

PROSPECTION OF GENES ASSOCIATED WITH ALUMINUM TOLERANCE IN GRASS SPECIES.

Geraldo Magela de Almeida Cancado¹, MAURICIO ANTONIO LOPES¹,
Newton Portilho Carneiro¹, Aluizio Borem Oliveira²

¹ Embrapa Maize and Sorghum, Rod. MG 424 Km 65, C.P. 151 35.701-970 - Sete Lagoas (MG), Brazil

² Federal University of Vicosa - Av P.H. Rolfs S/N Campus Universitario - Vicosa (MG), Brazil

The area of savanna in Brazil extend over 200 million ha, exhibiting high levels of aluminum that affect negatively many physiological, biochemical and metabolic processes in plants. In general, the Al tolerance trait is dominant and polygenic in plants. The development of molecular techniques allowed the study of individual components of quantitative traits, turning them into single units considered under the Mendelian concepts of segregation. Therefore, molecular markers have a great potential as assistant tools in breeding programs. In this work, RFLP technique was used as a tool to search for regions in the genomes of grass species that could be homologous to genes that have shown an altered expression after exposure to Al. The Al-tolerant maize genotypes used were the open-pollination variety CMS36 and the double-hybrid AG5011; as Al-sensitive genotypes, the endogamic lines L53 and L19, as well as the single-hybrid HS36x723 were used. Lines from other species were also investigated such as the sorghum BR007 and SC283 from EMBRAPA, the rice cultivar 'Urucuia', the wheat cultivar EMBRAPA 21, *Melinis minutiflora*, *Brachiaria decumbens*, *Pennisetum glaucum*, and *Imperata brasiliensis*. The probes used in this study were cDNAs obtained from isolated mRNAs, which had their levels of synthesis in the plant altered by the presence of Al. The results confirmed the existence of similar sequences in most, but not all genomes of the species investigated. The group of probes that rendered hybridization results were 1,3- β -glucanase, *wali3* and *wali5* (from wheat); pEARL1 5 and BCB (from *Arabidopsis thaliana*); and *csu359* (from maize), which yielded hybridizing signals for all samples analyzed. Further studies are now required to evaluate a possible variation in the expression of those genes under distinct conditions of Al-stress, if one intends to use them as assistant tools for breeding programs toward increased tolerance to Al toxicity. Supported by: CNPq, FINEP/PADCT, FAPEMIG and EMBRAPA