

FINE MAPPING OF TWO QTL FOR HETEROSIS IN MAIZE

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Although heterosis is widely exploited for crop improvement and breeding, a clear understanding of its genetic bases is still elusive. In a previous work undertaken to shed light on the genetic basis of heterosis in maize (*Zea mays* L.), we applied a joint classical genetic and QTL analysis to a population of Recombinant Inbred Lines (RIL-F_{12:13}) originated from the single cross B73 x H99. Level of heterosis for several agronomic traits and underlying genetic effects were evaluated, together with the relationship between level of heterozygosity and phenotypic performance, and several QTL with heterotic effects on phenotypes were detected. Based on these findings, we followed an introgression program employing marker-assisted breeding on residual heterozygous lines (RHL) to produce pairs of NILs homozygous either for one or the other parental inbred allele (i.e. B73 or H99) at the selected heterotic QTL regions. Large F₂ populations, each segregating only for the respective QTL region, were produced from F₁ hybrids obtained by crossing contrasting NILs for each QTL.

In this work we describe the results of our research work aimed at the fine mapping of two of the introgressed QTL mapped on chromosome 4 (bin 10) and 10 (bin 03). In particular, 3840 and 1152 F₂ plants were genotyped at markers flanking QTL 4.10 and QTL 10.03 respectively, and F₃ families were produced by selfing F₂ plants recombinant at the respective QTL region. The so obtained F₃ families are highly-informative and will be evaluated for agronomic traits in order to fine map their respective QTL.