SEARCHING RFLP MARKERS TO IDENTIFY GENES FOR ALUMINUM TOLERANCE IN MAIZE.[1] Giovana A. Torres[2], Paulo Roberto Martins[3], Maurício A. Lopes[4], Sidney N. Parentoni[4] and Edilson Paiva[4*]. [2]Graduate student, Departamento de Biologia, Universidade Federal de Lavras, Caixa Postal 37, CEP 37200-000, Lavras - MG, Brasil. [3]Trainee with schorlarship, from RHAE/CNPq. [4]Researchers from CNPMS/EMBRAPA, Caixa Postal 151, CEP 35701-970, Sete Lagoas - Mg, Brasil.

The objective of this study is to identify RFLP markers linked to QTLs that control Al tolerance in maize. The genetic material utilized consists of an F_2 population derived from a cross between the Al-susceptible line L53 and Al-tolerant line L1327. Both lines have been developed by the maize breeding program of the National Maize and Sorghum Research Center - CNPMS/EMBRAPA. The strategy used was Bulked Segregant Analysis (BSA), which is based on choosing homozygous F_2 individuals for bulking. The index Relative Seminal Root Length (RSRL) was used as the phenotypic measure of Al tolerance. The frequency distribution of RSRL of the F_2 population showed continuous distribution for RSRL, with skewing towards Al-susceptible individuals. The estimated heritability for the trait $[(\sigma^2_{F2} - \sigma^2_E)/ \sigma^2_{F2}]$ was found to be 60%. This moderately high heritability value suggests that although the character is of quantitative nature, it may be controlled by a small number of genes. Seedlings of the F_2 population which scored the highest and the lowest values for RSRL were subsequently selfed to obtain F_3 families. These families were evaluated in nutrient solution to identify the ones that weren't segregating. Based on the average and the genetic variance of these families, 5 individuals were chosen for each bulk. One hundred thirteen probes were selected at an average interval of 30 cM covering all the ten maize chromosomes. DNA was digested with Eco RI, Bam HI and HindIII. For hybridization, a nonradioactive labeling system, using dig-dUTP and alkaline phosphatase, proved to be quite efficient and reliable, resulting in Southern blots with good resolution and allowing the membranes to be stripped and reprobed at least three times. Forty six markers showed codominant effect identifying 56 RFLP loci, that could distinguish the parental lines. These 46 probes were hybridized with DNA from the two contrasting bulks. Three RFLPs went identifed at chromosome 8 that could distinguish the bulks. The linkage is being confirmed by segregation analysis in the F_2 population. Other informative markers are being searched in order to increase genome coverage and saturate the regions probably linked to the QTLs.

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