

Validation of aluminum tolerance QTL in 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 to associate QTL mapping, gene expression and allelic frequency shifts from a drift model to validate the chromosomal location of aluminum tolerance QTL. Al tolerance QTLs were mapped in a maize RIL population using the relative seminal root length obtained in nutrient solution as phenotypic index and a genetic linkage map composed by SSR, RFLP and STS markers. Allelic frequency shifts were evaluated across three cycles of recurrent selection for Al tolerance under nutrient solution. Gene expression profile was employed with one maize homologue of the Al tolerance gene cloned in sorghum *SbMATE*. QTL mapping detected six QTL explaining around 67.5% of the phenotypic variance. Some of these QTL were located at genomic regions syntenic with rice Al tolerance QTL and putative *SbMATE* homologs from sorghum. Other QTL were coincident with aluminum tolerance QTL mapped in the maize IBM population. A maize homologue gene to the *SbMATE* was mapped within the major Al tolerance QTL, located at chromosome 6 and explaining 18.2% of the phenotypic variance. This gene was highly expressed in the tolerant parental lines under aluminum stress, when compared to the sensitive line. The selection mapping strategy evaluated five SSR markers along the maize chromosome 5 in three selection cycles, and significant shifts in allelic frequencies were detected for the marker located near to the aluminum QTL explaining 16.1% 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. These results enforce the location of genetic factors controlling Al tolerance in maize, suggesting also that maize and sorghum share a common mechanism of Al tolerance.

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