



Plant & Animal Genomes XV Conference

January 13-17, 2007
Town & Country Convention Center
San Diego, CA

W73 : Challenge Program

Elucidating The Molecular Determinants Of Aluminum Tolerance In Sorghum And Maize

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Aluminum (Al) toxicity on acid soils represents a major constraint for crop production worldwide, thus understanding the genetic and molecular mechanisms of Al tolerance has been a major focus for a number of laboratories. Here, we report on the progress made from our Generation Challenge Program grant on the identification and characterization of Al tolerance genes and associated physiological mechanisms in sorghum and maize. With regards to sorghum Al tolerance, we have cloned via high resolution mapping a candidate Al tolerance gene, AltSB, that is a novel, Al-activated citrate transporter involved in the primary mechanism of sorghum Al tolerance. Evidence will be presented verifying that AltSB is a major sorghum Al tolerance gene. Also, sequence analysis of the parental AltSB alleles and the promoter region from selected members of a sorghum diversity panel, combined with determination of AltSB expression, Al tolerance and root citrate exudation indicates that differences in gene expression are a major determinant of sorghum Al tolerance. This research also has allowed us to identify superior AltSB alleles and work is now underway to use this information to facilitate improvements in sorghum Al tolerance via marker-assisted selection. In maize, we have employed an interdisciplinary approach based on maize root tip gene expression profiling, analysis of maize homologs of the wheat (ALMT1) and sorghum (AltSB) tolerance genes, and knowledge of physiological mechanisms of maize Al tolerance to identify candidate maize Al tolerance genes. Subsequent association and linkage analysis of these candidates has identified a number of putative tolerance genes.