

MAPPING NEW *ZMMATE1* ALLELE AND GENOMIC REGIONS ASSOCIATED WITH ALUMINUM TOLERANCE IN MAIZE

Gabriela Stefane Barbosa Mendes¹; Marcela Baroni de Rezende Costa²; Beatriz de Almeida Barros³; Marcos de Oliveira Pinto³; Jurandir Vieira de Magalhães⁴; Cláudia Teixeira Guimarães⁴

¹. Rodovia MG 424, Km 47, CEP: 35701-970, Caixa Postal: 56, Sete Lagoas - MG. Universidade Federal de São João del-Rei ; ². Av. Antônio Carlos, 6627, Pampulha - Belo Horizonte - MG - CEP 31270-901. Universidade Federal de Minas Gerais ; ³. Rodovia MG 424 - KM 65. Caixa Postal 151. CEP: 35702-098 - Sete Lagoas - MG. EMBRAPA - milho e sorgo ; ⁴. Rodovia MG 424 - KM 65. Caixa Postal 151. CEP: 35702-098 - Sete Lagoas - MG. EMBRAPA - milho e sorgo

Abstract:

Maize is a strategic crop in Brazil and the most produced cereal in the world, being used for human food, animal feed and industrial purposes. Maize is largely cultivated under acid soils where ionic forms of aluminum (Al) damage the root system, impairing water and mineral nutrients uptake. A few genomic regions and the gene *ZmMATE1* were identified controlling Al tolerance in maize. In our current work, a new F2 population of 280 individuals derived from two contrasting maize lines L228-3 (Al tolerant) x L53 (Al sensitive), was used to map genomic regions associated with Al tolerance. The F2 individuals were phenotyped for Al tolerance in hydroponics based on the inhibition of root growth by Al and genotyped with a *ZmMATE1* KASP marker (Kompetitive Allele-Specific PCR) and with SNP markers (Single Nucleotide Polymorphisms) developed with Illumina Infinium iSelect technology. The genetic map was composed of 477 mendelian SNP markers and the allele-specific marker for the *ZmMATE1* gene, covering 1152.95 cM along the 10 maize chromosomes. QTL mapping was performed by multiple interval mapping using the QTL Cartographer. Five Al tolerance QTLs were mapped on chromosomes 1, 5, 6, 7 and 9, as well as three epistatic interactions, which explained 47.8% of the total phenotypic variation. The QTL *qALT6* was mapped on chromosome 6, explaining 24.9% of Al tolerance and co-localized with the previously described *ZmMATE1* gene. The expression pattern of *ZmMATE1* evaluated in the parental lines, revealed that this superior allele was induced by Al in the root tip of L228-3, similarly as found in the Cateto Al237. However, the presence of only one copy of *ZmMATE1* in L228-3 differed from the three copies of this gene in the Cateto Al237, suggesting that L228-3 has a new allele of *ZmMATE1* that confer Al tolerance in maize. The second Al tolerance QTL with large effect was mapped to chromosome 9 (*qALT9*), explaining 7.5% of the trait, and presented epistatic interaction with *qALT6*. This genomic region may harbor important candidate genes controlling *ZmMATE1* expression that will be target for future studies. The other QTLs presented minor effects, epistatic interactions and were mapped in new genomic regions, which can also reveal new candidate genes to improve Al tolerance in maize.

Palavras-chave: Abiotic stress; *Zea mays* L; QTL.; ;