



Mapping of quantitative trait locus associated with maize tolerance to high seed drying temperature

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ABSTRACT. Quantitative trait locus (QTL) mapping and identification of traits of agronomic importance is important in the process of molecular marker-assisted selection in breeding programs. The molecular map of maize is well saturated and QTL and simple sequence repeat (SSR) markers have been identified, whereas few markers linked to seed quality traits are included. The present study aimed to identify QTL and the gene action and to quantify the effects of these regions in the phenotypic variation related to maize tolerance to high seed drying temperature. SSR markers and 129 segregating families of F₂ plants of the cross of intolerant and tolerant lines were used in regression and composite interval mapping methods. Three maize QTL associated with tolerance to high seed drying temperature were identified and mapped to chromosomes 6 and 8, explaining 39% of the phenotypic variation of the trait with additive, dominance and over-dominance gene action. These markers seem to be effectively associated with the evaluated trait, since all were mapped near genes whose expression products were associated with seed desiccation tolerance.

Key words: High temperature; Quantitative trait locus; Seeds; *Zea mays*; Desiccation tolerance