

# Genetic Analysis of Heterosis for Biomass in Rapeseed (*B. napus* L.)

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The heterosis observed in  $F_1$  hybrids from crosses between inbred lines is well known and extensively applied in plant breeding, but the basic understanding of heterosis is still not very advanced. Plant biomass, which is a complex, quantitative trait strongly exhibiting heterosis, is a suitable model for studying this phenomenon at the QTL level. To understand the genetic basis of heterosis in rapeseed QTL for early and late plant biomass were analysed by composite interval mapping using a genetic map of SSR and AFLP markers, which covers 1863 cM of the rapeseed genome. The

experimental population analysed, consists of 250 doubled haploid lines, developed from the  $F_1$  of a highly heterotic cross between the winter cultivar 'Express' and the resynthesized line 'R53' and their corresponding hybrids with the tester 'MSL-Express'. The use of one of the parents as a tester provided the opportunity for a straightforward determination of the additive and dominance effects of the localized QTL. The heterosis in early plant biomass of rapeseed was studied in a greenhouse trial with four replications, while plant height, used as a proxy for late plant biomass, was

analysed in a field experiment replicated at four locations. Both of the trials were based on incomplete block designs including the doubled haploid population and the corresponding  $F_1$  hybrids of the doubled haploid lines with the tester 'MSL-Express'. QTL mapping with the data derived from the greenhouse and the field trials resulted in the localization of QTL for biomass and in an assessment of their genetic effects. From this, the relative contributions of different gene actions, e.g. dominance, overdominance and epistasis to the expression of heterosis in rapeseed were estimated.

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