

# #038

## Uncovering the scope of fixed homoeologous recombination events in Brassica napus using long read sequence data

*Isobel Parkin*

Chu Shin Koh, Erin Higgins, Andrew Sharpe

Agriculture and Agri-Food Canada, Saskatoon, Canada

The promiscuous nature of the progenitor A and C genomes of Brassica napus has recently been characterised. Multiple exchanges between these genomes, leading to fixed duplication and deletion of large chromosomal stretches, were apparent in the first reference sequence published in 2014. The influence of such events on the adaptation of crop type has indicated their importance and recent studies in additional genotypes have shown that this mechanism for evolutionary change is continuing at a consistent but variable pace. Some of the identified homoeologous exchanges appear to be common to multiple genotypes, yet the overall prevalence and maintenance of these events in a wider set of lines is unknown. The advent of long read technology which can span rearrangement end points and allows unique matching of reads to the polyploid genome offers a powerful platform to study this phenomenon. Utilising Oxford Nanopore Technology (ONT) sequencing of multiple B. napus genotypes a catalogue of homoeologous exchange events has been created along with smaller structural variants that differentiate the genome. Two of the same genomes were also de novo sequenced using short read Illumina based technology allowing a comparison of the approaches. The extent and range of these potentially adaptive changes will be discussed in the context of the underlying gene content and their possible role in influencing traits of importance.

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