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Towards deciphering genetic and physiological cues associated to nitrogen and water stress tolerance in oilseed rape

Winter oilseed rape is a very nitrogen-fertilizer consuming crop and is characterized by low nitrogen use efficiency (NUE). It is also very reactive to and penalized by water deficit insofar functional interactions occur in plants between N nutrition and water acquisition. A high proportion of absorbed N remains immobilized in senescent leaves and is returned to the soil failing to contribute to sink functioning and seed production. Improvement of N remobilization efficiency (NRE) during leaf senescence is likely to improve significantly the overall plant NUE, particularly in oilseed rape in which organic N recycling is rather inefficient. Water stress strongly impacts yield and water use efficiency is partly associated to efficient N and C recycling, allocation and partitioning. In order to decipher functional traits involved in nitrogen and water use efficiencies optimization, searching for genetic variation in physiological and molecular key determinants such as genes, enzymes and metabolites, we are developing a multi-disciplinary approach based on genetic, physiology and functional genomic strategies that will be described in the talk.

Recent years have mainly allowed the development of experimental systems and phenotyping tools as well as the exploration of the existing genetic material in trials conducted under controlled or field conditions. Genetic analysis is being developed and has led to the identification of QTL for oil yield, yield components and NUE parameters under different fertilization regimes. Some of the variables are also being acquired at key stages on a panel of genotypes to initiate association analysis.

At critical stages of resource allocation, metabolomic and transcriptomic fingerprints of source and sink tissues are performed during sequential senescence to highlight networks discriminating source leaf from sink leaf and during monocarpic senescence to compare leaf draining and seed filling under different fertilization regimes. Works are designed either under controlled or field conditions to permit discovering essential nodes of regulation and new candidates for both vegetative tissue NRE performance and seed oil accumulation. Efforts are also devoted to the development and the improvement of efficient phenotyping tools dedicated to NUE, WUE and leaf and root development.

The functional value of metabolism known to be induced under stress conditions is sought. These include the metabolic pathways involved in mobilizing glutamate and directed to glutamine, proline and gamma-aminobutyric acid (Gaba) production and utilization. Proteases and protease inhibitors are also being studied as key effectors of nitrogen remobilization whose regulation by stress is investigated. Besides these targeted investigations more comprehensive transcriptomic and metabolomic approaches are performed in oilseed rape under stress and in related species more or less adapted to adverse conditions with the prospect of discovering molecular markers of tolerance.

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KEYNOTE THEME D

The Climate Corporation St. Louis, MO, USA

P. Das

Confluence of data science and precision ag: Bringing digital agronomic insights to increase yield and minimize risk on the farm

Current unfettered access to relatively inexpensive data on a massive scale, advent of advanced sensor technologies, proliferation of high-end big data analytics, and availability of powerful seed genetics are ushering in globally the next wave of productivity and efficiency to our agricultural farms.

Demand to meet burgeoning global food and feed security needs under limited agricultural land and stretched input resource conditions, sustainably, requires new knowledge, insights, tools and practices that can illuminate and respond to the fast-changing landscape of the farms. Increasing need for long term soil security and climate-resilience while continuously boosting agricultural output is calling for adoption of digital ag tools that are coming into the marketplace at a very opportune time.

In this presentation, we seek to highlight how the confluence of big Data Science and Precision Ag technologies could be harnessed to increase productivity and minimize risks on the farm through prospective digital insights derived from sensor-based measurements, data analytics, and powerful data science models.

KEYNOTE THEME D

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Next generation phenotyping for quantitative analyses of key productivity traits of crops: Challenges and opportunities for plant phenomics and plant breeding, from controlled environments to the field

It is widely accepted that continued development of both high-throughput and mechanistic, plant phenotyping methodologies are required to add value to genomic discovery and improve crop productivity by supporting plant breeding programs. We have developed a unique infrastructure for 2D, 3D and 4D quantitative analyses, which is currently applied to tackle research questions addressing the identification and selection of key shoot, root and seed traits of selected crops including rapeseed. This presentation provides highlights of our research, first focusing on an overview of state-of-the-art methodologies for non-invasive phenotyping under controlled environment and proximal or remote sensing in the field. Current challenges regarding data acquisition, analysis and interpretation will be discussed. Next, we will present case studies demonstrating the applicability of these methods to characterize genetic resources in various crop species as well as their phenotypic plasticity to the environment. The overarching research questions concentrate on assessing trait networks for improved acquisition and use efficiency of water and nutrients, nitrogen and phosphorous in particular. Emphasis will be given to rapeseed by introducing detailed studies of lateral root development in response to nitrogen limitation supporting association mapping efforts.

POSTERS THEME E

KEYNOTE THEME D

N. Harker

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Canola weed management systems – Mitigating weed resistance to herbicides

Background: Weed management systems in canola (*Brassica napus L.*) have improved markedly since canola was first grown in Canada. Herbicidal weed control in canola is now relatively simple, but the repeated use of the same herbicide tools favours the selection of weeds that resist our most common herbicides and decreases the prospect for long-term, sustainable canola production.

Evolution of Weed Management in Canola: In the 1970s, when the first canola-quality *B. napus* and *B. rapa* varieties were developed in Canada, canola was usually seeded on land with low weed populations with pre-plant incorporated herbicides such as trifluralin, and later ethalfluralin, to control a good portion of the weed spectrum. Post-emergence graminicides were introduced in the 1980s and provided a high level of grassy weed control. Clopyralid was also introduced in the 1980s and controlled difficult species such as *Cirsium arvense, Sonchus arvensis* and *Polygonum convolvulus*. In 1990 ethametsulfuron was introduced to control weedy *Brassica* relatives to canola and was often tank-mixed with graminicides and clopyralid for full-spectrum weed control. Almost all of these herbicide options were rapidly abandoned when imidazolinone-, glyphosate- and glufosinate-tolerant canola were introduced in the mid-1990s. The latter herbicide systems provided a high level of weed control for the most important weeds in canola and continue to dominate weed management systems in canola today.

The Risk of Repeated Herbicide Use: While plenty of western Canada farmland harbours ALS-resistant (Group 2) weeds, much less land contains glyphosate-resistant (Group 9) weeds (only *Kochia scoparia* in western Canada); and, thus far, glufosinate-resistant weeds have not been detected here. However, whereas glyphosate- and glufosinate-tolerant canola have provided somewhat of a reprieve from Group 1 (ACCase)- and Group 2 (ALS)-resistance selection pressure, their overuse in high frequency canola rotations threaten additional weed resistance to glyphosate and new resistance to glufosinate.

Mitigating Weed Resistance to Herbicides: Rotating different effective herbicide modes of action and tank-mixing different effective herbicide modes of action delays selection of resistant weed populations. However, using alternatives to herbicides halts selection for weed resistance to herbicides. Combining optimal cultural practices (e.g. diverse crop rotations and higher crop seeding rates) against weeds and determining the utility and viability of harvest weed seed control techniques (e.g. Harrington seed destructor and chaff collection/baling) will provide growers with non-herbicidal weed control options that will prolong the life of valuable herbicide tools; relatively non-renewable resources.

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J. McKay

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Genetics underlying variation in drought adaptation in *Brassica napus*

The long-term goal of my research is to provide detailed functional knowledge of mechanisms regulating drought responses and water use efficiency. I will report on results of using natural variation in drought tolerance among diverse lines of the important crop *Brassica napus*. This focuses on detailed physiological screens in segregating families to understand physiological mechanisms and identify causal polymorphisms underlying differences in drought adaptation. These findings will facilitate ongoing efforts to improve productivity of *B. napus* and other crop plants under drought and expand understanding of the evolution and physiology of drought adaptation and acclimation. My long term goal in *Brassica napus* is to understand the mechanisms underlying drought acclimation and adaptation at the molecular, physiological and population scale. These efforts will be facilitated by the close relationship to *Arabidopsis thaliana*, where existing functional data and molecular tools can be employed to dissect variation in *Brassica* spp.

KEYNOTE THEME D

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PHENOME, the French Plant Phenomic Network, a tool for rapeseed phenotyping

Background: Phenotyping has become the major limitation in programs aimed at building genotypes that maintain / increase crop performance under climate change and reduced inputs. The goal of Phenome is to provide France with an up-to-date, versatile, high-throughput infrastructure and suite of methods allowing characterization of panels of genotypes of different species under climate change scenarios.

Methodology and facilities: The Phenome consortium gathers 12 academic groups (mainly from INRA), two farmer-funded applied research organizations (ARVALIS and CETIOM), and subcontractors from public organizations specialized in sensor or imaging developments. It also indirectly involves, through research projects, the major European-based seed companies working in France.

The five locations of Phenome involve: i) two platforms in controlled conditions, able to individually characterize 300 genotypes in a single experiment (1900 plants) with the possibility to measure individual plant growth, architecture (shoots and roots) and transpiration; ii) two field platforms with strong control of environmental conditions, in particular one free-air carbon enrichment) (FACE) system, (800 individual plots). (iii) three field platforms with higher throughput (2000 individual plots). They are equipped with soil and climate sensors, and a 'phenomobile' designed by Phenome to capture functional images of each individual plot at high throughput. (iv)Two supporting "omic" platforms allow us to centralize and optimize high throughput metabolomic and structural measurements associated with the experiments in the phenotyping platforms. Several methodological projects are working to: i) improve our capacity to measure plant traits and environmental conditions with accurate and high throughput methods; ii) Organize phenotypic data originating from different nodes in a coordinated way iii) Handle very large datasets comprising data at different time scales and plant organization levels, and the interface between data collection and plant / crop models. Phenome will be an essential tool for (i) the academic community for original programs of genetics/genomics, (ii) private seed companies, which will have access to the infrastructure via collaborations and bilateral contracts, (iii) French SMEs involved in markets of phenotyping and precision agriculture.

Rapeseed experimentations: CETIOM has the lead on Dijon field Platform. 800 rapeseed plots designs and methodological trials were carried out the last two cropping seasons using drones flights for NDVI measurements for Biomass and LAI at different plant development stages, or flowering earliness with RGB acquisition. Comparisons with classical or pedestrian technics have been done to evaluate this new high throughout put technological opportunity. A new multicoptere drone and a Phenomobile V2 adapted to a wider number of plant species will be developed in the next two following years.

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