

**POSITIONAL CLONING AND ASSOCIATION ANALYSIS OF A MATE GENE THAT CONFERS ALUMINUM TOLERANCE IN *Sorghum* VIA THE *ALT<sub>SB</sub>* LOCUS**

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Crop yields are significantly reduced by aluminum toxicity on highly acidic soils, which comprise up to 50% of the world's arable land. However, the molecular basis underlying the most accepted tolerance mechanism based on Al-induced organic acid release by root apices is only now being elucidated. Candidate aluminum tolerance proteins include organic acid efflux transporters, with the organic acids forming non-toxic complexes with rhizosphere aluminum. Initially, a single major Al tolerance gene, *Alt<sub>SB</sub>*, was mapped to the end region of sorghum chromosome 3. In this study, we used positional cloning to identify the gene encoding a member of the multidrug and toxic compound extrusion (MATE) family, an aluminum-activated citrate transporter, as responsible for the major sorghum (*Sorghum bicolor*). Aluminum tolerance locus, *Alt<sub>SB</sub>*. We sequence scanned the entire 25 Kbp region defined by high resolution mapping across the 'Al tolerant' and 'Al sensitive' reference alleles from SC283 and BR007, respectively, and found that allelic effects on the phenotype are controlled by polymorphisms on regulatory regions, which primarily affect gene expression. Among the candidate QTNs is a MITE insertion in the promoter region of the gene, whose large size variations were correlated with Al tolerance across members of a sorghum diversity panel. However, preliminary data obtained with near-isogenic lines suggest that the MITE insertion alone is not enough to fully explain the observed allelic effects at *Alt<sub>SB</sub>* and that trans-acting factors elsewhere in the sorghum genome can play an important role to provide extreme levels of Al tolerance in sorghum. We are now applying association genetics to dissect the molecular nature of the causative polymorphism(s) of *Alt<sub>SB</sub>*. We are also defining elite *Alt<sub>SB</sub>* haplotypes using SNPs and indels associated with Al tolerance and generating tagging SNPs, which will be used to deploy these haplotypes into acid soil breeding programs throughout the world.