

Quantitative Trait Locus (QTL) Mapping of a High Temperature Germination Locus in Lettuce

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Lettuce (*Lactuca sativa*) is the most important salad crop grown in the United States with annual per capita consumption exceeding 10 kg and sales of over US\$2.3 billion. Seed thermoinhibition (failure to germinate at high temperatures) leads to stand establishment problems in lettuce. In cultivar 'Salinas', seed germination is inhibited at temperatures above $\sim 27^{\circ}\text{C}$. In contrast, PI251246, a primitive lettuce (*L. sativa*) genotype, exhibits tolerance of high temperature during germination. The pronounced difference in germination phenotype in the parental genotypes (Salinas versus PI251246) at high temperatures enabled QTL analysis of the seed thermoinhibition trait using a recombinant inbred line (RIL) population. The RIL mapping population consisting of 159 F_8 families revealed a major QTL (*Htg9.1*) from three seed production environments that described 23% of the total phenotypic variation for high temperature germination. Based on lettuce genomic and transcriptomic sequences, some germination-related genes involved in hormonal regulation (brassinosteroid, ethylene, and gibberellin) are located within the *Htg 9.1* region. Fine mapping to refine the QTL region and identify candidate genes is underway. RNA-Seq analyses have been conducted to identify genes exhibiting differential expression patterns at different germination temperatures.