

Topic: **Sequence Analysis**  
PI: SA04

## ALUMINUM-INDUCED GENES IN GRASS SPECIES

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The toxicity caused by aluminum (Al), intrinsic to acid soils, influences negatively the stability of crop production. Under toxic levels of Al, plant roots paralyze their development and become unable to explore the deeper layers of the soil, affecting nutrient and water acquisition and reducing crop yield. This study aimed to identify genes associated with Al tolerance mechanisms in grasses, using cDNA and subtractive libraries derived from roots of maize, rice, sorghum, oat, barley, wheat and brachiaria tolerant genotypes submitted to critical levels of Al in nutrient solution. We analyzed 5,304 sequences, of which 3,869 were considered of good quality (Phred score: 13 and minimum number of bases: 70). Additionally, 391 sequences without quality scores that showed similarities in BLASTn against public database sequences were added to the clustering process. A total of 4,260 quality sequences were clustered with CAP3, generating 567 contigs and 1,009 singletons. The contigs ranged from 2 to 92 sequences. BLAST2GO was used to determine the putative roles and ontologies of the sequences combining results from BLAST, InterProScan, Gene Ontology (GO), and KEGG metabolic pathways. Out of the 1,576 unique sequences (contigs + singletons), 953 received GO terms by BLAST2GO annotation. Al tolerance mechanisms are divided into two main types: (1) exclusion, which prevent the Al uptake into the cell; and (2) simplastic, that immobilize or neutralize the Al in specific locations inside the cells. Therefore, we focus our initial search in sequences associated with transport, biotic and abiotic stress, and membrane components. Next we searched for sequences related to organic acids compounds such as malate, citrate and oxalate. The “transport” term appears under GO terms in 113 unique sequences, “membrane” in 335, and “stress” in 45, while the combination of “transport and membrane” were found in 82, “membrane and stress” in 19, “transport and stress” in nine, and “stress, transport and membrane” in four. For organic compounds, “malate” appears under GO terms in four unique sequences, “citrate” in three and “oxalate” does not appear. Using KEGG, 12 sequences showed similarity with nine enzymes of the TCA cycle. A large number of genes were induced under Al stress in grass roots, including genes commonly found in other abiotic stresses. This strategy will allow us to identify Al tolerance mechanisms common to several grass species.

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