Grau, N. Brichet, C. Welcker</i>	



Recent progress in drought tolerance

from genetics to modelling

Le Corum - Montpellier - France

8 & 9 June 2015



Program

Program June 8th, 2015

8:00 - 9:15	Registration	<i>Antigone room</i>
9:15 - 9:30	Opening Claude Welcker, INRA, Chair of the Conference Official welcome Laurent Bruckler, INRA, Chair of the INRA research center of Montpellier Andreas Boerner, IPK, chair of the cereals section of Eucarpia	<i>Einstein Auditorium</i>
9:30 - 10:40	Session 1: Coping with drought in crop improvement : a global perspective	
	The nature and patterns of drought in Europe E. Fereres, <i>Universidad de Cordoba, Spain</i> A multi scale multi environment approach F.Tardieu, <i>INRA, France</i>	<i>Einstein Auditorium</i>
10:40 - 11:10	<i>Coffee break</i>	<i>Antigone room</i>
11:10 - 12:55	Session 2: Traits-base strategies for dealing with drought	<i>Einstein Auditorium</i>
	Roots traits beyond architecture X. Draye, <i>Université Catholique de Louvain, Belgium</i> • “Quantitative imaging of root water uptake” M. Zarebanadkouki, <i>Georg-August University of Göttingen, Germany</i> • “Linkage mapping for root system architecture in durum wheat” N. Ghasemali, <i>Islamic Azad University, Iran</i>	
	Control of expansive growth in water deficit: from phenotyping to field simulations B. Parent, <i>INRA, France</i> • “Using modelling and GWAS to support the genetic and physiological dissection of a complex trait, toward ideotype exploration - Case of rice early vigor response to drought” D. Luquet, <i>CIRAD, France</i>	
12:55 -14:30	<i>LUNCH time</i>	
14:30 - 16:15	Modeling kernel abortion in maize CH. Messina, <i>Pioneer, USA</i> • “Grain abortion and yield stability under drought: a key role for growth processes in reproductive organs” O. Turc, <i>INRA, France</i> • “Predicting maize kernel number using genetic information” A. Amelong, <i>Universidad Nacional de Rosario, Argentina</i>	<i>Einstein Auditorium</i>
	Genotypic variation in water use efficiency and related physiological traits WJ. Davies, <i>Lancaster University, England</i> • “High resolution mapping of traits related to whole-plant transpiration under increasing evaporative demand in wheat” W. Sadok, <i>Université Catholique de Louvain, Belgium</i>	

16:15 - 16:45	<i>Coffee break</i>	<i>Antigone room</i>
16:45 - 17:45	Aquaporines: physiological roles and variability F. Chaumont, <i>Université Catholique de Louvain, Belgium</i>	<i>Einstein Auditorium</i>
	Investigating drought resistance using metabolic phenotyping Y. Gibon, <i>INRA, France</i>	
18:00 - 19:00	Poster session 3: Variation for target traits and phenotyping methods Poster Viewing	<i>Antigone room</i>
19:00 - 20:30	<i>Cocktail</i>	<i>Antigone room</i>

Program June 9th, 2015

8:45 - 9:00	Message of welcome	
9:00 - 10:30	Session 4: Dealing with Genotype x Environment interaction	<i>Einstein Auditorium</i>
	Analysis of GxE in maize by multi-environment GWAS and genomic selection F. van Eeuwijk, <i>Wageningen Universiteit, Netherlands</i>	
	Investigating the unstability of yield-related QTL in wheat D. Fleury, <i>ACPFPG, Australia</i>	
	<ul style="list-style-type: none">• “Genetic variability of the sensitivity of grain number to drought and high temperature in maize” E. Millet, <i>INRA, France</i>• “Genetic and ecophysiological dissection of tolerance to drought and heat stress in bread wheat: from environmental characterization to QTL detection” B. Bouffier, <i>Limagrain Europe, France</i>	
10:30 - 11:00	Coffee break	<i>Antigone room</i>
11:00 - 11:45	Modelling G x E x M with explicit genotypic information G. Hammer, <i>University of Queensland, Brisbane, Australia</i>	
	<ul style="list-style-type: none">• “Precision agriculture for SAT - near future or unrealistic effort?” J. Kholova, <i>ICRISAT, India</i>	
11:45 - 13:00	Poster session 5: QTL, functional genomics, allelic diversity and breeding application Posters viewing	<i>Antigone room</i>
13:00 - 14:30	LUNCH time	
14:30 - 17:00	Session 6: Breeding for drought, strategies, choices	<i>Einstein Auditorium</i>
	Genomics-assisted breeding to enhance drought resistance in cereals R. Tuberosa, <i>Università di Bologna, Italy</i>	
	<ul style="list-style-type: none">• “Genetics and breeding for rice that use less water” A. H. Price, <i>University of Aberdeen, UK</i>• “Extending the phenotype - crop modeling to estimate the ‘unobservable’” S. Chapman, <i>CSIRO, Australia</i>• “Breeding for drought: Outputs and lessons learnt from the GCP experience” J. M. Ribaut, <i>CGIAR, Mexico</i>• “100 years of wheat selection in Switzerland decreased rooting depth but increased plasticity in response to drought” A. Hund, <i>Institute of Agricultural Science, Switzerland</i>	
16:20 - 16:50	Coffee break	<i>Antigone room</i>

17:00 - 18:10

Panel of discussion:
Designing new variety for drought-prone environments

Einstein Auditorium

- A. Murigneux, *Limagrain Europe, France*
- J. Betran, *Syngenta, France*.
- M. Cooper, *Pioneer, USA*
- D. Jordan, *University of Queensland, Australia*
- B. Usadel, *University Aachen, Germany*

Open discussion

18:10 - 18:30

Closing summary

Einstein Auditorium

Claude Welcker, *INRA, Chair of the Conference*

Closing remarks

- Domagoj Simic, *Agricultural Institute Osijek, Chair of the maize and sorghum section of Eucarpia*
- François Tardieu, *INRA, Chair of Interdrought*

**June 12th: 9:00 - 13:00 Conference extension/Technical session
Phenotyping for the responses to environmental conditions**

Venue: Campus SupAgro - 2 place Viala, Montpellier