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Potential of rutabaga (Brassica napus var. napobrassica) gene pool for use in the breeding of B. napus canola

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ABSTRACT

The narrow genetic diversity in Brassica napus L. (AACC, $2n = 38$) canola is considered one of the limitations for continued improvement of this crop. Among the different primary gene pools of canola, rutabaga (B. napus var. napobrassica) is genetically distinct from spring canola. The potential value of this gene pool for broadening the genetic base of B. napus canola was investigated in the present study. A total of 93 advanced generation inbred lines with a spring growth habit were developed from F2 and BC1 populations of two rutabaga × spring canola crosses, and evaluated in replicated field trials for agronomic and seed quality traits, and heterosis for different traits by developing test hybrids with their spring canola parent. These inbred lines were genotyped with polymorphic SSR markers for assessing the extent of allelic diversity and the level of introgression from rutabaga into the inbred lines. Some of the inbred lines gave higher yield and had greater seed oil content than the spring canola parent. Molecular marker analysis showed that genetically distinct B. napus canola lines carrying unique alleles of the A and C genomes of rutabaga could be obtained from both F2- and BC1-derived populations. The majority of the test hybrids displayed positive MPH for seed yield, and a number of test hybrids surpassed seed yields of the spring canola parents. Thus, the results from this study demonstrate the potential of using the rutabaga gene pool for broadening the genetic base of B. napus canola, and for the development of genetically distinct heterotic groups for exploitation of heterosis in hybrid cultivars.