

# #003

## Understanding and exploiting the dynamic Brassica napus genome

ADDRESS

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The first genetic mapping analyses of Brassica napus in the 1990s revealed surprising exchanges among homoeologous chromosomes donated by the two progenitor species, Brassica rapa and Brassica oleracea. Two decades later, the genome assembly of the winter oilseed rape accession Darmor-bzh (Chalhoub et al. 2014, Science), together with whole-genome resequencing of diverse natural and synthetic B. napus accessions (Schmutzer et al. 2015, Scientific Data), provided unprecedented insight into the extent and causes of genome restructuring in the allopolyploid rapeseed genome, revealing its important role in the rapid evolution of B. napus into a diverse and successful global crop. Genome sequences are now available for thousands of world-wide B. napus accessions, but we still have a lot to learn about the dynamics of structural genome diversity in B. napus and how to capture, exploit and manage such diversity for breeding. In particular, there is growing evidence that genome restructuring is ongoing in modern cultivars, and that there are specific genetic factors which influence the rate and extent of genomic rearrangements. This presents both opportunities and challenges for breeders: While de novo structural variants potentially create novel diversity as a basis for crop improvement and heterosis, they can also potentially cause instability and unwanted variation within cultivars. Understanding the genetic control of genome dynamics in rapeseed and how it influences key traits is likely to play an important role in future breeding efforts.

PLENARY TALKS

ORALS

POSTERS

WORKSHOPS