

## **QTLs Associated with Aluminum Tolerance in a Kenyan Maize Population**

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Maize yield is greatly reduced by aluminum (Al) toxicity in acid soils, which comprise over 50% of the global arable lands. The toxic form of Al ( $Al^{3+}$ ) present in the soil solution limits root growth, water and nutrient uptake. The current work aimed to dissect the genetics of Al tolerance in 180  $F_{2:3}$  families derived from a cross between Kenyan maize lines contrasting for Al tolerance, 203B-14, tolerant and SCH3, sensitive. Al tolerance was evaluated using the relative net root growth (RNRG) in nutrient solution with  $\{39\} \mu M Al^{3+}$  activity. Variance analysis for RNRG revealed significant genetic variability and high heritability based on family means (97.07%). The genetic linkage map was constructed using 152 SNP markers and the multiple interval mapping was applied using QTL Cartographer 2.5. Five Al tolerance QTLs were mapped on chromosomes 1, 5, 8, 9 and 10, explaining ~50% of the phenotypic variance for RNRG, including the epistatic effects. New Al tolerance QTLs were identified on chromosomes 1 and 9, whereas the QTLs mapped on chromosomes 5, 8 and 10 were previously detected by other studies. The *ZmNrat1*, a homolog to *OsNrat1*, which encodes an  $Al^{3+}$  specific transporter involved in rice Al tolerance, was co-localized with the QTL on chromosome 5. However, no association was detected on chromosome 6, where the *ZmMATE1* underlies a large-effect Al tolerance QTL in a Brazilian population. Thus, this Kenyan maize line is likely to harbor new Al tolerance genes that can be further validated and used for breeding purposes.

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