SEQUENCING OF GENES EXPRESSED IN THE ROOT APEX OF AN ALUMINUM TOLERANT MAIZE LINE CULTIVATED UNDER ALUMINUM STRESS

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Tropical savanna soils are usually characterized as having low fertility, low pH and high levels of toxic aluminum. The latter has been identified as one of the main factors limiting food production in the tropics. Despite a large amount of research in this area, the physiological, biochemical and molecular mechanisms involved in AI tolerance in maize (Zea mays L.) are far from being completely elucidated. Lately, however, high throughput DNA sequencing has turned out to be one of the major strategies to identify genes related to different biological processes. In order to study the molecular basis of the aluminum tolerance in maize we have utilized this approach to identify genes expressed in the root apex of two Al-tolerant maize lines. cDNAs were prepared from plants grown for either 4 or 24 hours in a complete nutrient solution with pH 4.2 containing 222 ?M AlCl₃. They were cloned and sequenced in an ABI 3100 DNA Sequencer (Applied Biosystems). Based on homology, 2400 cDNA clones were compared to sequences deposited in the NCBI GenBank, representing 500 expressed genes that were categorized as involved in signal transduction, membrane transport and stress-tolerance mechanisms. Functionally, some of these genes were related to biotic stresses such as resistance to nematode infestation and abiotic stresses such as oxidative, chemical, drought and heavy metal. From these data, more than 20 genes have been selected for further functional analysis. These genes may be useful to elucidate the mechanisms of aluminum tolerance in maize and to carry out functional genomics in maize.

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