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W4 : Abiotic Stress

Joint Linkage-Association Analysis Of Aluminum Tolerance In Maize

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Aluminum (Al) toxicity is a profound limitation to crop production worldwide, reducing yields on up to 50% of potentially arable lands. Breeding for Al tolerance and agronomic practices aimed at ameliorating soil acidity have historically been productive avenues for improved crop production. However, it is widely recognized that additional improvements in crop Al tolerance will depend on biotechnology. We undertook an experimental plan integrating statistical genetic, genomic and proteomic approaches, building upon our previous work on the genetic and physiological bases for Al tolerance in maize. We identified 6 Al tolerance QTL in the Intermated B73 x Mo17 (IBM) recombinant inbred population, which together explain nearly 65% of the variance observed. Al exclusion from the root tip correlates highly with Al tolerance as estimated by root growth. We used microarray analysis to characterize the root tip transcriptome, together with a limited use of proteomics to validate the gene expression work. The results of the microarray experiments have been analyzed with respect to the physical and genetic maps of maize and in a comparative sense with the rice genome. Based on all of these experiments, we selected candidate Al tolerance genes to evaluate using association analysis. We identified several single nucleotide polymorphisms in multiple genes that are associated with Al tolerance. The significance of these results and of this approach will be discussed. NSF Plant Genome Award DBI #0419435, a CGIAR Generation Challenge grant, a McKnight Foundation Collaborative Crop Research Program and USDA-ARS base funds support this work.