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