



Plant & Animal Genomes XV Conference

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

W355 : QTL Cloning

Positional Cloning And Characterization Of AltSB, A Major Aluminum Tolerance Gene In Sorghum: Toward The Identification Of The Molecular And Physiological Basis Of Allelic Effects

Jurandir Magalhaes¹, Jiping Liu², Vera Alves¹, Claudia Guimaraes¹, Yihong Wang^{2, 3},
Ubiraci Lana¹, Robert Schaffert¹, Patricia Klein⁴, Owen Hoekenga², Miguel Piñeros²,
Leon Kochian²

¹ Embrapa Maize and Sorghum, Rod. MG 424, Km 65, 35701-970, Sete Lagoas, Brazil

² U.S. Plant and Soil Nutrition Laboratory, Cornell University, Ithaca, NY 14853

³ Current Address: Biology Program, School of Science, Penn State Erie, the Behrend College, Erie, PA 16563

⁴ Institute for Plant Genomics and Biotechnology and Dept. of Horticulture, Texas A&M University, College Station, TX 77843

Aluminum toxicity is a major constraint for agriculture on acid soils, which comprise over half of the world's potentially arable lands. 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. A single major Al tolerance gene, AltSB, was mapped to the end of sorghum chromosome 3. Subsequently, high-resolution mapping allowed us to define a target region of 25 Kbp containing three ORFs. One of these ORFs (ORF7) corresponds to a member of a family of membrane transporters previously implicated in the efflux of low molecular weight solutes. The following evidence indicates that this gene corresponds to AltSB: (i) among all three ORFs, ORF7 is the only one expressed in sorghum root apices. (ii) ORF7 is expressed at high levels only in a tolerant near-isogenic line for AltSB and expression is inducible over time of exposure to Al, which is consistent with the pattern of citrate release. (iii) ORF7 expression in transgenic Arabidopsis conferred increased Al tolerance and Al-induced citrate release. Sequence scanning of the 25 Kbp region indicated that allelic effects on the phenotype are controlled by polymorphisms in regulatory regions, which primarily affect gene expression. Interestingly, a MITE insertion in the promoter region was found to be highly variable in size and correlated with Al tolerance across members of a sorghum diversity panel. The allelic basis for differences in Al tolerance is now under investigation by association analysis on a diverse sorghum core collection.