

Repeated polyploidy drove different levels of crossover suppression between homoeologous chromosomes in *Brassica napus* allohaploids

Eber F.¹, Cifuentes M.², Lucas M.O.¹, Lodé M.¹, Chèvre A.M.¹, Jenczewski E.²

¹ INRA, UMR 118 Amélioration des Plantes et Biotechnologies Végétales, BP35327, 35653 Le Rheu cedex, FRANCE

² INRA, Station Génétique et d'Amélioration des Plantes-Institut Jean-Pierre Bourgin, 78026 Versailles cedex, FRANCE

Introduction

Brassica napus (AACC; 2n=38) is a young allopolyploid species with multiple origins; it was formed by repeated interspecific hybridization between ancestors of *B. oleracea* (CC, 2n=18) and *B. rapa* (AA, 2n=20). It was shown that AC *B. napus* allohaploid plants produced from some varieties displayed few univalents (fu) whereas those produced from other varieties displayed Mostly Univalents (MU). This trait is controlled by major locus (*PrBn*: Jenczewski et al., 2003) localized on linkage group C9 and 4-6 other additive or epistatic loci (Liu et al., 2006). It is directly linked to variation of homeologous recombination (Nicolas et al. 2009). Here, our goal is to decipher whether the diversity of meiotic behavior found among a wide range of *B. napus* allohaploid accessions is related to the polyphyletic origin of this species and diversity at the *PrBn* locus (Cifuentes et al., 2010).

Diversity of meiotic behaviour among *B. napus* allohaploids

A total of 363 allohaploid plants were isolated from 29 varieties representing different types of cultivars and a major part of *B. napus* genetic diversity. We analyzed the meiotic behavior at Metaphase I (MI) of all allohaploids and one raw *B. oleracea* × *B. rapa* interspecific hybrid, which have a similar karyotype (10 A and 9 C chromosomes). This plant showed the lowest number of univalents while two clear-cut meiotic phenotypes were identified among all *B. napus* allohaploids (Figures 1 and 2). These two main meiotic behaviors were randomly distributed with respect to the winter and spring oilseed types (Fisher's exact test P>0.05). Only eight plants showed an intermediate meiotic phenotype, most of which originated from open pollinated varieties that produced a mixture of MU and fu allohaploids.

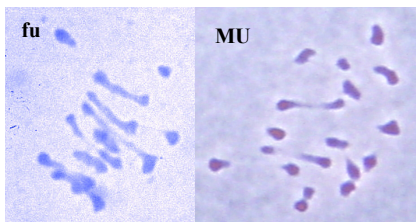


Figure 1: Metaphase I from few univalents (fu) and Mostly Univalents (MU) allohaploids

Diversity of plastid haplotypes and their distribution with respect to allohaploid meiotic behavior

We analyzed the genetic diversity of the chloroplast genome in order to gain insight into the maternal origins of the 29 *B. napus* accessions. Sequencing both the *ndhC-trnV* and *rbcL-accD* chloroplast intergenic regions showed exactly the same distribution of chloroplast diversity. Only two plastid genome (ptDNA) haplotypes were found; they differed by a total of nine SNPs and three indels, including a 10bp deletion.

These two plastid haplotypes were not randomly distributed with respect to the two main meiotic behaviors (Fisher's exact test P=0.0123). 18 out of 19 fu accessions displayed ptDNA haplotype 1 while a more balanced mix of ptDNA haplotypes was found among MU accessions (Figure 2). This suggests that the dichotomy of meiotic behaviors among *B. napus* allohaploids could be related to *B. napus* multiple origins.

Nuclear DNA marker diversity in the *PrBn* region with respect to the allohaploid meiotic behavior

We analyzed the genetic diversity of eight molecular markers spanning the region of *PrBn* (defined in the *Darmor-bzh* × *Yudal* segregating population). (Figure 3).

Although MU accessions appeared more diverse than fu accessions, the meiotic phenotype of twenty two accessions (out of 29) was consistent with their multilocus genotype in the region surrounding *PrBn* (Figure 3). Half of these displayed the same multilocus genotype as did *Darmor-bzh* or *Yudal*, while the other half was recombinant in the interval with alleles at the peak of the QTL being in agreement with the meiotic phenotype.

These results confirm the most likely position for *PrBn*. They also demonstrate that, although some accessions certainly segregate for different loci other than *PrBn*, this locus is still the main determinant for natural variation of homeologous recombination (in allohaploids) at the species level.

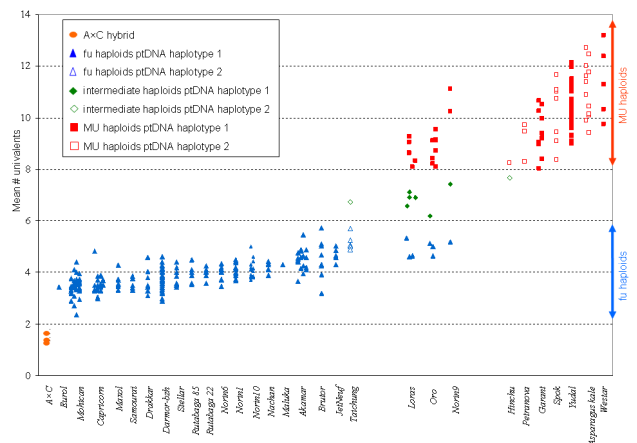


Figure 2: Diversity of meiotic behaviour and plastid haplotypes in *B. napus* allohaploids

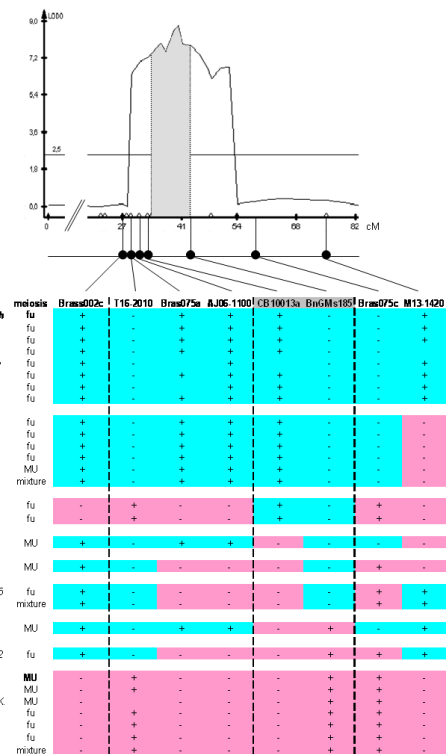


Figure 3: Genotype of the varieties in the region of *PrBn*, the main determinant for the number of univalents among *B. napus* allohaploids

Cifuentes M.*, Eber F.*, Lucas M.O., Lodé M., Chèvre A.M., Jenczewski E., 2010. Repeated polyploidy drove different levels of crossover suppression between homeologous chromosomes in *Brassica napus* allohaploids. The Plant Cell doi:10.1105/tpc.109.072991

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Nicolas S., Leflon M., Monod H., Eber F., Coriton O., Huteau V., Chèvre A.M., Jenczewski E., 2009. Genetic regulation of meiotic crossovers between related genomes in *Brassica napus* haploids and hybrids. Plant Cell 21: 373-385.