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Allele-specific expression in resynthesized *Brassica napus* lines

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Background:

Interspecific hybridization between *Brassica rapa* (AA = 20) and *Brassica oleracea* (CC = 18) can produce resynthesized *B. napus* lines, which is a possible way to increase genetic variation in rapeseed. Most resynthesized lines produced so far have been meiotically unstable with low fertility. However, we identified some progeny of resynthesized lines which appear to have higher meiotic stability.

Objective:

We aimed to identify differences in allele-specific gene expression between resynthesized rapeseed lines with higher and lower meiotic stability and established rapeseed (*B. napus*).

Methods:

We undertook resequencing followed by copy number variation (CNV) analysis (number of gene copies present) and allele-specific expression analysis (expression of specific alleles of each gene copy) from transcriptomic data in order to identify differences between higher stability and lower stability resynthesized rapeseed as well as cultivars of *B. napus*. Data was generated from leaf, bud and open flower tissues collected from four plants from each of six resynthesized rapeseed genotypes, the three genotypes of *B. rapa* and three genotypes of *B. oleracea* that represented their parent cultivars, and two genotypes of *B. napus* all grown together under controlled glasshouse conditions.

Results:

We found differences in expression of alleles from the A genome relative to the C genome (subgenome expression level dominance) in the resynthesized lines, with differences between genotypes in the level of this effect. We also observed allele-specific expression (ASE), with but not all some genes showing ASE also correlated with CNVs. ASE was also different between different genotypes of resynthesized rapeseed.

Conclusions:

Correlation of ASE with CNVs is not unexpected, as CNVs result in changes of copy number of the genes involved, which can affect expression. However, ASE was not solely explained by allele dosage, indicating cis gene regulation plays an important role in allele expression in the resynthesized lines. Difference between genotypes observed may also indicate a role of ASE in genome stability. Further investigation of these lines may reveal the mechanisms underlying differences between genotypes in genome stability.