

IDENTIFICATION OF GENOMIC REGIONS THAT CONFER ALUMINUM TOLERANCE IN MAIZE

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Abstract:

Maize is a strategic crop in Brazil and the most produced cereal in the world. Maize is used for various purposes such as human consumption, animal feed and to produce biofuels. Corn is largely cultivated in acidic soils regions where ionic aluminum (Al) causes root damage, impairing water and mineral nutrient absorption by the plant. A few genomics regions and the gene *ZmMATE1* were associated with Al tolerance in maize. In our current work, a new F2 population of 280 individuals derived from two contrasting maize line L228-3 x L53 was used to map genomic regions associated with Al tolerance phenotyped as Relative Net Root Growth (RNRG) was evaluated based on individual plant in nutrient solution with and without aluminum. The genetic map was composed by 477 mendelian SNPs (Single Nucleotide Polymorphisms) markers developed with Illumina Infinium iSelect technology and the allele-specific KASP marker for the *ZmMATE1* gene. For that, QTL mapping was undertaken in an F2 population of 280 individuals derived from the lines, L228-3 (Al tolerant) and L53 (Al sensitive). Individuals from the F2 population were phenotyped for Al tolerance in hydroponics based on Al inhibition of root growth, and genotyped with a *ZmMATE1* KASP (Kompetitive Allele-Specific PCR) marker and with 3000 SNPs (Single Nucleotide Polymorphisms) markers distributed in the maize genome. QTL mapping was performed via multiple interval mapping (MIM) using QTL Cartographer. The genetic map covered 1152.95 cM (centimorgans) along the 10 maize chromosomes and five Al tolerance QTLs were mapped on chromosomes 1, 5, 6, 7 and 9 including 3 epistatic interactions explaining 47.8% of the phenotypic variance. The most effective QTL (qALT6) was mapped on chromosome 6, explained 24.9% of the Al tolerance and co-localized with the previously described *ZmMATE1* gene. The second most effective QTL was mapped to chromosome 9 (qALT9), explaining 7.5% of the trait. Three epistatic effects among the QTLs explained from 1.9% to 2.4% of the phenotypic variance, with dominance x dominance effects, as shown in Table 2. The qALT7 showed significant interaction with two other QTLs (qALT1 and qALT6). The QTLs mapped to chromosomes 1, 5 and 9 explained the smaller effect on phenotypic variance. The QTL of chromosome 9 (qALT9), however, showed a spastatic effect with the QTL of chromosome 6 (qALT6), the QTL with the greatest effect. And the QTL of chromosome 7 is present in two epstatic iterations (qALT1 x qALT7 and qALT5 x qALT7), demonstrating the presence of possible candidate genes and also of epistatic interactions that control Al tolerance in maize. In subsequent research the genetic map will be used to identify Al tolerance genes.

Palavras-chave: abiotic stress; aluminum tolerance; *Zea mays*; QTL;