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Analysis of the role of RcaE during complementary chromatic adaptation in the cyanobacterium *Fremyella diplosiphon*.

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The cyanobacterium *Fremyella diplosiphon* shows complementary chromatic adaptation (CCA). The gene *rcaE* complemented the black mutant **FdBk**. The amino-terminal half of RcaE contains a region similar to the tetrapyrrole chromophore binding domains of the phytochromes, including a cysteine (C) at position 198 that is in a similar location to the C used in phytochromes for the covalent attached of the bilin chromophore. RcaE is proposed to act as a photoreceptor controlling CCA.

We used zinc blots to examine RcaE isolated from *F. diplosiphon* for the presence of a covalently attached chromophore. RcaE covalently associates with a tetrapyrrole chromophore *in vivo*. Mutagenesis of C198 to alanine (A) results in loss of chromophore attachment.

We examined the ability of RcaE/C198A to functionally complement **FdBk**. RcaE/C198A restored CCA in red light, but not in green light. These data suggest that another, red light absorbing chromophore may be involved in regulating CCA.

RcaE was overexpressed in both *F. diplosiphon* and *E. coli*. We are currently determining the structure of the tetrapyrrole of RcaE.

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CHARACTERIZATION OF TWO NOVEL TRIHELIX PROTEINS

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GT-box binding proteins are transcription factors that have trihelix motif(s) as DNA-binding domain(s) and bind to various promoters which respond to environmental signals including light and pathogen. We have cloned two novel Arabidopsis cDNA clones encoding GT-box binding protein, GTR1 and GTR2, both of which show striking similarity to trihelix motif of AtGT-1. Both GTR1 and GTR2 are expressed in all tissues tested. Gel shift assay using recombinant proteins revealed that GTR1 and GTR2 bind to GT-boxes but their binding specificity are different from that of AtGT-1. GFP fusion of both proteins showed nuclear localization activity in onion epidermal cells. Transient assay using luciferase reporter genes suggested that GT-1 and GTR1 are involved in boxII mediated transcriptional regulation.

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TARGET GENES AND FUNCTIONAL DOMAINS OF MAIZE TRANSCRIPTION FACTOR, Dof1

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Dof proteins are plant transcription factors with a Dof DNA binding domain that recognizes an AAAG sequence (1, 2). Maize Dof1, which displayed different activities in greening and etiolated protoplasts, appeared to be a regulator of the C4-type phosphoenolpyruvate carboxylase gene expression (3). By transient expression assays with a plasmid for expression of Dof1-specific antisense RNA, I show that Dof1 also might regulate multiple light-responsive promoters of the genes that are associated with carbon metabolism. In addition, the Dof domain (46-98 a.a.) alone showed different activities in two types of protoplasts. The C-terminal region of Dof1 (175-238 a.a.) functioned as a transcriptional activation domain that was unable to be dissected further, and a basic region (120-129 a.a.) was sufficient to direct nuclear localization of a reporter protein (GFP). (1) Yanagisawa (1996) Trends Plant Sci., 1, 213-214. (2) Yanagisawa & Schmidt (1999) Plant J., 17, 209-214. (3) Yanagisawa & Sheen (1999) Plant Cell, 10, 75-89.

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DIFFERENT PHOTOREGULATION OF TWO GENES FOR PROTOCHLOROPHYLLIDE REDUCTASES IN GAMETOPHYTE OF THE LIVERWORT *Marchantia paleacea* var. *diptera*.

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A cell line of suspension culture from the liverwort *Marchantia paleacea* var. *diptera* showed high level of chlorophyll in the light but much reduced level in the dark. The expression of *por* and *chlL/N/B* encoding protochlorophyllide reductase in dark-grown cells, which had been subcultured for more than one year under heterotrophic conditions, was light-dependent.

To investigate expression pattern of these genes in parental plants, we determined transcript levels of both genes in gametophytes in the light and in the dark. 1) The level of *por* transcript was greatly reduced in the dark and recovered on transfer of dark-incubated plants to light. On the other hand, the level of *chlL* transcript was increased in the dark. 2) The same expression pattern was found in photoautotrophic cells. 3) The level of *por* transcript in photoheterotrophic cells, which had been subcultured in the light, was slightly reduced in the dark, while that of *chlL* was not changed. These facts indicate that *por* and *chlL* in gametophytes are differently photoregulated.