Division of Biochemistry
– Molecular Biology –

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Scope of Research

This laboratory aims at clarifying molecular bases of regulatory mechanisms for plant development, especially plant morphogenesis, with techniques of forward and reverse genetics, molecular biology, and biochemistry. Current major subjects are phospholipid signalings in cell morphogenesis, the transcriptional network for cytokinin responses, COP9 signalosome modulating signal transduction in the nuclei, and the endoreduplication cell cycle in cell differentiation.

KEYWORDS

Morphogenesis
Signal Transduction
Phospholipid
COP9 Signalosome
Cytokinin

Selected Publications

Lin, Q.; Aoyama, T., Pathways for Epidermal Cell Differentiation via the Homeobox Gene GLABRA2: Update on the Roles of the Classic Regulator, *J. Integr. Plant Biol.*, **54,** 729-737 (2012).

Aki, S.; Nakai, H.; Aoyama, T.; Oka, A.; Tsuge, T., *AtSAP130/AtSF3b-3* Function is Required for Reproduction in *Arabidopsis thaliana*, *Plant Cell Physiol.*, **52,** 1330-1339 (2011).

Taniguchi, Y. Y.; Taniguchi, M.; Tsuge, T.; Oka, A.; Aoyama, T., Involvement of *Arabidopsis thaliana* Phospholipase Dζ2 in Root Hydrotropism through the Suppression of Root Gravitropism, *Planta*, **231,** 491-497 (2010).

Kusano, H.; Testerink, C.; Vermeer, J. E. M.; Tsuge, T.; Shimada, H.; Oka, A.; Munnik, T.; Aoyama, T., The *Arabidopsis* Phosphatidylinositol Phosphate 5-kinase PIP5K3 Is a Key Regulator of Root Hair Tip Growth, *Plant Cell*, **20,** 367-380 (2008).

Menon, S.; Tsuge, T.; Dohmae, N.; Takio, K.; Wei, N., Association of SAP130/SF3b-3 with Cullin-RING Ubiquitin Ligase Complexes and Its Regulation by the COP9 Signalosome, *BMC Biochem.*, **9,** 1 (2008).

Taniguchi, M.; Sasaki, N.; Tsuge, T.; Aoyama, T.; Oka, A., ARR1 Directly Activates Cytokinin Response Genes That Encode Proteins with Diverse Regulatory Functions, *Plant Cell Physiol.*, **48,** 263-277 (2007).

Regulatory Network for Epidermal Cell Differentiation in Plants

The epidermal cells of *Arabidopsis thaliana*, including trichomes and root hairs, are excellent subjects for studies on pattern formation and morphological differentiation in plant cells. It has been revealed that the regulation of cell differentiation pattern involves cell lineage, positional cues from subepidermal tissues, and lateral inhibition between neighboring cells, and that elaborate transcriptional networks play an integrative role in the regulation. Interestingly, of such transcriptional networks, those for various epidermal tissues share a common structure consisting of transcription factor genes encoding MYB proteins, bHLH proteins, the WD40 protein TRANSPARENT TESTA GLABRA1 (TTG1), and the homeodomain leucine-zipper protein GLABRA2 (GL2) (Figure 1). In the conserved network structure, the *GL2* gene is placed furthest downstream, targeted by a transactivating complex consisting of R2R3-type MYB, bHLH, and TTG1 proteins, and negatively regulated by R3-type MYB proteins. Although *GL2* is assumed to be a bottleneck in the regulatory pathway for cell differentiation in various epidermal tissues, both its physiological outputs in cell differentiation and downstream target genes of GL2 almost remain unclear. Therefore, the total picture of the regulatory pathway for differentiation into each cell type is still obscure.

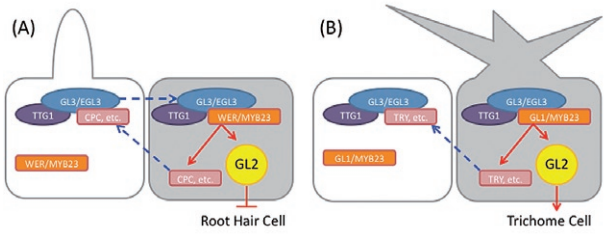

Figure 1. Regulatory Pathways for Epidermal Cell Differentiation. Pathways upstream of GL2 are schematically illustrated for hair and non-hair cells in the root epidermis (A), pavement and trichome cells in the leaf epidermis (B). Red arrows and T-bars indicate positive and negative transcriptional regulation, respectively. Blue arrows indicate protein movement between cells. Arrows with dashed lines indicate assumed regulation and movement. Cells that strongly express the *GL2* gene are shown in glay color.

To clarify the regulatory pathway for epidermal cell differentiation in plants, we are studying on the transcriptional network downstream of GL2, and have identified several its direct target genes, including a phospholipase D (PLD) gene, *PLDζ1*. PLDs are known to play roles in intracellular signal transduction via their product, phosphatidic acid (PA). Artificial down-regulation of the *PLDζ1* gene caused abnormalities in root hair cell morphogenesis. Recent studies on plant signal transduction revealed that PA signaling links to protein kinase cascades containing the 3'-phosphoinositide-dependent kinase PDK1 and AGCVIII-type kinases in plant cells. The finding suggests that AGCVIII-type kinases mediate the PA signal produced by PLDζ1 to promote root hair cell development in *Arabidopsis*. Candidate AGCVIII-type kinases include AGC2-1/OXI1 and PID, which have been reported to be involved in signals of reactive oxygen species (ROS) and the phytohormone auxin, respectively. PLDζ1-RFP fusion protein expressed using the *PLDζ1* promoter was localized to inner membrane structures in root hair cells, suggesting that PA activates PDK1 on the inner membrane (Figure 2). Downstream of *GL2*, PLDζ1 may accelerate signal transduction, including those mediated by ROS and auxin, which are involved in root hair development.

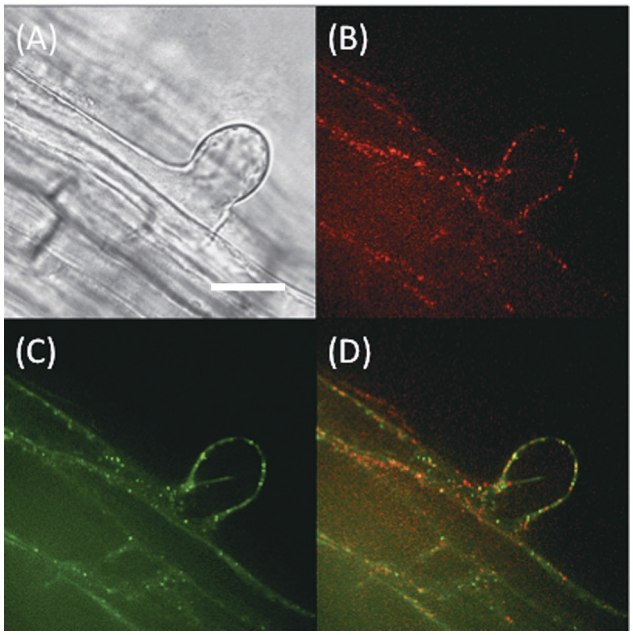

Figure 2. Intracellular Localization Pattern of PLDζ1-RFP. Fluorescence signals of PLDζ1-RFP and GFP-ARA7, an endosome marker, in a root hair cell were observed with confocal laser scanning microscopy. A bright field image (A), and fluorescence images of PLDζ1-RFP (B), GFP-ARA7 (C), and their overlay are shown. PLDζ1-RFP was partially co-localized with GFP-ARA7. Bar = 20 μm.