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Cloning and *in silico* characterization of *PHOSPHORUS STARVATION TOLERANCE1* in sorghum

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PHOSPHORUS STARVATION TOLERANCE1 (*OsPSTOL1*) was cloned in rice and enhances P acquisition and grain yield under low P by modulating early growth. In sorghum, six homologs of OsPSTOL1 were recently shown to contribute to P acquisition and grain yield under low P in sorghum via a similar root related mechanism. Here we show a comparative protein domain analysis of PSTOL1 proteins in rice and sorghum, which suggested striking feature differences between the PSTOL1 proteins. Roots were collected from the sorghum line BR007 after 13 days in nutrient solution with low P (2.5 µM P). Total RNA was isolated and complete coding cDNA sequences were obtained for Sb07g002840, Sb03g031670, Sb03g031690, and Sb07g006765 based on the *Sorghum bicolor* gene model Sbi v1.4. Protein domain predictions were carried out using Pfam (http://pfam.xfam.org/), and SMART (http://smart.embl-heidelberg.de/) tools, indicating that the kinase domain is commonly present in OsPSTOL1 and in all selected SbPSTOL1 proteins. However, distinctly different features were predicted for the SbPSTOL1 proteins, namely a signal peptide suggesting a secretory pathway, a transmembrane domain, and cell wall interaction domains (GUB_WAK_bind domain, and WAK_association domain). These features are typical of Ser/Thr wall-associated kinase (WAK) proteins. We are now using RACE-PCR to clone the full-length cDNA from these genes and efforts are also underway to verify the predicted subcellular localization and to identify potential SbPSTOL1 partners. Establishing how and where these proteins exert their biochemical activities is crucial for understanding the sorghum adaptive response to low P availability.

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