Assessment of genetic relationship among resynthesized, semi-resynthesized and natural *Brassica napus* L genotypes

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Selective breeding of B. napus, especially for canola quality, has reduced its variation, particularly for traits of breeding interest. Resynthesized Brassica napus L. obtained by interspecific hybridization between genotypes of B. rapa L. and B. oleracea L. can create a valuable source for broadening genetic diversity in oilseed rape. Despite these achievements, the synthesized allotetraploids of *B. napus* have not been readily used in breeding programs due to low seed yield, low oil content and non-canola quality. The existing methods of interspecific hybrid formation are limited by the fact that one of the parents used for resynthesis of B. napus, B. oleracea, has never been domesticated as an oilseed crop. This mean that resynthesized (RS) lines require improvement, e.g. by developing semi-resynthetic (semi-RS) plants or through backcrossing and other methods of breeding, before they can be used by breeders. In this study, we determined the extent of DNA polymorphism among natural accessions of oilseed rape, resynthesized B. napus, their parental genotypes and double-low quality semi-RS lines carrying the Rfo gene. Using 10 selected primer combinations, 522 polymorphic AFLP markers were scored in the complete set of 100 studied genotypes. To detect relationships between genotypes resynthesized, semi-resynthesized and natural B. napus L. The natural oilseed rape group, which consists of 49 cultivars and lines, is characterized by lower genetic diversity than 33 lines of artificially synthesized oilseed rape and the analysis showed that the double-low quality semi-RS lines represent a specific genetic variation of B. napus. The de novo synthesized B. napus lines and the semi-RS of double-low quality generated from them, which are genetically distinct from the natural cultivars and accessions, provide a significant opportunity for enrichment of the oilseed rape gene pool.

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