ABSTRACT

Aluminum (Al) toxicity on acid soils adversely affects maize yields, which can be overcome by combining soil amendments with genetic tolerance. In maize, ZmMATE1 confers Al tolerance via Al-activated citrate release, whereby citrate forms non-toxic complexes with Al^{3+} in the rhizosphere. Here, we investigated Al tolerance mechanisms in maize germplasm originated from Kenya based on quantitative trait loci (QTL) mapping. Five QTLs and four epistatic interactions explained ~51% of the phenotypic variation for Al tolerance. The lack of Al tolerance QTL on chromosome 6 and the much lower expression of *ZmMATE1* in both Kenyan lines than in Cateto Al237, which donates the superior allele of *ZmMATE1*, strongly indicate that this gene does not play a significant role in Al tolerance in neither parent. In turn, maize homologs to genes previously implicated in Al tolerance in other species, *ZmNrat1*, *ZmMATE3*, *ZmWRKY* and *ZmART1*, co-localized with Al tolerance QTL and were more highly expressed in the parent that donate favorable QTL alleles. However, these candidate genes will require further studies for functional validation on maize Al tolerance. The existence of Al tolerance mechanisms independent from *ZmMATE1* suggests it is possible to develop highly Al tolerant cultivars by pyramiding complementary Al tolerance genes in maize.