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Poster: Maize, Sorghum, Millet, Sugar Cane, and related

QTL And Selection Mapping For Aluminum Tolerance In Tropical Maize

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Aluminum toxicity is one of the major constraints for agriculture on acid soils, which occupy large regions of the world's agricultural area. This work aimed at validating the chromosomal location of aluminum tolerance QTL mapped in a maize RIL population using allelic frequency shifts from a drift model, across three cycles of recurrent selection for this trait. The phenotypic index employed was relative seminal root length obtained in nutrient solution. A genetic linkage map composed by 162 SSR markers was used to detect five QTL explaining around 60% of the aluminum tolerance. Some of these QTL were located at syntenic regions with rice Al tolerance QTL and putative AltsB homologs from rice and sorghum. Other QTL were coincident with aluminum tolerance QTL mapped in the maize IBM population. The selection mapping strategy evaluated five SSR markers along the maize chromosome 5 in three selection cycles, significant shifts in allelic frequencies were detected for the marker located near to the aluminum QTL explaining 13% of the phenotypic variance. Significant associations detected by QTL and selection mapping support the presence of genetic factors controlling aluminum tolerance on maize chromosome 5. Additionally, within this genomic region there is sequence homologous to AltsB, which is a major aluminum tolerance gene in sorghum, suggesting that maize and sorghum share a common mechanism of Al tolerance. Financial support for this project was provided by FAPEMIG, CNPq, McKnight Foundation, GCP, IFS and Embrapa

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