



# Genetic analysis of maize kernel thickness by quantitative trait locus identification

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**ABSTRACT.** Kernel thickness is one of the most important traits in kernel structure, and is related to yield. To ascertain its genetic information more clearly, an immortal recombinant inbred line segregation population was used to map the quantitative trait loci (QTLs) for kernel thickness. As a result, two QTLs were identified on chromosome 9; both of them had negative additive effects, and could decrease kernel thickness to some extent. The QTLs explained 25.8% of the total phenotypic variation. These results advance our understanding of the genetic basis of kernel thickness in maize-breeding programs.

**Key words:** Maize (*Zea mays* L.); Quantitative trait locus; Recombinant inbred line; Kernel thickness