

CONGRESS KEYNOTE

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High throughput plant phenotyping approaches to improving yield potential, biomass, radiation and water use efficiency in grain crops

Plant Phenomics provides new opportunities for using non-destructive, high throughput tools to select germplasm with enhanced growth, biomass and nutrient use efficiency and determine the genes underpinning these important traits. In this presentation, the utility of a variety of tools based on proximal and remote sensing, is demonstrated for trait quantification and determination of genes and mechanisms in controlled environments and the field. In particular, examples of digital growth analysis for high resolution genetic analysis of nutrient use efficiency, chlorophyll fluorescence and hyperspectral reflectance for photosynthetic characterization, LiDAR for canopy architecture and radiation use efficiency optimisation and distributed canopy temperature sensors and aerial thermal imaging for water use efficiency, are shown for grain crops such as wheat and canola.

The importance of canola from a global customer perspective

G. Crockett

M. Smith

US McDonald's Corporation, USA

Rapeseed (Canola) Oil and McDonald's Perspective

The presentation will provide a topline summary of McDonald's global markets and their use of rapeseed oil as well as how McDonald's projects plan to utilize rapeseed oil in the future. This includes consideration of customer preferences and the necessary characteristics of rapeseed oil in blends that enable restaurants to provide consistent quality foods that meet McDonald's established sensory standards for color, flavor, and texture..

An overview of McDonald's food evolution to remain relevant with today's customers and how rapeseed oil fits into that evolution will also be provided.

Milestones on the road to the future

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The milestones on the way to establishing the oilseed *Brassicac*s as major crop species are many, with most having occurred since the 1960s. The oilseed *Brassicac*s crops (*B. napus*, *B. rapa* and *B. juncea*) are now established as the world's third most important source of edible oil. Since 1960 the area of production in all major producing regions has grown exponentially with seed production increasing by 40 fold in Canada, 21 fold in Europe, and 13 fold in China. Seed and oil yield per hectare have also increased year over year. In addition, canola oil, in both its traditional and high oleic/low linolenic forms, can claim to be the world's most nutritious oil. Moreover, canola quality meal is now considered the protein supplement of choice for dairy cows. The demand for *Brassicac* oilseed and its products has provided producers with an alternative crop to cereals and other crop species. In Canada at least, the crop's expansion has also established a growing, rural based, canola crushing industry.

Innovation and discovery are the basis of the crop's success. Scientific advances have not been limited to genetics, the tools of detection and changes in how the crop is grown and managed have also been key to rapid development. Some of milestones will be highlighted such as the impact of gas chromatography, modified fatty acid composition, herbicides, haploid breeding, hybrids, NMR, NIR, gene and genome sequencing, gene transfer and marker assisted selection, to name a few.

However, the crop's success has not been without evolving problems such as diseases, insects, weeds and the requirement for more intense management. Can we keep up with Mother Nature's worldwide evolutionary resources? Nature is always ready to take advantage of the lush plate we place before canola's multiplicity of hungry pests. The almost complete loss of Australia's 1972 crop to blackleg or the devastation of the 2014 UK crop by flea beetles are reminders that we can't let our guard down. Fortunately technology has armed us with an ever growing arsenal of tools, techniques and knowledge to fight such hazards.

We don't know what the future may bring by way of new challenges, such as the identification of *Verticillium longisporum*, clubroot and the Swede midge on the Canadian prairies, or what new innovations may become available to protect or accelerate future advances. The rapid and revealing knowledge of the plant's genetic makeup and the increasing effectiveness of marker assisted selection together with the potential internal and external use of RNAi's and microbiome modification bode well for the future. The ability to image root growth and morphology in situ will add a new dimension to our understanding of plant growth and productivity. Aptomictic hybrids could reduce seed costs and overcome concerns of gene flow. Full resistance to shattering, introduction of yellow seeded hybrids and the elimination of secondary dormancy are clearly desired and attainable targets. In addition, the harnessing of large agronomy data sets and the use of unmanned aerial vehicles (UAV's) could result in increased farm efficiencies.

As bright as the future may seem, it is critical that we find ways of countering misinformation while building public trust in scientific advances. One of the most effective and powerful tools at our disposal, gene transfer, lies largely idle due to a misinformed public and an onerous and expensive regulatory framework. If we are to fully benefit from our current and future knowledge this battle must be won.

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The impact of genomics on *Brassica* genetics and breeding – a sequence level view of the triangle of U

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Background: *Brassica* research has benefited greatly from the close relationship between the Brassica crops and the crucifer model *Arabidopsis thaliana*, the first plant species to have a fully sequenced and annotated genome (The Arabidopsis Genome Initiative 2000). The availability of the *A. thaliana* sequence allowed the rapid identification of candidate genes for traits of interest and through comparative mapping provided novel insights into the larger genomes of the *Brassica* crops (Wang et al. 2011; Town et al. 2006; Navabi et al. 2013). Yet, the genome of the weed is still an imperfect model for the crops, the current promise of access to whole genome sequences for each agronomically important Brassica species will revolutionise research and development of Brassica crops in the coming decade.

Objectives: In the 1940's using cytogenetics U defined the unique relationship between six of the *Brassica* species, three diploids and three allopolyploids, formed from each possible pairwise hybridization. The objective is to understand at the sequence level how each of these species relates to one another and what has been the consequence of the interspecific hybridization events.

Methods: Each species that forms the triangle of U has now been sequenced, assembled and annotated (Wang et al. 2011; Parkin et al 2014; Chalhoub et al, 2014; Parkin, Sharpe et al, unpublished) All the genome sequences were generated using next generation sequencing technologies (Roche 454 and Illumina), using different combinations of libraries with varying insert sizes and relative genome coverage.

Results and Conclusions: The relative ease and cost of sequencing has allowed the impact of evolution and agronomic selection among the Brassica species to be studied at the DNA level. The genome sequences offer unprecedented insights into the impact of genome doubling on gene retention and correspondingly on trait divergence in polyploid genomes. Further the canola genome shows the impact of the high prevalence of illegitimate exchanges between the constituent genomes, with the selection of such events being responsible for some of canola's distinguishing attributes. The B genome *Brassica* species appear excluded from this type of event with multiple rearrangements distinguishing this diploid genome from its relatives. The genomes provide not only insights into polyploid evolution but provide a foundation for the application of the next generation of breeding tools.

References:

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