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Large-scale identification of lettuce and cucumber phloem proteins

Xiong-Yan Chen¹, Su Hwa Kim³, Chunlin Shi¹, Yeonggil Rim², Juyeon Moon¹, Jin-Hee Jung¹, Hey-Jin Kwon², Sunseon Kim², Seonok Kwon², Zee Yong Park³, Jae-Yean Kim^{1,2,*}

¹Division of Applied Life Science, Department of Molecular Biology, Plant Molecular Biology & Biotechnology Research Center, ²Environmental Biotechnology National Core Research Center, Gyeongsang National University, Jinju 660-701, Korea. ³Department of Life Science, Kwangju Institute of Science and Technology, Gwangju 500-712, Korea

Objectives

To analyze phloem proteome and to understand long distance signaling through plant phloem.

Materials and Methods

1. Material

Plant - Lattuce(*Lactuca sativa* L.), Cucumber (*Cucumis sativus*).

2. Methods:

Phloem sap was extracted from lattuce and cucumber stem.

A nano-high-performance liquid chromatography/mass spectrometry (nano-HPLC/MS) system.

Results and Discussion

The phloem of higher plants is not only a principal conduit for transporting macromolecule signals that coordinate growth and development between distant tissues and organs but also a conduit for transporting organic and inorganic nutrients from source leaves to sink organs. Phloem is composed of companion cells(CCs) and sieve elements(SEs). Protein exchange between CCs and SEs seems to be controlled tightly and selectively and a limited number of proteins found in phloem sap are capable of dilating the size exclusion limit (SEL) of PD. Here we describe a proteomic analysis of lettuce and cucumber phloem proteins. Using a nano-high-performance liquid chromatography/mass spectrometry (nano-HPLC/MS) system, we constructed a comprehensive peptide maps for lettuce and cucumber phloem proteins. In this study a total of over 600 different proteins from lettuce and cucumber phloem proteins were identified. These proteins were grouped into more than 15 categories based on their predicted functions: HSPs, eIFs, eEFs, metabolic enzymes, RNA-binding proteins, nuclear transporting proteins, protein kinases, cytoskeleton-associated proteins and protein degradation-associated proteins etc. The comprehensive analysis of them will greatly enhance our current knowledge of phloem functions and help us uncover new physiological and intercellular communication processes, coordinating nutrient allocation, defence and development in higher plants.

* Corresponding author : Jae-Yean Kim, TEL: 055-751-6253, E-mail: kimjy@gsnu.ac.kr
Zee Yong Park, TEL: 062-970-2496, E-mail: zeeyoung@gist.ac.kr