Resumos do GENÉTICA 2016 - 62º Congresso Brasileiro de Genética • 11 a 14 de setembro de 2016
Hotel Glória • Caxambu • MG • Brasil
www.sbg.org.br - ISBN 978-85-89109-06-2

Functional characterization of *PHOSPHORUS STARVATION TOLERANCE1 genes in sorghum (SbPSTOL1)*

Maciel, LS[1,2]; Barros, BA[2]; Damasceno, CMB[2]; de Sousa, SM[2]; Guimarães, CT[2]; Magalhães, JV[2]

[1] Departamento de Biologia Geral do Instituto de Ciências Biológicas, UFMG; [2] Embrapa Milho e Sorgo, Rod. MG 424, Km 45 - Sete Lagoas, MG

laianesm@gmail.com

Keywords: Abiotic stress tolerance, genetic functional, PSTOL1, WAKL, sorghum

Low phosphorus (P) availability on tropical soils is one of the major limiting factors for agricultural production. Phosphorus starvation tolerance 1 (PSTOL) genes in rice (*OsPSTOL1)* and sorghum (*SbPSTOL1)* were associated with enhanced P acquisition and grain yield under low P availability. Here we show the structure of these genes and their predicted protein architecture, in addition to the *SbPSTOL1* expression profile under low P. Roots were collected from the sorghum line BR007 after 13 days in nutrient solution with low P (2.5 uM P). Total RNA was isolated and full-length cDNAs were obtained using rapid amplification of cDNA ends (RACE) for the following *SbPSTOL1 genes:* Sb07g002840, Sb03g031670, Sb03g031690, and Sb03g006765. An *in silico* analysis of conserved domains performed with the Pfam (http://pfam.xfam.org/) and SMART (http://smart.embl-heidelberg.de/) tools indicated that the kinase cytoplasmic domain is conserved among OsPSTOL1 and the SbPSTOL1 proteins. However the N-terminal of SbPSTOL1 proteins diverge from OsPSTOL1 by a putative extracellular domain containing a signal peptide, a cysteine-rich galacturonan_binding domain (GUB-WAK_bind), a wall-associated receptor kinase domain (WAK_assoc domain) and a transmembrane domain. Proteins with this domain architecture are commonly classified as wall-associated receptor kinase like (WAKL) proteins. WAKL proteins can interact with pectins in the cell wall and are involved in the activation of signaling pathways in response to pathogens, abiotic stress, and cell expansion. SbPSTOL1 contains the non-narginine (non-RD) kinase domain, typically found in receptors related with plant innate immune response. Phylogenetic and structural analysis showed that the SbPSTOL1 are highly similar to ZmWAKRLK from maize, which confers resistance to *Exserohilum turcicum* and represents a new class of immune receptors in monocots. Quantitative real time analysis (qRT-PCR) was carried out using six sorghum lines contrasting for root morphology. Expression analysis showed a tendency towards increased expression of *SbPSTOL1* genes under low P in lines that have higher root surface area. These results support the hypothesis that SbPSTOL1 is associated with root system modulation, consequently conferring more efficient phosphorous acquisition under low P. We are now conducting subcellular localization studies to confirm whether SbPSTOL1 interacts with the cell wall and, after that, a split ubiquitin system will be used to identify putative partners for interaction with SbPSTOL1.

Financial Support: CNPq, Fapemig and Embrapa