Quantitative trait loci influencing heterosis for seedling biomass and seed yield in oilseed rape

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Understanding the genetic basis of early developmental and biomass traits in oilseed rape (Brassica napus) and investigation of possible relationships to seed yield could be potentially useful with respect to hybrid breeding. One interesting aspect that to date has not been fully elaborated is whether heterosis for seedling traits can be related to heterosis for seed yield. In this study we have mapped quantitative trait loci (QTL) influencing heterosis for morpho-physiological traits in oilseed rape seedlings grown under controlled conditions. Our aim is to compare these loci to QTL influencing heterosis for seed yield in field experiments.

A set of doubled-haploid (DH) lines was developed from a cross between the 00quality winter oilseed rape variety 'Express' and the high erucic acid, high glucosinolate inbred line 'V8'. This DH population was used to develop a set of test hybrids segregating for heterosis by controlled crossing of all DH lines with the male-sterile tester 'MSL-Falcon'. A genetic map comprising 167 SSR and 313 AFLP markers was generated from the DH population and used to locate relevant QTL. Data for seedling biomass were collected 17 and 28 days after sowing (*das*) from a triple-replicated greenhouse experiment where performance of the test hybrids was compared to the DH lines. Field trials of the same materials were conducted in 2004-2005 at two locations to estimate yield and yield heterosis.

Quantitative trait loci (QTL) for per se performance with additive effects were obtained using the data from the DH lines, while QTL for heterosis effects could be localised based on the difference between test hybrid and mid-parent data. Three QTL for heterosis in seedling traits were detected along with one QTL for seed yield heterosis. A strong additive QTL on chromosome N17 was found to have a significant effect on seedling dry weight at 17 days after sowing (das), however at 28 das no QTL was found at this position and a different locus on chromosome N10 had the main effect on this trait. Two different QTL were detected with significant heterosis effects on hypocotyl length at 17 das and stem length at 28 das. This suggests a shift in the genetic control of heterosis for seedling development during the first four weeks after germination. Only one QTL for heterosis in seed yield was detected, and this QTL was not in the same position as the main QTL for *per se* yield. The QTL for seed yield heterosis did not colocalise with the QTL for seedling biomass heterosis.

It was obtained that biomass heterosis can be measured at early developmental stages in oilseed rape. It appears that the genetic control of heterosis changes in different developmental stages. One significant QTL for seed yield heterosis could be located. The investigations are currently being continued with a different set of test hybrids and compared with data from a different mapping population. Ultimately we hope to gather information which will help in determining the genetic mechanisms underlying developmental and yield heterosis in *B. napus*.

Keywords

heterosis, QTL analysis, early morphological trait, oilseed rape.

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