Division of Biochemistry
- Molecular Biology -

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Visitors

Dr MELE, Giovanni	National Research Council of Italy, Italy, 7 February–6 March 2007
Prof SCHWECHHEIMER, Claus	University of Tübingen, Germany, 12–15 April 2007
Prof von ARNIM, Albrecht G	The University of Tennessee, USA, 4–7 July 2007
Prof GU, Hongya	College of Life Science, Peking University, China, 8–15 July 2007
Prof QU, Li-Jia	College of Life Science, Peking University, China, 11–24 July 2007
Mr WANG, Wei	College of Life Science, Peking University, China, 30 July 2007–31 January 2008
Ms LI, Ruixi	College of Life Science, Peking University, China, 30 July 2007–1 March 2008
Prof PETERS, Janny L	University of Nijmegen, The Netherlands, 3–17 September 2007

Scope of Research

This laboratory aims at clarifying the framework of regulatory network between genetic programs and environmental stress responses through the study on structure-function relationships of genetic materials and cellular proteins in higher plants. The current major subjects are the two-component response regulators involved in cytokinin signaling, HD-Zip proteins and phosphatidyl-inositol 4-phosphate 5-kinases required for phospholipid signaling, COP9 signalosome modulating protein degradation, and cyclins and CDKs controlling cell cycle.

Research Activities (Year 2007)

Presentations

Regulation of the COP9 Signalosome, a Repressor of Photomorphogenesis, Tsuge T, The 1st Workshop for Young Researchers – Scientific Research on Priority Areas "Plant Movement Regulation by LOV-Domain Photoreceptors", 17–18 January 2007 (Kyoto).

ARR1 Directly Activates Cytokinin Response Genes that Encode Proteins with Diverse Regulatory Functions, Taniguchi M, Tsuge T, Aoyama T, Oka A, Trends in Plant Hormones – RIKEN Plant Science Center International Symposium, 1–2 March 2007 (Yokohama).

Identifying Novel Regulation beyond Proteolysis of the COP9 Signalosome, Tsuge T, Aki S, Taniguchi M, Dohmae N, Menon S, Pick E, Wei N, Oka A; *Arabidopsis* CSN1 Binds SAP130, a Component of the mRNA Splicing Machinery, Aki S, Oka A, Tsuge T; *Arabidopsis AtPIP5K3* Gene Controlling Root-hair Morphogenesis, Kusano H, Yasuda K, Shimada H, Oka A, Aoyama T, 2007 Ann Meeting of Jpn Soc Plant Physiol, 28–30 March 2007 (Matsuyama).

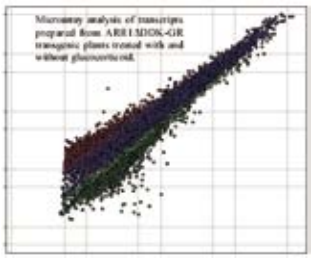
Towards Overall Architecture of Cytokinin Signaling and the Subsequent Responses

Cytokinin plays pivotal regulatory roles in plant development, including shoot regeneration from plant tissues, the release of axillary buds from apical dominance, leaf expansion, delay of senescence, vascular cell development, and the differentiation and proliferation of chloroplasts. In these processes, plant cells respond to the cytokinin signal by changing their gene expression patterns. Genome-wide analyses of *Arabidopsis* transcripts have revealed a number of genes responsive to exogenous cytokinin.

Intracellular signal transduction of cytokinin involves a histidyl-aspartyl phosphorelay among three components, *i.e.* sensor histidine kinases anchored at the plasma membrane, response regulators, and histidine-phosphotransfer (HPt)-type mediaotors. There are several paralogs with functional overlap for each component. Cytokinin triggers autophosphorylation of the histidine kinases whose phosphate is transferred to the response regulators *via* the mediators, and eventually activates the response regulators. The plant response regulators include two subtypes, type A and type B. Of 23 *Arabidopsis* response regulators (ARRs), 10 and 11 belong to types A and B, respectively. Type A ARRs lack known functional structures, except for the signal receiver domain, and constitute one clade in the phylogenic tree of plant response regulators. Exogenous cytokinin up-regulates steady-state levels of all type A transcripts examined, independent of *de novo* protein synthesis, suggesting that all type A *ARR* genes primarily respond to cytokinin. On the other hand, type B ARRs work as transcription factors. Although their gene themselves are not responsive to cytokinin, type B ARRs activate transcription of type A *ARR* genes upon cytokinin treatment.

Although molecular framework of phosphorelay signaling itself has become apparent, it is still hard to depict the overall architecture of the signal cascade leading to cytokinin-responsive phenomena in plant cells, mainly because the connections between the phosphorelay and downstream phenomena are unclear. Particularly, it is not known which of a number of genes immediately responsive to cytokinin are directly up-regulated by type B ARRs. To reveal events immediately downstream from the phosphorelay-mediated transcriptional activation, we searched for genes directly targeted by a type B ARR, ARR1, that has been most intensively studied in terms of both its molecular and biological functions [1]. Our approach used ARR1ΔDDK-GR, a chimeric transcription factor that is able to activate transcription of genes targeted by ARR1 in transgenic plants with treatment of glucocorticoid instead of cytokinin. We identified 23 such target genes, most of which were primarily responsive to cytokinin. Defect in the *ARR1* gene clearly affected the primary cytokinin response in at least 17 genes. This result imply that the majority of the genes primarily responsive to cytokinin are transactivated through the function of ARR1. The 17 genes encode proteins with diverse functions, including type A response regulators, cytokinin metabolic enzymes and putative disease resistance response proteins. The histidyl-aspartyl phosphorelay is thus connected to diverse regulatory levels of cytokinin-responsive phenomena through genes directly targeted by ARR1 and possibly its paralogs [2].

[1] Aoyama T, Oka A, *J. Plant Res.*, **116**, 221–231 (2003).
[2] Taniguchi M, Sasaki N, Tsuge T, Aoyama T, Oka A, *Plant Cell Physiol.*, **48**, 263–277 (2007).



Grants

Aoyama T, Development of Light Molecular Switch for Analyzing Intracellular Information Network, Grant-in-Aid for Exploratory Research, 1 April 2007–31 March 2009.

Tsuge T & Qu LJ, Molecular Mechanism Involved in Maintaining the Flatness of the Leaf Blade, Japan-China Scientific Cooperation Program (JSPS), 1 April 2007–31 December 2009.

Tsuge T, Novel Functions of COP9 Signalosome, the Key Signaling Component Is Conserved in both Human Carcinogenesis and Plant Photomorphogenesis, Research Grant (Research Foundation for Opto-Science and Technology), 1 April 2007–31 March 2009.

Tsuge T, Comparative Analysis of the Regulatory Mechanism Involved in Signal Transduction in Responses to Environmental Stimuli, among the Plant and Animal Kingdoms, Collaborative Research Grant (The Kyoto University Foundation), 1 April 2007–31 March 2008.

Aki S, Novel Functions of COP9 Signalosome, Plant Protein Analysis Research Project Graduate-Student-Grant (NAIST Science Research and Education Promotion Unit), 1 April 2007–31 March 2008.