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Expression patterns of oligopeptide transporters in *arabidopsis thaliana*

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Peptide transport is a universally observed cellular mechanism employed by both prokaryotes and eukaryotes to transport peptides (2-6 residues) across cellular membranes in an energy-dependent manner. These peptides, upon internalization, are rapidly hydrolyzed into amino acids, which can be used for protein synthesis or as alternative sources of carbon and nitrogen. The OPT (Oligopeptide Transporter) family is involved in transport of tetra- and penta-peptides and was first identified in yeast. A distinct subfamily of nine putative *Arabidopsis thaliana* OPT orthologs (AtOPT1-AtOPT9) were identified by comparison to fungal OPTs. The function of OPT proteins in plant growth and development is largely unknown. One approach to help elucidate their physiological function is to determine the tissue-specific localization of each AtOPT, as well as factors that affect their expression. To accomplish this, promoter-GUS fusions of seven of the AtOPTs were utilized. The transgenic plants were stained for GUS to characterize gene expression at various stages of development, as well as under different growth conditions. Each of the AtOPT fusions exhibited similar tissue-specific expression. The AtOPTs were preferentially expressed in the vascular tissues of vegetative organs but were not expressed in root hairs and root tips. However, differential expression of the AtOPTs was observed under limiting iron conditions.