Role of PHABULOSA in *Arabidopsis* root vascular differentiation

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Over the past few decades, enormous achievement has been made in understanding the fundamental molecular mechanism underlying plant development, especially thanks to *Arabidopsis thaliana*, the most popular model organism in the research field of plant biology. *Arabidopsis*, a common thale cress native to Europe, Asia, and northwestern Africa, has a rapid life cycle and one of the smallest genomes among land plants making it useful for genomic studies. *Arabidopsis* can complete its entire life cycle within six weeks, and has five chromosomes with a genome size of 157 Mbps, whereas size of the human haploid genome, for example, reaches over three billion base pairs. It is strikingly interesting that the number of genes in *Arabidopsis* is estimated to be around 27,000 whereas around 23,000 genes are found in the human genome. Since the whole sequencing was completed in the year of 2000 by the Arabidopsis Genome Initiative, a new era in plant biology has begun with a focus on the fundamental genetic and molecular mechanisms of plant development, promising a bright future in connection to not only the evolutionary aspects but also to the potential application in agricultural studies.

The root of *Arabidopsis* has been widely used for studying tissue patterning in plants by virtue of its relatively simple structure and compatibility in genetic analysis, and this study particularly focuses on the vascular developmental aspects in the *Arabidopsis* roots in relation to PHABULOSA (PHB), a member of the class III transcription factors of the Homeodomain-Leucine Zipper family (HD-Zip III). Carlsbecker *et al.* have recently shown that endodermally produced microRNA165/166 (miR165/166) acts non-cell-autonomously to degrade mRNA of HD-Zip III transcription factors, resulting in a differential distribution of HD-Zip III transcripts in the xylem-forming procambial cells, which, in turn, determines the mutually exclusive metaxylem and protoxylem cell fates of the xylem tissue in a dosage-dependent manner.

However, up to now the direct or indirect role of the HD-Zip III transcription factors and miRNAs on determining the identity of xylem cells in the root vasculature is not yet fully explored, and this study is dedicated to enhance our knowledge of how the development and patterning of the vasculature is coordinated by the HD-Zip III transcription factors and miR165/166, and also to explore the HD-Zip III transcription factors potential downstream targets in order to better understand their elaborate working mechanism during the whole process.

Utilizing a β-estradiol inducible XVE system, this study shows that formation of metaxylem is mediated by PHB in a dosage-dependent manner in the vascular system, which suggests the direct involvement of PHB in the regulatory mechanism of cell type patterning, and analyses of loss-of-function ARGONAUTE (AGO) mutants reveal involvement of AGO1 and AGO10 in the same process, wherein AGO proteins are known to play crucial roles in microRNA regulation. Performed global transcriptome analyses could not identify potential downstream targets of HD-Zip III transcription factors due to inconsistency of data sets, and comparison with a previously published microarray data proves treatment of β-estradiol is not the source of observed discrepancy. In addition, this study suggests that phenotype of *phb-7d*, a gain-of-function of PHB mutant, could be mediated through increased level of cytokinin signaling, and it is possible that ARABIDOPSIS HISTIDINE PHOSPHOTRANSFER PROTEIN 6 (AHP6)-independent pathways in protoxylem formation exist.

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