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GWAS of a maize *Phosphorus-Starvation Tolerance 1* homolog expression in a tropical diverse panel

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Maize is one of the most cultivated crops in the world and low phosphorus (P) availability is a major constraint for its production in tropical regions. Changes in root morphology are key strategies for plants to enhance P acquisition. Recently, our group performed a multiple interval QTL mapping in a maize recombinant inbred line population derived from a bi-parental cross of lines L3 and L22, P-efficient and inefficient, respectively, under low-P condition. The QTL mapping revealed candidate genes as maize homologs to *Phosphorus-Starvation Tolerance 1* (*Pstol1*) that is a gene responsible to enhance root surface, P acquisition and grain yield in rice under P deficiency. One of the candidates is the *ZmPstol3.06* that co-localizes with multiple root morphology traits and is more expressed in the root of the efficient genotype (L3) which contributes with positive alleles for root:shoot ratio QTL. In the present study, we aimed to characterize *ZmPstol3.06* expression in maize. 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. The expression data, eGWAS results and promoter sequence corroborate with a higher expression of the *ZmPstol3.06* gene in the efficient genotype. Further studies are required to comprehend the regulation of ZmPstol homologs in the maize root system.

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