

# #036

## Specific chromosome rearrangements and allelic variants influence fertility and genome stability in novel Brassica allohexaploids

ADDRESS

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PLENARY TALKS

Allohexaploid Brassica is a promising new crop type which offers to combine useful agronomic traits from all six cultivated Brassica "U's Triangle" species, with the potential for additional hybrid vigour provided by an extra genome and set of alleles. However, most allohexaploid Brassica material is genomically unstable, with recombination between the A, B and C genome chromosomes during meiosis resulting in loss of chromosome fragments and hence loss of plant fertility and viability. In order to identify factors affecting genome stability, we genotyped several populations of allohexaploid Brassica resulting from the cross combination (B. napus × B. carinata) × B. juncea and recorded self-pollinated seed fertility in these lines. Seed fertility was highly correlated with regular meiosis in a subset of lines studied ( $r \sim 0.8$ ). Surprisingly, predictive models suggested that one of the best indicators of increased fertility was the replacement of C-genome chromosome segments with A-genome chromosome segments in unbalanced translocation events, while replacement of A-genome chromosome segments with C-genome chromosome segments had a negative effect on plant fertility. Also predictive of fertility were the presence of univalents (mixed effect; generally negative but positive in some cases if the alternative was complete loss of the chromosome pair) and accumulation of genomic rearrangements (negative effect). Using genome-wide association analysis, we identified several QTL containing meiosis genes with putatively causal variants between the parents of the mapping population, including a stop codon gain in a copy of SMC1 in one of the B. carinata lines, and an effect apparently due to an unbalanced translocation between the top of chromosomes A03 and C03 in one population. Our results suggest that a combination of allelic variants and gene copy numbers (possibly modulated by additional translocation events) could play a role in stabilizing meiosis in novel allohexaploid types. Better understanding of the genetic factors underlying genomic stability could allow pre-selection of putatively stable material from the parent species for production of allohexaploid germplasm pools.

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