

# Comprehensive analysis of regulatory elements of maize *Phosphorus-Starvation Tolerance 1*

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Palavra-chave: Keywords: Root, Nutrient solution, gene expression.

Cereal production on a significant fraction of the soils in developing countries is limited by phosphorus (P) deficiency due to P fixation in the soil as well as low levels of total P. Modifications in root morphology are important strategies to maximize soil exploitation under P starvation in plants. 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 *ZmPstol8.02* that co-localizes root length, root surface area, root:shoot ration and P content and was highly expressed in roots of L22, the donor line of the favorable QTL alleles. In the present study, we aimed to characterize *ZmPstol8.02* regulatory cis-elements of the promoter region. The upstream region (-1 to -2039 bp) was analyzed using SIGNALSCAN program provided by NEW PLACE database in order to identify their *cis*-regulatory elements (CREs). Using this approach, we found 450 and 444 CREs in the promoter of L3 and L22, respectively. Five CREs were found in a larger number in L3. One of them is an ABRE-related sequence, a key component of *Mem1* (Mesophyll expression module 1). Another key component of *Mem 1*, CACTFTPPCA1, was the most frequent element in both lines, and the other three elements are RY repeats. All elements that were found in a higher number in L3 are related to abscisic acid (ABA) that regulates many aspects of plant growth and development, including inhibition of root elongation. In order to validate the promoter region and better comprehend its regulation; we cloned around 2 Kb of L3 and L22 promoter region in pTF102 using *Bar* gene as a selective marker and *Gus* as a reporter. Maize HiII plants were genetically transformed via *Agrobacterium tumefaciens* EHA101 strain and regenerated from selected callus in shooting and rooting medium. Fragments of the *Bar* gene (~400 bp) and *Gus* gene (~700 bp) were amplified by PCR, confirming integration of the cassettes in the transformed plants. Currently putative transgenic maize plants harboring the different genetic cassettes are in the greenhouse and are going to be used for molecular and functional analysis.

Fonte de financiamento: Embrapa, CNPq and Fapemig