USE OF RFLPs TO IDENTIFY GENES FOR ALUMINUM TOLERANCE IN MAIZE. Giovana A. Torres[1]; Maurício A. Lopes[2]; Sidney N. Parentoni[2] and Edilson Paiva[2]. 1)Depto. de Biologia - UFLA, Lavras, MG, 2) CNPMS/EMBRAPA, CP 151, 35701-970 , Sete Lagoas - MG.

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 showed continuos 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. Ninety two 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 our hybridization work, 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. Thirty three markers showed codominant effect identifying 56 RFLP loci, that could distinguish the parental lines. These 33 probes were hybridized with DNA from the two contrasting bulks. We identified three RFLPs (two at chrom. 8 and one at the chrom. 2) that could distinguish the bulks. The linkage will be confirmed by segregation analysis in the F_2 population. Also, other informative markers are being searched in order to increase genome coverage and saturate the regions probably linked to the QTLs.

Financial support: CNPMS, FAPEMIG, IAEA.

ESTUDO DA VARIABILIDADE GENÉTICA ENTRE CULTIVARES DE SORGO (*Sorghum bicolor* (L.) Moench) ATRAVÉS DE MARCADORES MOLECULARES RAPD. Maria José Vilaça de Vasconcelos[1] e Fredolino Giacomini dos Santos[1] 1) CNPMS, Caixa postal 151, 35701-970 - Sete Lagoas (MG).

Nos programas de melhoramento genético usam-se análises fenotípicas para evidenciar variabilidade genética entre indivíduos. Nos últimos anos têm-se utilizado marcadores como Isoenzimas, RFLP e Microssatélites para estudar a distância genética entre cultivares de várias espécies vegetais. Neste trabalho propõe-se o uso de marcadores moleculares do tipo RAPD ("Random Amplified Polymorphic DNA") como potente ferramenta na caracterização de linhagens e de potenciais progenitores em programa de melhoramento de Sorgo. Foram selecionados pelo programa de melhoramento de sorgo do CNPMS 20 materiais para um estudo inicial. O DNA total de folhas desses materiais foi purificado e amplificado utilizando-se iniciadores de sequência aleatória, onde as reações de amplificação consistiram de 40 ciclos de desnaturação a 94° C por 15 seg, pareamento a 35° C por 30 seg e alongamento a 72° C por 1min e uma etapa de 7 min a 72° C para o alongamento final. Todos os iniciadores utilizados geraram pelo menos uma banda polimórfica. Os dados obtidos foram utilizados para a determinação da distância genética entre os genótipos, sua separação em grupos ("clusters") e em análise multivariada.

Apoio Financeiro: EMBRAPA