

MAIZE PHOPHORUS-STARVATION TOLERANCE 1 (ZmPSTOL1_3.06) GENE IS RELATED TO ROOT HAIR FORMATION AND PHOSPHORUS STARVATION

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Phosphorus (P) is an essential macronutrient, however tropical soils are deficient in readily available forms of P, which limits cereal production. A multiple interval QTL mapping in a maize recombinant inbred line population derived from a bi-parental cross between contrasting lines for P-efficiency revealed maize homologs to *Phosphorus-Starvation Tolerance 1* (*OsPstol1*) that enhances root surface area, P acquisition and grain yield under P deficiency in rice. Of these candidate genes, *ZmPSTOL1_3.06* co-localized with QTLs for root morphology, biomass accumulation and/or P content on chromosome 3 and is highly expressed in the root of L3 maize line, the donor line of the favorable QTL allele. To gain insights on the role of *Phosphorus-Starvation Tolerance 1* in maize roots we cloned and characterized the transcriptional control of the *ZmPSTOL1_3.06* gene. *ZmPSTOL1_3.06* was more expressed in L3 primary root, especially at the differentiation zone. We verified the expression of *ZmPstol3.06* in 77 genotypes from a maize diversity panel genotyped with over 300,000 GBS based-SNPs and in order to detect possible genomic regions related to *ZmPstol3.06* expression we performed an eGWAS analysis. We found an extend gene expression variation within the genotypes. The most significant SNP (Single Nucleotide Polymorphism) associated with *ZmPstol3.06* expression in the GWAS (Genome Wide Association Studies) was the closest to the target gene, indicating that the variation in this gene expression was mainly controlled by cis elements. Furthermore, sequencing around 2 Kb of L3 and L22 promoter region revealed an insertion of a MITE transposon (*PIF/Harbinger*) in the promoter of L22 line around -800 bp, which probably disrupted the *ZmPstol3.06* expression in the inefficient genotype. Cis-regulatory elements (CREs) related to phosphorus deficiency and root hairs were found in this region using Genomatix MatInspector software. To confirm the region responsible for transcriptional regulation of *ZmPstol3.06*, 2,282 Kb upstream of ATG from L3 line was isolated and cloned on pTF102 vector with *Gus* as a reporter gene for permanent expression assays. *GUS* activity driven by the *ZmPSTOL1_3.06* promoter was higher under low P, corroborating with expression analysis. *Histochemical* staining of the transgenic plants showed that *GUS* was specifically expressed in maize root hairs. It is interesting to notice that L3 presented longer and denser root hairs than L22. We speculate that *ZmPSTOL1_3.06* is related to root hair formation and adaptation to the low-P environment.

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