

Abstract

The *teosinte branched1* (*tb1*) gene is a major QTL controlling branching differences between maize and its wild progenitor, teosinte. The insertion of a transposable element (*Hopscotch*) upstream of *tb1* is known to enhance the gene's expression, causing reduced tillering in maize. Observations of the maize *tb1* allele in teosinte and estimates of an insertion age of the *Hopscotch* that predates domestication led us to investigate its prevalence and potential role in teosinte. We assessed the prevalence of the *Hopscotch* element across an Americas-wide sample of 837 maize and teosinte individuals using a co-dominant PCR assay. Additionally we calculated population genetic summaries using sequence data from a subset of individuals from four teosinte populations and collected phenotypic data using seed from a single teosinte population where *Hopscotch* was found segregating at high frequency. Genotyping results indicate the *Hopscotch* element is found in a number of teosinte populations and linkage disequilibrium near *tb1* does not support recent introgression from maize. Population genetic signatures are consistent with selection on this locus revealing a potential ecological role for *Hopscotch* in teosinte, but a greenhouse experiment does not detect a strong association between *tb1* and tillering in teosinte. Our findings suggest the role of *Hopscotch* differs between maize and teosinte. Future work should assess *tb1* expression levels in teosinte with and without the *Hopscotch* and more comprehensively phenotype teosinte to assess the ecological significance of the *Hopscotch* insertion and, more broadly, the *tb1* locus in teosinte.

Key words: domestication; maize; teosinte; *teosinte branched1*; transposable element