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Foreword

Brassica 2016 – Phenomics to genomics and everything in between

Angela Van de Wouw[A] *and Jacqueline Batley*[B]

[A]School of BioSciences, the University of Melbourne, Victoria 3052, Australia.
[B]School of Biological Sciences, University of Western Australia, Crawley, WA 6009, Australia.

Introduction

In October 2016, Melbourne, Australia hosted the international Brassica 2016 conference, a merge between the Crucifer Genetics and Australian Research Assembly of Brassicas meetings. The conference was attended by 246 delegates, representing 15 different countries and highlighted world class *Brassica* research ranging from genetic structure and diversification of the various *Brassica* species to advances in disease and pest control.

The conference included 58 oral presentations representing 12 themed sessions and included nine plenary speakers. The presenters highlighted the use of various genomics technologies to understand the role copy-number and presence-absence variation plays in selection of genetic traits, the evolution of the *Brassica* species and the advantages and need for pan-genomes to advance our understanding. The impact of diseases such as Club Root (*Plasmodiophora brassicae*), Sclerotinia stem rot (*Sclerotinia sclerotiorum*) and Blackleg (*Leptosphaeria maculans*) on yield in Australia, Canada and Europe were discussed and the advances that have been made to reduce this effect were highlighted. Lastly, it was shown how farming systems have changed immensely in recent years and how there is still limited information on the impact of these changes on phenology of crops and therefore yields.

In association with the conference, a round-table forum was held to initiate discussions around nomenclature issues for resistance genes associated with control of blackleg disease, conferred by *L. maculans*. The discussion, led by Dr Thierry Rouxel, highlighted the various issues with nomenclature whereby the same gene has been given multiple names by various groups, for example the confusion around the resistance gene(s) in Surpass400 which have been identified as *LepR3, RlmS, Rlm1, BLMR1* and *BLMR2* (Balesdent *et al.* 2005; Van de Wouw *et al.* 2009, 2014; Long *et al.* 2011; Larkan *et al.* 2013). In addition, it was highlighted that we now have the added confusion that the same nomenclature used for major resistance genes, *Rlm* (resistance to *L. maculans*), has been used for quantitative or minor gene resistance, with the first locus of this kind identified and named *Rlm12* (Raman *et al.* 2016). A consensus amongst the group was that the *Rlm* nomenclature should be exclusive for the major genes.

It was identified by the group that one of the major factors driving this confusion is the lack of common resources such as control isolates and cultivars that all researchers can have access to. For example, two groups had independently identified an avirulence gene conferring resistance to *B. juncea,* one naming the gene *AvrLm5* and the other *AvrLmJ1*. It was only once these groups were able to share resources, could they confirm that indeed these genes were the same and have since been renamed as *AvrLm5* (Balesdent *et al.* 2005; Van de Wouw *et al.* 2014; Plissonneau *et al.* 2017). The biggest issue associated with sharing resources are quarantine implications for importing isolates and cultivars which limits research groups ability to request the material. The second issue is that if there is a common source of isolates and cultivars, these need to be maintained and distributed from a single agency/research group which requires funding and capacity.

This special issue has been put together to emphasise some of the research that was presented at the Brassica 2016 conference, highlight the diversity of the conference and the impact that the various science fields are having on improving the *Brassica* crops.

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