

## Spatial and temporal gene expression of *ZmPSTOL1* genes in maize

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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 context, *Phosphorus-starvation tolerance 1 (Pstol1)* was identified as the gene underlying the *Pup1* locus, which encodes a protein kinase responsible for enhanced early root growth, P uptake and, consequently, grain yield in rice. Recently, we performed 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 (*ZmPSTOL1*, *ZmPSTOL4*, e *ZmPSTOL6*) to the rice *PSTOL1 (OsPSTOL1)* based on QTL co-localization with root and P efficiency traits. In the present study, we aimed to verify the spatial and temporal gene expression of these maize *Pstol1* homologs in two P contrasting maize genotypes (L3 – efficient and L22 – inefficient). Gene expression was determined through quantitative PCR (qPCR-RT) using TaqMan assays in adult plant grown in pots with soil at the greenhouse and plantlets grown in nutrient solution (low P – 2,5 µM) in a paper pouch system. First, the expression profile of the candidate genes was assessed in different maize tissues (inflorescence, leaves, stem, seeds and roots) that were harvest during flowering, revealing that *ZmPSTOL1* and *ZmPSTOL6* were more expressed in roots and inflorescence of the inefficient line (L22) while *ZmPSTOL4* was more expressed in these same tissues but of the efficient line (L3). 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. 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 *ZmPSTOL1* and *ZmPSTOL6* were more expressed in all root types of L22 line and *ZmPSTOL4* was more expressed in L3 primary root. These results shed a light on the illusive *Pstol1* pathway; however, further functional studies are required to comprehend the actual pathway leading to root system modulation by *Pstol1*.

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