## Light stimulation/Biological clock

### 334(1aG01)

RPT2: SIGNAL TRANSDUCER OF THE PHOTOTROPIC RESPONSE IN ARABIDOPSIS

Tatsuya SAKAI, Kiyotaka OKADA, Dept. Botany, Grad. Sch. Sci., Kyoto Univ., Kyoto 606-8224

The blue light receptor *NPH1* (for *nonphototropic hypocotyl1*) has been considered to be the only UV-A/blue light receptor that induces a phototropic response by the hypocotyl and root of Arabidopsis. By analysis of *root phototropism* (*rpt*) mutants, we show, however, the involvement of another blue light receptor as well as the existence of two separate signaling pathways working downstream of these receptors in the phototropic response. A newly isolated gene, *RPT2*, controls one of these pathways. The *RPT2* gene is light inducible; encodes a novel protein with putative phosphorylation sites, nuclear localization signal, a BTB/POZ domain, and a coiled-coil domain; and belongs to a large gene family that includes the recently isolated *NPH3* gene. From genetic, physiological, and biochemical evidence, we propose a genetic model of signaling pathways to induce the phototropic response in Arabidopsis.

### 335(1aG02)

Target Gene Analysis of the Transcription Factor ATHB-2

Maki Ohgishi, Atsuhiro Oka and Takashi Aoyama; Institute for Chemical Research , Kyoto University , Uji 611 , Japan

The HD-Zip-type homeobox genes of Arabidopsis are considered to be involved in signal transduction of developmental responses to environmental stimuli. Among those, *ATHB-2* has been shown to be rapidly and strongly induced by far-red-rich light, and considered to play a regulatory role in light-mediated cell growth. We constructed a chimeric gene, *HDZip2-VG*, which encodes a transcription factor consisting of the ATHB-2 DNA-binding domain, the VP16 transactivating domain, and the rat GR hormone-binding domain. Using the transgenic Arabidopsis carrying the *HDZip2-VG* genes, we are now searching genomic sequences on a micro array for gene(s) of which transcription is induced by DEX treatment .

### 336(1aG03)

ISOLATION AND CHARACTERIZATION OF SUPPRESSORS OF *cop1*

Takeshi YOSHIZUMI [1,2], Yoshiharu Y. YAMAMOTO[1], Hiroaki SHIMADA[2], Minami MATSUI[1], [1] Plant Function Exploration Team, Plant Functional Genomics Research Group, GSC, RIKEN, [2]Dept. Biol. Sci. Tech., Sci. Univ. Tokyo

Plant development is finely regulated by environmental conditions. Light is one of the important factors. Arabidopsis *cop1* mutant exhibits light-grown phenotype in darkness. This suggests that COP1 is a repressor of photomorphogenesis.

In order to identify the downstream pathway from COP1, we screened for suppressors of *cop1* mutant using an *En-I* transposon system. Five suppressor candidates have been isolated, and one of them was characterized in detail. The suppressor elongated hypocotyl in not only darkness but also in various light conditions including white light, red, far-red, and blue light. *cop1* accumulates anthocyanin and causes photobleaching after transfer to white light condition. The suppressor repressed these *cop1*-specific phenotypes.

### 337(1aG04)

**A NOVEL NUCLEAR PROTEIN, CIP4, IS A POSITIVE REGULATOR OF PHOTOMORPHOGENESIS.**

Yoshiharu Y. YAMAMOTO[1], Xing-Wang DENG[12], Minami MATSUI[1]; [1]GSC, RIKEN, [2]MCDB, Yale Univ.

*CONSTITUTIVELY PHOTOMORPHOGENIC1* (*COP1*) is a master switch for photomorphogenesis in *Arabidopsis*, and the nuclear-cytoplasmic partitioning of the COP1 protein plays an important role in light regulation of gene expression. In order to understand the function of COP1, we did far-western screening for COP1 interacting proteins. Among the isolated genes, *CIP4* encodes a novel nuclear protein. Presense of a functional transcriptional activation domain in CIP4 suggests that CIP4 is a transcriptional coactivator. A reverse genetic approach revealed that *CIP4* is actually involved in photomorphogenesis of *Arabidopsis* seedlings and that *CIP4* is a promoter of photomorphogenesis rather than repressors like *COP1*. Several lines of evidence indicate that CIP4 is a downstream factor of COP1 as another putative coactivator, CIP7. The light signals from PHYA, PHYB, and CRY1 are reported to merge at the upstream of COP1. Our results strongly suggest that the merged signal again makes a branch point just after COP1 to lead CIP4-dependent and CIP7-dependent pathways.