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ANALASIS OF INTERACTION BETWEEN TRANSCRIPTIONAL ACTIVATOR RSG CONTROLLING GA BIOSYNTHESIS AND ITS REGULATOR 14-3-3

Sarahmi ISHIDA, Jutaro FUKAZAWA, Yohsuke TAKAHASHI; Dept. Biological Sci., Grad. Sch. Sci., Univ. Tokyo

RSG is a bZIP transcriptional activator controlling shoot growth by regulation of GA biosynthesis. To understand a transcriptional network of RSG dominating shoot growth, we have sought RSG-interacting proteins by two-hybrid screen. One class of screened clones is the family of 14-3-3 proteins that are conserved among eukaryotes and regulating its ligand proteins by recognition of a phosphorylated serine residue of the target. We have demonstrated that the residue S114 of RSG plays an important role in the interaction between RSG and 14-3-3 with site-directed mutagenesis. Thus, phosphorylation of S114 of RSG seems to modulate the binding of RSG to 14-3-3. Transient trans-activation assay has suggested that 14-3-3 regulates negatively RSG because S114A mutant RSG exhibits higher transcriptional activity than wild RSG. For elucidation of the mechanism by which 14-3-3 controls RSG activity, transgenic tobaccos expressing RSG-GFP fusion protein are produced and the role of 14-3-3 in the intracellular localization of RSG is analyzed.

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FAS1, FAS2 and AtMSI1 proteins form a complex which has chromatin assembly activity *in vitro*.

Hidetaka Kaya1, Kei-ichi Shibahara2,3, Yasushi Kobayashi1, Tetsuo Meshi1, Masaki Iwabuchi1, 4, Bruce Stillman3 and Takashi Araki1

1. Dept. Bot., Grad. Sch. Sci., Kyoto Univ., 2. TOREST, JST, 3. CHSL, 4. RIBS, Okayama

We have previously shown that *Arabidopsis FAS1* and *FAS2* genes maintain organization of the shoot and root apical meristems. FAS1 and FAS2 proteins have similarity to p150 and p60 subunits, respectively, of human Chromatin Assembly Factor-1 (hCAF-1). However, biochemical activity of FAS1 and FAS2 proteins has remained to be shown. AtMSI1 protein has highest homology to the third subunit of hCAF-1, p48, among four AtMSI proteins. Based on these, we first demonstrated that FAS1, FAS2, and AtMSI1 proteins form a complex *in vitro*. Then, using two-step assay system by Shibahara and Stillman (2000), we showed that the FAS1/FAS2/AtMSI1 complex has nucleosome assembly activity on newly replicated DNA *in vitro*.

These results strongly suggest that FAS1, FAS2, and, most likely, AtMSI1 are the component of the Arabidopsis counterpart of CAF-1.

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Target Gene Analysis of Arabidopsis ATHB-1

Takuya MURAMOTO, Mayumi TSUKUDA, Atsuhiro OKA, Satoshi TABATA[1], Ida Ruberti[2], Giorgio Morelli[3], Takashi AOYAMA, Inst. Chem. Res., Kyoto Univ., [1]Kazusa DNA Res. Inst., [2]Centro di studio per gli Acidi Nucleici, Italy, [3]Unita di Nutrizione Sperimentale, Istituto Nazionale della Nutrizione, Italy

The Arabidopsis ATHB-1 is a member of HD-Zip type transcriptional factors, which contain a homeobox. followed by a leucine zipper. Although ATHB-1 is thought to be involved in leaf development, its role is not clear. Development in plants are regulated not only according to its own programmed processes but also responding to environmental stimuli. These factors are integrated to regulate the formation of plant body. To clear the role of ATHB-1 and understand the integrity of complicated factors in the plant development, we analyse the target genes of ATHB-1. In this report, we present the candidates of ATHB-1 target genes and discuss the role of ATHB-1 in plant development.

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CHARACTERIZATION OF THE HOMEOBOX GENE, *ATHB-10/GL2*

Yohei Ohashi, Atsuhiro Oka, Ida Ruberti[1], Giorgio Morelli[2], Takashi Aoyama; Institute for Chemical Research, Kyoto University, Japan. [1]Centro di studio per gli Acidi Nucleici, c/o Dipartimento di Genetica e Biologia Molecolare, Universita di Roma La Sapienza, Italy. [2]Unita di Nutrizione Sperimentale, Istituto Nazionale della Nutrizione, Italy

An *Arabidopsis* homeobox gene, *ATHB-10* has been isolated by virtue of sequence conservation within the homeobox and is known to be identical to the *GLABRA2*(*GL2*) gene. Because mutations at the *ATHB-10/GL2* locus result in aborted trichomes and ectopic root hairs, this gene is thought to regulate the trichome morphogenesis positively and the root hair formation negatively. To understand these regulations, it is important to identify target genes which are transcriptionally regulated by *ATHB-10/GL2*. So far, we have been trying to identify the target genes using GR-induction system. The result will be discussed.