



Analysis of Phosphorus-Starvation Tolerance 1 *cis*-acting regulatory DNA elements from rice, maize and sorghum

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Low soil phosphorus (P) availability is a major constraint for crop production in tropical regions and changes in root morphology are key strategies for plants to enhance P acquisition. Phosphorus-Starvation Tolerance 1 (*OsPstol1*) is a gene responsible to enhance root surface, P acquisition and grain yield in rice under P deficiency. Multiple *Pstol1* homologs in sorghum also play a role in the root morphology and architecture, leading to grain yield gain under low P availability. In maize, candidate genes were pointed out as *Pstol1* homologs based on Quantitative Trait Loci co-localization with root and P efficiency traits and gene expression. In the present study, we aimed to identify *in silico* the non-coding region of *Pstol1* gene from rice and their homologs in maize and sorghum. The upstream region (-1 to -2039 pb) was analyzed using SIGNALSCAN program provided by NEW PLACE database in order to identify their *cis*-regulatory elements (CREs). Using this approach, 175 types of CRE were identified and 29 CREs were common among the three species. Some of these CREs such as ARR1AT, CAATBOX1, CACTFTPPCA1, DOFCOREZM and WRK710S elements were also identified in all rice Phosphate Transporter genes. These elements have between 6 and 39 duplications in each *cis*-regulatory sequence. In addition, each *Pstol1* gene has typical CREs that can only be found in the respective genes. These results shed light on the elusive path of signaling *Pstol1*; however, more studies are required to comprehend the pathway leading to the activation of *Pstol1* genes.

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