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Identification of QTL Controlling Flooding Tolerance in Reducing Soil Conditions in Maize (*Zea mays* L.) Seedlings

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Abstract: We investigated the tolerance to flooding in reducing conditions of five maize inbred lines and identified a quantitative trait locus (QTL) for the trait. Flooding treatment with 0.1% to 0.4% starch solution for 14 d reduced soil redox potential to about — 200 mV, mimicking reducing conditions in soil. Treatment with 0.2% starch revealed wide varietal differences in dry matter production among the five maize inbred lines. We identified the QTL for flooding tolerance in reducing conditions in a population of 178 F_2 plants derived from a cross of inbred lines F1649 (tolerant) and H84 (sensitive). Flooding tolerance, evaluated as the degree of leaf injury following treatment with 0.2% starch solution, revealed wide variation in the F_2 population. Amplified fragment length polymorphism (AFLP) markers linked to flooding tolerance gene(s) were screened with 64 AFLP primer combinations using 15 of the 178 F_2 plants from each extreme representing the 'tolerant' and 'sensitive' plants, and found 11 AFLP markers associated with flooding tolerance. Of these, 10 co-segregated and were assigned to chromosome 1. Six SSR primer pairs around these markers were used to construct a linkage map. Composite interval mapping analysis revealed that a single QTL for degree of leaf injury was located on chromosome 1 (bin 1.03-4). Another QTL for flooding tolerance, evaluated as dry matter production under flooding with 0.2% starch, was located at the same position. These results suggest the potential to increase productivity by transferring flooding tolerance genes from F1649 to elite maize inbred lines.

Keywords: Flooding, Quantitative trait locus, Reduction, Starch

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