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ORIGINAL PAPER

Genetic and physical mapping of flowering time loci in canola (*Brassica napus* L.)

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Abstract We identified quantitative trait loci (QTL) underlying variation for flowering time in a doubled haploid (DH) population of vernalisation—responsive canola (*Brassica napus* L.) cultivars Skipton and Ag-Spectrum and aligned them with physical map positions of predicted flowering genes from the *Brassica rapa* genome. Significant genetic variation in flowering time and response to vernalisation were observed among the DH lines from Skipton/Ag-Spectrum. A molecular linkage map was generated comprising 674 simple sequence repeat, sequence-related amplified polymorphism, sequence characterised amplified region, Diversity Array Technology, and candidate gene based markers loci. QTL analysis indicated that flowering time is a complex trait and is controlled by at least 20 loci, localised on ten different chromosomes. These loci each accounted for between 2.4 and 28.6 % of the total genotypic variation for first flowering and response to vernalisation. However, identification of consistent QTL was found to be dependant upon growing environments. We compared the locations of QTL with the physical positions of predicted flowering time genes located on the sequenced genome of *B. rapa*. Some QTL associated with flowering time on A02, A03, A07, and C06 may represent homologues of known flowering time genes in *Arabidopsis*; *VERNALISATION INSENSITIVE 3, APETALA1, CAULIFLOWER, FLOWERING LOCUS C, FLOWERING LOCUS T, CURLY LEAF, SHORT VEGETATIVE PHASE, GA3 OXIDASE,* and *LEAFY*. Identification of the chromosomal location and effect of the genes influencing flowering time may hasten the development of canola varieties having an optimal time for flowering in target environments such as for low rainfall areas, via marker-assisted selection.

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