SYMP-18

Regulation of cortical microtubule organization by mitogen-activated protein kinase phosphatase-like Gene in Arabidopsis

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One of major interests in Prof. Hashimoto's group is cortical microtubule-mediated process that control the morphological plasticity in plant. Previous studies from our and other groups have shown that a transverse cortical microtubule arrays is essential for establishment of plant axial growth. To be able to align at desirable transverse arrays, by exploiting process of disorganization and reorganization, the cortical microtubule required the actions from distinct group of regulator proteins that directly bind to the microtubule structure, designated as microtubule-associated proteins (MAPs). Several animal literatures have shown that phosphorylation or dephosphorylation affects microtubule binding affinity of MAPs therefore, microtubule dynamic or structure can be regulated. Consistent with animal findings, through identification of Arabidopsis mutants, the group of phosphatase genes that is responsible for organizing the cortical microtubule arrays has been reported, suggesting the protein phosphorylation could in fact be a recurring mechanism deployed for microtubule regulations in both plant and animal.

Propyzamide-hypersensitive1 (*phs1*) screening strategy is based on the phenotypic sensitivity upon propyzamide (microtubule-disrupting drug) treatment. At low dose of propyzamide, *phs1-1* mutant shows 1) severely reduced elongation and radial swelling of seedlings and 2) heavily fragmented cortical microtubule arrays with random distribution in the swollen cells. PHS1 encodes a novel protein similar to mitogen-activated protein kinase (MAPK) phosphatases. The *phs1-1* mutation caused R64C amino acid substitution in the putative kinase docking motif of PHS1. Transgenic plants expressing phs1-1 mutation phenocopied propyzamide hypersensitive phenotype of *phs1-1*, suggesting PHS^{R64C} act dominant negatively to disrupt microtubule function.

However, the precise mechanism of how cortical microtubule is regulated by PHS1 is still largely unknown. We have been working on isolating of the potential substrate(s) and/or interacting partner(s) of PHS1 using suppressor screening, phenotypic analysis of T-DNA insertion lines of other Arabidopsis MAPK phosphatase genes and yeast two hybrid screen strategies with the aim of understanding how protein phosphorylation affects behavior of cortical microtubule. This will ultimately provide the better picture of how plant cell shape is determined during their growth and development.