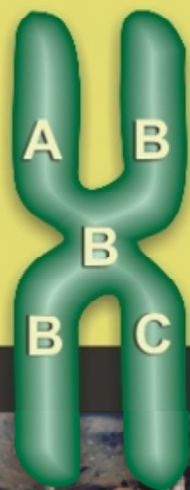


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DATA MINING AND PHYLOGENY TO SELECT CANDIDATE GENES RESPONSIBLE FOR ALUMINUM TOLERANCE IN MAIZE

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Bioinformatics is an essential tool for handling biological data and has been useful in many plant breeding applications. Aluminum toxicity on acid soils is a major factor limiting yield of many important crops such as maize. In acidic conditions ($\text{pH} \leq 5.0$) ionic forms of Al are released into the soil solution, inhibiting root growth and plant development. Recently, one Al tolerance gene was isolated in sorghum, *SbMATE*, which encodes a membrane transporter responsible for Al-activated citrate release, and is a member of the multidrug and toxic compound extrusion (MATE) family. MATE genes have also been identified in other species such as arabidopsis (*AtMATE*), rice (Os01g69010), barley (*HvMATE*) and soybean (*GmAlTsb1*), wheat (*TaMATE*) as associated with aluminum tolerance. Considering that the MATE is a multigenic family with a wide range of biological functions, our major goal was to use Bioinformatics strategies in order to select MATE genes most likely to be associated with Al tolerance in maize. A search for MATE homologs in maize was undertaken by means of sequence similarity analysis against the maize genome sequence based on *SbMATE*. BLAST searches were performed in Phytozome v. 5.0. Using the identified maize homologs as query, new searches were carried out using the tool Peptide Homologs in Phytozome in order to expand the search for MATE homologs in maize. A total of 44 MATE homologs were identified and a phylogenetic study was based on the predicted protein sequences was performed, including protein sequences of genes described in the literature as responsible for Al tolerance in other crops. The protein sequences were subjected to multiple alignments using the program T-Coffee and a neighbor-joining tree was generated based on the genetic distance matrix using the Phylemon website (<http://phylemon.bioinfo.cipf.es>). Five maize homologs were clustered with MATE genes responsible for aluminum tolerance in other species and showed similarity from 24 to 61% with the *SbMATE*. In order to improve the selection criteria, the five predicted proteins were submitted to topological analysis based on the HMMTOP program (<http://www.enzim.hu/hmmtop>). Out of them, only one member presented a unique large intracellular loop between the second and third transmembrane domains, shared among plant citrate transporters. This member is the second best hit compared with the *SbMATE*, sharing 50% of similarity, and is a citrate transporter activated by aluminum in maize root tip according to data of the literature. Then, the proposed approach identified precisely one putative Al tolerance gene in maize, named as *ZmMATE1*. Additionally, *ZmMATE1* is co-localized with a major Al tolerance QTL in maize. Thus, we showed that combining Bioinformatics tools is an important strategy to select candidate genes to be further validated.

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