



MARKER-ASSISTED INTROGRESSION OF *ZmMATE1* GENE TO IMPROVE ALUMINUM TOLERANCE IN MAIZE ELITE LINES

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Key words: Marker-assisted breeding, Al toxicity, maize

Aluminum (Al) toxicity is one of the major limiting factor to crop yield in acid soils, which comprise over 50% of the global arable lands. The toxic forms of Al present in the soil solution limits root development and its ability to uptake water and nutrient. Al tolerance is a quantitative inherited trait in maize, but we mapped a major Al tolerance QTL on chromosome 6, which is controlled by the *ZmMATE1*. This gene encodes a citrate transporter and is induced by Al in the root apices of tolerant genotypes. The introgression of this QTL, and consequently the *ZmMATE1*, was responsible to improve Al tolerance in an Al sensitive line (L53). In order to accelerate the marker-assisted introgression of this gene, one SNP in the promoter of *ZmMATE1* was identified and converted to KASP assay (Kompetitive Allele-Specific PCR). This simple PCR assay was able to differentiate the superior allele of *ZmMATE1*, which presents high expression in root apex under Al stress. Thus, a marker-assisted backcross (MABC) was carried out for a maize elite line that contributes with several Embrapa's commercial hybrids. The BC1 progenies were genotyped with the *ZmMATE1*-SNP marker and with 27 SNP markers randomly distributed along the maize genome, been selected one progeny heterozygous for the *ZmMATE1* and presenting 85% of the recurrent genome. The backcross cycles were followed selecting only for the *ZmMATE1* until the generation BC3F3. Thus, we expect that the maize elite line introgressed with *ZmMATE1* will present a superior yield performance under acid soils.



Supported by Fapemig, CNPq, CAPES, Embrapa and Generation CP.