

Mapping QTLs Associated with Salinity Tolerance in Maize at Seedling Stage

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Abstract : Salinity stress is one of the most important abiotic factors contributing to crop growth and yield loss. Exploring the genetic basis is necessary to develop maize varieties with salinity tolerance. In order to discover the inherent basis for salinity tolerance traits in maize, 121 polymorphic SSR markers were used to analyze 163 F₂ individuals derived from a single cross of inbred line B73 (a salt susceptible inbred line) and CZ-7 (a salt tolerant inbred line). A linkage map was constructed and the map covered 1195.2 cM of maize genome with an average distance of 9.88 cM between marker loci. Ten salt tolerance traits at seedling stage were evaluated for QTL analysis in maize seedlings. A total of 41 QTLs associated with seedling shoot and root traits were detected, with 16 and 25 QTLs under non-salinity and salinity condition, respectively. And only 4 major stable QTLs were detected in two environments. The detected QTLs were distributed on chromosomes 1, 2, 4, 5, 6, 7, 8, 9, and chromosome 10. Phenotypic variability for the identified QTLs for all the traits was in the range from 6.27 to 21.97%. Fourteen QTLs with more than 10% contributions were observed. Our results and the markers associated with the major QTL detected in this study have the potential application for genetic improvement of salt tolerance in maize through marker-assisted selection.

Keywords : salt tolerance, seedling stage, root shoot traits, quantitative trait loci, simple sequence repeat, maize

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