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Molecular and Physiological Analysis of Aluminum Tolerance in Maize Recombinant Inbreds

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Abstract

Aluminum (Al) toxicity is a major constraint for crop production on acid, Al toxic soils, that occupy over 50% of the potentially arable lands in the world. Aluminum is ubiquitous in soils and when solubilized at pH values below 5.0, becomes highly phytotoxic as Al3+, causing severe yield reduction to sensitive crops. Al tolerance in species such as wheat, barley and sorghum appears to rely largely on a small number of genes within each species. However, quantitative inheritance for Al tolerance appears to be the general pattern observed in rice and maize. In maize, citrate exudation has been suggested as an important tolerance mechanism. However, lack of correlation between citrate exudation and differential Al tolerance observed in some maize lines suggests that other Al tolerance mechanisms may take place in maize. In this study, we undertook a physiological study of Al tolerance mechanisms focusing on citrate exudation in selected maize recombinant inbred lines for which a QTL map had been previously developed. Our results are being assessed in light of the genetic constitution of these RILs for the major Al tolerance QTLs segregating in the population. Our results support the role of citrate exudation as a major Al tolerance mechanism in maize but suggest that other mechanisms probably take place in this population.

One of the most important factors limiting agriculture in developing countries involves the large areas of acid soils found therein. On acid soils, toxic levels of aluminum (Al) ions are released into soil solution, where they damage roots and impair their growth and function. This results in reduced nutrient and water uptake, with concomitant reductions in crop yield, thus representing a food security problem worldwide. Al tolerance in sorghum has been reported to be conferred by a single, major Al tolerance gene, *Alt*$_{SB}$ (Magalhaes et al. 2004). In addition, the genetics of Al tolerance in members of the Triticeae tribe as wheat, barley and rye also appears to be rather simple, with one or a few loci controlling the trait (Kochian et al. 2004). Our group has recently cloned, via high resolution mapping, a major aluminum tolerance gene in sorghum (Magalhaes et al. 2007). This gene, *Alt*$_{SB}$, encodes the root citrate efflux transporter that underlies an important physiological mechanism of sorghum aluminum tolerance based on Al exclusion from sensitive sites in the root apex. In wheat, the *ALMT-1* gene was cloned and characterized as a member of a new family of membrane proteins (Sasaki et al. 2004), which is likely to correspond to the major Al tolerance locus, *Alt*$_{BH}$.

Al tolerance in maize has been reported as a quantitative trait (Ninamango-Cárdenas et al. 2003) but the physiological basis underlying maize Al tolerance QTLs is largely unknown. The physiological mechanism underlying Al tolerance in maize has been suggested to involve citrate release into the rhizosphere (Pellet et al. 1995). However, more recently, Piñeros et al. (2005) investigating a broader range of maize lines suggested that multiple Al tolerance mechanisms may be taking place in maize.

Here we undertook an integrated genetic/physiological approach to get insights into the role of organic acid exudation in providing Al tolerance in maize. For that we used selected members of the recombinant inbred line population used in the QTL mapping study by Ninamango-Cárdenas et al. (2003) for which the reaction to Al toxicity was known. Al-tolerance as measured by Al inhibition of root growth, Al accumulation in root apices, root tip and bulk solution organic acid exudation were assessed in the parents and the selected RILs. These results are being analyzed jointly with the graphical genotypes for the selected RILs for the major Al tolerance QTLs identified in the mapping study. Our results support the role of citrate exudation as a major Al tolerance mechanism in maize but suggest that other mechanisms probably take place in this population.

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