

CLONING AND CHARACTERIZATION OF THE GENE EXPRESSION PROFILES OF MAIZE *PHOSPHORUS-STARVATION TOLERANCE 1* GENES

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Maize is generally considered to have a high fertility soil requirement, so the development of phosphorus-efficient maize genotypes would be beneficial in low-input agroecosystems and would improve the sustainability of high-input agroecosystems. Plants developed several mechanisms to adapt to low phosphorus (P) conditions, indicating that this is a complex trait. The main mechanism that has been implicated with increased P acquisition efficiency involves changes in root morphology. In this, the gene underlying the Pup1 locus, was identified as *Phosphorus-starvation tolerance 1 (Pstol1)*, which is responsible for enhanced early root growth, P uptake and grain yield in rice and sorghum. We performed a comprehensive QTL mapping in maize recombinant inbred line population (RIL) in nutrient solution under low-P conditions and pointed out candidate genes as maize homologs (*ZmPSTOL8.05*, *ZmPSTOL3.06*, e *ZmPSTOL8.02*) to the rice *PSTOL1* (*OsPSTOL1*) based on the co-localization with root and P efficiency traits. In the present study, we aimed to clone and verify the temporal and spatial expression of maize *Pstol1* genes in two maize lines that contrast for P efficiency, L3 – efficient and L22 – inefficient. First, we sequenced the coding region of the three candidate genes in the donor line of the allele. Then, we did an in silico analysis using ExPasy Prosite software to predict protein domains. All three proteins have, as *OsPSTOL1*, a serine/threonine kinase domain, an active site of ATP and serine/threonine predicted active site. Temporal expression revealed that all genes start to express, in nutrient solution, at 7 days after germination (DAG) and had their peak of expression at 17 DAG. Based on this information we harvested different root parts (primary, lateral, non-embryonic seminal, embryonic seminal, crown) of L3 and L22 grown in nutrient solution at 17 DAG. These results showed that *ZmPSTOL8.05* and *ZmPSTOL8.02* were more expressed in all root types of L22 line and *ZmPSTOL3.06* was more expressed in L3 primary root. Receptor-like kinases comprise the largest family of receptors in plants and the diverse structures in the receptor domains suggest that there are likely to be several biological functions for these proteins.

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