

Detecting the genes controlling homologous recombination in *Brassica napus*

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Background:

Homoeologous recombination between the A and C sub-genomes of *Brassica napus* occurs at low levels in established cultivars but is prevalent in newly resynthesised *B. napus*. The resulting chromosomal exchanges which generally lead to presence/absence variation and concomitant changes in gene expression have been linked to a number of important traits in the crop. Utilising a cross between an established and resynthesised *B. napus* line loci controlling this genetic phenomenon were identified (Higgins et al, 2021).

Objective:

In order to further dissect the loci controlling homologous recombination in *B. napus* and potentially determine the genes underlying the trait, a comprehensive picture of the gene expression landscape during meiosis of both cultivated and resynthesised *B. napus* was developed.

Methods:

Meiocytes were staged and extracted from DH12075 (a canola quality *B. napus*) and RB1 (resynthesised *B. napus*) during six stages of prophase I, when recombination would be occurring. RNASeq libraries were generated and sequenced in triplicate for each stage. Comparative differential gene expression analyses and WGCNA was used to identify genes differentially expressed between the two lines. Homologues of known meiosis-specific genes from *Arabidopsis thaliana* were identified and their expression pattern determined across prophase I.

Results:

Although gene expression during prophase I of *B. napus* could be separated into the six stages in both lines, pachytene, considered a meiotic checkpoint in some species, was a clearly defined transition stage. Contrary to similar studies in cereal species, gene expression did not appear to be suppressed during meiosis and there was no evidence of novel intergenic meiotic transcripts. There were distinct changes in expression profiles of genes involved in controlling inter-homologous bias and crossover/non-crossover formation between the two lines. Study of those genes underlying the loci controlling homologous chromosome pairing suggested a candidate gene that could be manipulated in the crop to generate novel variation through homoeologous exchange.

Conclusions:

The ability to control homologous recombination in *B. napus* would provide a mechanism to generate novel variation exploiting the underlying sub-genome structure, potentially encouraging chromosomal exchange with the more distantly related B genome. The described study provides a comprehensive landscape of recombination in two *B. napus* lines differing in their ability to control homologous recombination. The results point to candidate genes that could be targeted through gene editing to manipulate the recombination process and lead to the generation of novel and potentially valuable germplasm.

References:

Higgins, E. E., Howell, E. C., Armstrong, S. J., & Parkin, I. A. P. (2021). A major quantitative trait locus on chromosome A9, *BnaPh1*, controls homoeologous recombination in *Brassica napus*. *New Phytologist*, 229: 3281–3293.