

USE OF RFLPs TO IDENTIFY GENES FOR ALUMINUM TOLERANCE IN MAIZE.

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The genetic material utilized consists of an F₂ population derived from a cross between the Al-susceptible line L53 and Al-tolerant line L1327. The strategy used was Bulk Segregant Analysis (BSA). The index Relative Seminal Root Length (RSRL) was used as the phenotypic measure of Al tolerance. Seedlings of the F₂ population which scored the highest and the lowest values for RSRL were subsequently selfed to obtain F₃ 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, extreme individuals were chosen to build Al-tolerant and Al-susceptible bulks. One hundred and twenty probes were selected at an average interval of 30 cM covering all the ten maize chromosomes. DNA from L53, L1327 and F₁ was digested with Eco RI, Bam HI and HindIII. Forty seven markers showed codominant effect identifying 73 RFLP loci, that could distinguish the parental lines. These 47 probes were hybridized with DNA from the two contrasting bulks. The ones that were able to distinguish the bulks were then probed with DNA from each individual of the two bulks. We identified three RFLPs at chrom. 8 that could distinguish the bulks.

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