

# #014

## Long reads reveal small scale genome structural variations in Brassica napus

ADDRESS

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There is increasing evidence that genome structural variation (SV) contributes significantly to phenotypic variation for many important agronomic traits. Most crop plants derive from ancient or recent polyploidisation events and carry extensive SV. However, difficulties in describing this kind of variation with common genetic marker systems or short-read DNA sequencing mean that SV has been largely neglected when it comes to explaining observable phenotypes. Accurate long-read sequencing provides new opportunities to detect SV at the scale of single-genes and associate such variants to traits. Here we describe the use of Oxford Nanopore sequencing for precise detection of small scale SV and association with Verticillium stem striping resistance in Brassica napus (canola, rapeseed), a recent allopolyploid species with a complex, rearranged genome. Whole genome sequencing was performed for a commercial cultivar along with a synthetic B. napus line carrying interesting trait variation for breeding, in order to identify the distribution and frequency of small-scale SVs and investigate associations with known QTL in crosses between these lines.

Using this data we were able to identify small-scale SVs (down to single-gene level) associated with quantitative disease resistance.

PLENARY TALKS

ORALS

POSTERS

WORKSHOPS