COP9: A New Genetic Locus Involved in Light-Regulated Development and Gene Expression in Arabidopsis

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We report here the identification and characterization of a new Arabidopsis light-regulatory locus, COP9, mutation that leads to a constitutive photomorphogenic phenotype. Dark-grown cop9 seedlings exhibit many morphological characteristics of light-grown seedlings, including short hypocotyls and open and enlarged cotyledons with cell-type and chloroplast differentiation. Furthermore, the cop9 mutation leads to high-level expression of light-inducible genes in the absence of light, probably by altering the promoter activities of these genes. These properties imply that the mutation in the COP9 locus uncouples the light/dark signals from morphogenesis and light-regulated gene expression. In addition, light-grown cop9 mutants are severely dwarfed and are unable to reach maturation and flowering. This adult-lethal phenotype indicates that the COP9 locus also plays a critical role for normal development of the light-grown plant.

Similar to cop1 mutants, but not def, the cop9 mutants show (1) no effect on the phytochrome control of seed germination and (2) deficiency in the dark-adaptive change of expression of light-regulated genes. Our results suggest that the cop9 and cop1 mutations result in the same range of phenotypes and therefore COP9 and COP1 loci may encode closely related components in the same regulatory pathway.

INTRODUCTION

Higher plants, such as Arabidopsis, are intrinsically programmed with two developmental plans: skotomorphogenesis and photomorphogenesis (for review, see Kendrick and Kronenberg, 1986). Dark-grown seedlings have long hypocotyls, apical hooks, and unopened and undeveloped cotyledons with etioplasts (skotomorphogenesis). Conversely, light-grown seedlings have short hypocotyls and opened and enlarged cotyledons with distinct chloroplast and cell-type differentiation (photomorphogenesis). At the molecular level, the expression of a group of genes, such as most photosynthesis-related genes, is significantly increased; whereas others, such as genes encoding type A phytochrome, are repressed in the light-grown plants (Kendrick and Kronenberg, 1986; Sharrock and Quail, 1989; Gilmartin et al., 1990; Bruce et al., 1991; Thompson and White, 1991). The switch between skotomorphogenesis and photomorphogenesis in early plant development is naturally triggered by light signals. It is known that the light signals are perceived by at least three types of photoreceptors in higher plants: phytochromes, blue light (UVA) receptors, and UV-B receptors (Kendrick and Kronenberg, 1986; Quail, 1991). However, the mechanisms of how the signals, once perceived, are integrated to dictate the switch between these two morphogenic pathways are just beginning to be unraveled.

Genetic approaches have been taken to identify the signaling components involved in the light-regulated development of Arabidopsis (recently reviewed by Okada and Shimura, 1992). Two general groups of mutants defective in coupling light signals with morphogenesis have been isolated. One group of mutants, such as those derived from hy and blu loci, shows dark-grown seedling characteristics (long hypocotyls) when grown under either white or blue light conditions (Koornneef et al., 1980; Chory et al., 1989b; Liscum and Hangarter, 1991). Mutants derived from several of these loci are defective in the functional photoreceptors (Chory et al., 1989b; Parks and Quail, 1991; Somers et al., 1991). The other group of mutants exhibits light-grown seedling characteristics when grown in the dark. Three such genetic loci have been described and are as follows: deetiolated-1 (DET1) (Chory et al., 1989a), DET2 (Chory et al., 1991), and constitutive photomorphogenic-1 (COP1) (Deng et al., 1991; Deng and Quail, 1992). Mutations in these three loci also lead to constitutive expression of normally light-regulated genes in dark-grown seedlings. These phenotypes suggest that these genetic loci are directly involved in coupling light perception to morphogenesis and gene expression during different stages of plant development. The recessive nature of all three mutations implies that their wild-type gene products act to repress photomorphogenic development in the absence of light.

Several interesting features distinguish these three constitutive photomorphogenic mutants from one another. First, mutations in COP1 and DET2, but not DET1, result in lack of dark-adaptive change of gene expression in light-grown adult plants. Second, cop1 mutations do not affect phytochrome

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control of seed germination, whereas det1 seeds germinate even in the absence of active phytochromes. Third, both det1 and cop1 mutations, but not det2, lead to chloroplast differentiation of dark-grown seedlings.

The COP1 gene encodes a protein with a Zn binding motif and a domain homologous to the β subunit of trimeric G-proteins (Deng et al., 1992). This novel structure suggests that the COP1 gene product not only has the potential to directly bind DNA through its Zn binding domain, it may also have the ability to interact with other protein components through its G-protein homologous domain. These interactions can be two-fold: that is, the other regulatory components could either modulate COP1 activity in response to light signals or be controlled by COP1. Depending on the nature of interaction, mutations in the genes encoding these components may give a cop1-like phenotype. To understand the molecular mechanism of COP1 function in the light signal transduction pathway, it will be necessary to identify the regulatory components that interact with COP1. Toward this goal, we report here the characterization of a new genetic locus, designated COP9, mutation that leads to the constitutive photomorphogenic phenotype which is identical to that of cop1 mutants.

RESULTS

Identification of the COP9 Locus

A new Arabidopsis mutant line, carrying a single recessive cop mutation, was isolated during our screening of new cop mutants (see Methods). Complementation tests between this new cop mutation and cop1, det1, and det2, as shown in Table 1, indicated that it was able to complement the mutant phenotype of each of the three mutations. We have further shown that this new cop mutant is also distinct from other COP loci (COP2 to COP8) thus far identified in our laboratory (Y. Hou, A.G. Arnim, and X.-W. Deng, manuscript submitted; N. Wei and X.-W. Deng, unpublished results). These results establish that the new cop mutation defines a new locus, designated as COP9. This mutant line, designated as the cop9-1 allele, is used in all of the experiments described in this report.

Homozygous cop9-1 seedlings growing in the dark exhibit many morphological characteristics normally associated with light-grown seedlings. Figure 1 shows 10-day-old dark- and light-grown cop9 seedlings (Figures 1A and 1B) as compared with 6-day-old dark- and light-grown wild-type seedlings (Figures 1C and 1D). It is obvious that dark-grown, as well as light-grown, cop9 seedlings develop opened and enlarged cotyledons and short hypocotyls. These features are typical of a light-grown wild-type seedling and are in sharp contrast to the dark-grown wild-type seedlings. Both dark- and light-grown mutant seedlings are substantially smaller in size than wild-type light-grown seedlings, and they accumulate high levels of anthocyanins as evidenced by the purple color.

Dark-Grown cop9-1 Seedlings Display Characteristics of Light-Grown Seedlings at Cellular and Subcellular Levels

Figure 2 shows cotyledon cross-sections of mutant and wild-type seedlings growing in the dark and light. The cotyledon expansion in dark-grown cop9 seedlings (Figure 2A) is similar to that of their light-grown siblings (Figure 2B) and is significantly greater than that of dark-grown wild-type (Figure 2C). Further, the overall cellular differentiation in the dark-grown mutant cotyledons, as evidenced by air space between mesophyll cells and by cell-type differentiation, is more similar to those found in cotyledons of light-grown seedlings than to those of dark-grown wild-type seedlings.

The cellular differentiation pattern of the epidermal cell layer was further examined by scanning electron microscopy, as shown in Figure 3. The dark- and light-grown (Figures 3C and 3D) cop9 mutant cotyledons have enlarged and differentiated epidermal cells of irregular shape, and mature opened stomata. These properties are similar to those found in light-grown wild-type cotyledons (Figure 3B). By contrast, the dark-grown wild-type seedlings have smaller and more regularly shaped epidermal cells and immature stomatal structures with no detectable openings (Figure 3A). Close examination of an immature stomatal structure under transmission electron microscopy (Figure 3E) revealed that there is a substantial amount of intercellular matrix between the two guard cells. A functional stomatal structure would at least require the removal of this intercellular matrix. We also noticed that the hypocotyl cells in dark-grown cop9 mutants (Figure 3F) are significantly shorter (approximately fivefold to eightfold) than those of dark-grown wild-type seedlings (Deng et al., 1992), and are slightly longer than that of light-grown mutants (Figure 3G). This suggests that lack of cellular elongation rather than cell division is primarily responsible for the short hypocotyl of dark-grown cop9-1 mutant seedlings as shown in Figures 1 and 3F.

The effect of the cop9 mutation on plastid development was examined by transmission electron microscopy. Figure 4A
Figure 1. Morphologies of Dark- and Light-Grown cop9-1 and Wild-Type Arabidopsis Seedlings.

(A) Ten-day-old dark-grown cop9-1 mutant seedling.
(B) Ten-day-old light-grown cop9-1 mutant seedling.
(C) Six-day-old dark-grown wild-type seedling.
(D) Six-day-old light-grown wild-type seedling.

The same magnification (×7.5) was used for all panels with the exception of (C), which has two-thirds (×5) of the magnification used for the others.
Figure 2. Morphogenetic Comparison of Cotyledon Cross-Sections.

(A) Cotyledon cross-section of a 9-day-old dark-grown cop9-1 mutant seedling.
(B) Cotyledon cross-section of a 9-day-old light-grown cop9-1 mutant seedling.
(C) Cotyledon cross-section of a 6-day-old dark-grown wild-type seedling.
(D) Cotyledon cross-section of a 6-day-old light-grown wild-type seedling.

Light micrographs were taken from 1-μm sections of the fixed and embedded seedlings. Bars = 0.2 mm.

shows the morphology of a typical etioplast of dark-grown wild-type seedlings. The most characteristic feature of an etioplast is the presence of a large paracrystalline assembly of tubules, termed the prolamellar body (Kirk and Tilney-Bassett, 1978).

Mature chloroplasts, as found in the cotyledons of normal light-grown seedlings, contain parallel and highly stacked membrane systems. These fully developed chloroplasts are predominant in light-grown cop9-1 mutants (Figure 4B). In the dark-grown cop9-1 mutant seedlings, most of the plastids do not have prolamellar bodies but are filled with parallel and unstacked membranes instead (Figure 4C). This morphology resembles the plastids found in the dark-grown cop1 mutants (Deng et al., 1991; Deng and Quail, 1992). Occasionally, however, a prolamellar body of significantly reduced size was observed in small fractions of plastids of dark-grown mutants (Figure 4D). These observations indicate that the chloroplast differentiation has been initiated, although not completed, in the dark-grown cop9-1 mutants.

Mutation in the COP9 Gene Results in Constitutive Expression of Light-Inducible Genes in the Dark

The expression pattern of a group of light-regulated genes in wild-type Arabidopsis seedlings changes dramatically following the switch from skotomorphogenesis to photomorphogenesis upon exposure to light. Because the cop9-1 mutation leads to photomorphogenic development in the absence of light, it was interesting to see whether it would also uncouple light signals from the regulation of gene expression. As shown in Figure 5, we examined the expression of four nuclear-encoded genes (rbcS, fedA, cab, and chs) and one plastid-encoded gene (psbA), all of which are positively regulated by light in wild-type plants (see legend to Figure 5 for explanation of abbreviations). The mRNA levels of rbcS, fedA, cab, and psbA were very low, yet detectable, in dark-grown wild-type seedlings, and elevated drastically in light-grown seedlings. In the cop9-1 mutant, however, no change in the level of expression was observed between dark- and light-grown seedlings. It appeared that the expression of cab genes in both dark- and light-grown cop9-1 seedlings is greatly repressed compared with light-grown wild-type seedlings. We have previously observed a similar suppression of cab expression in cop1 mutants. The degree of suppression seems to correlate with the severity of individual alleles (Deng et al., 1991, 1992). Because the cop9-1 mutants have a more severe phenotype (see sections below) than most of the cop1 mutations, a strong suppression of the cab mRNA levels may not be unexpected. We also noticed an abnormally higher chalcone synthase mRNA level in the mutant seedlings growing under either dark or light conditions than in wild-type seedlings. This result is consistent with the high level of anthocyanin accumulation observed in both dark- and light-grown cop9-1 seedlings (Figure 1), because chalcone synthase is the first committed enzyme in the anthocyanin biosynthetic pathway.
Figure 3. Epidermal Cell Morphology and Differentiation.

Epidermal cells were examined by scanning electron microscopy, as shown in (A), (B), (C), (D), (F), and (G), and by transmission electron microscopy, as shown in (E).

(A) Cotyledon epidermal surface of a 10-day-old dark-grown wild-type seedling.
(B) Cotyledon epidermal surface of a 10-day-old light-grown wild-type seedling.
(C) Cotyledon epidermal surface of a 10-day-old dark-grown cop9-1 seedling.
(D) Cotyledon epidermal surface of a 10-day-old light-grown cop9-1 seedling.
(E) A cross-section view of an immature stomatal structure from a 6-day-old dark-grown cop9-1 seedling. The upper side of the micrograph corresponds to the cotyledon surface. The guard cells (g) and intercellular matrix (see arrow) are shown.
(F) Ten-day-old dark-grown cop9-1 seedling: morphology of the whole seedling and its surface cells.
(G) Ten-day-old light-grown cop9-1 seedling: morphology of the whole seedling and its surface cells.

Bars = 10 μm in (A) to (E) and 200 μm in (F) and (G).
Constitutive Expression of Light-Inducible Genes Is Modulated by Promoter Activation in the Dark-Grown cop9 Mutants

Light modulates the expression of most light-regulated genes at the level of transcriptional initiation (Kuhlemeier and Chua, 1987; Quail, 1991; Thompson and White, 1991). It is likely, therefore, that the high mRNA levels of these genes observed in dark-grown cop9 mutants result from increased transcriptional activity in the dark. To test this possibility, promoter-β-glucuronidase (GUS) reporter fusion constructs, which were carried in Arabidopsis transgenic lines (Deng et al., 1991), were introduced into the cop9-1 mutant by genetic crossing. Thus, the in vivo activities of the test promoters can be determined by measuring the corresponding GUS activity.

Two light-regulated promoters (rbcS-1A and cab1) and a control promoter (the cauliflower mosaic virus [CaMV] 35S promoter) were selected for our experiments, and the results are summarized in Figure 6. The GUS activities of dark-grown cop9 seedlings were comparable to (in the case of cab1 promoter, Figure 6B), or even slightly higher than (the rbcS promoter, Figure 6A), those of light-grown mutants. In contrast, wild-type seedlings showed a dark/light increase of approximately threefold or 10-fold for rbcS or cab1 promoters, respectively. The CaMV 35S promoter was more active in dark-grown than in light-grown plants, but the dark/light ratios of
the activity were almost the same in wild-type and mutant seedlings (Figure 6C). However, much lower absolute GUS activity of the CaMV 35S promoter–GUS fusion in mutant than in wild-type seedlings was consistently observed. Such lower overall GUS activities were also noticed for cab and rbcS promoter-fusion constructs in both dark- and light-grown mutant seedlings. It implies that the suppression of GUS expression in the mutant is a general property of the mutant plants rather than a gene-specific modulation. Qualitatively, the activities of the fused promoters correlate well with the mRNA level of corresponding genes shown in Figure 5. This suggests that the elevated expression of these light-regulated genes in dark-grown cop9-1 mutants results from increased transcriptional activity of their promoters.

The cab1 promoter–GUS transgenic line used in this experiment contained a minimal light-responsive promoter (−250 to +67) (Deng et al., 1991). This promoter fragment has been shown in both transgenic tobacco (Ha and An, 1988) and Arabidopsis (Deng et al., 1991) to be sufficient for full light-regulated and tissue-specific expression. We have previously shown that this small promoter fragment contains all necessary information for mediating the response to copl mutations (Deng et al., 1991). The result shown in Figure 6B suggests that the fragment also contains sufficient information for mediating the response to the cop9-1 mutation. It is therefore probable that both the cop1 and cop9 loci modulate cab1 expression through the same promoter element.

COP9 Locus Also Plays an Essential Role during Normal Arabidopsis Development under Light Conditions

The cop9-1 mutation not only leads to a constitutive photomorphogenic phenotype in dark-grown seedlings, but also has a severe effect on light-grown adult plants. Even under optimal light conditions, plants homozygous for the cop9-1 mutation develop at most four pairs of tiny rosette leaves (rosette diameter of less than 0.5 cm) and senesce before maturation and transition to reproductive development. We have so far not observed a single mutant plant (of hundreds of cop9-1 mutants) that had a life span of more than 5 weeks and/or initiated reproductive development, such as flower bud formation or bolting. Such an adult-lethal phenotype in the light-grown cop9 plants strongly indicates that the COP9 locus plays an essential role during normal growth and development of Arabidopsis under light conditions. It is worth noting that the T-DNA insertional mutant allele (cop1-5, presumably a null allele) of the COP1 locus also leads to a similar adult-lethal phenotype (Deng et al., 1992).

It has been reported that light-grown def1 and cop1 mutant plants develop chloroplasts instead of amyloplasts in the root cells, resulting in greenish roots (Chory and Peto, 1990; Deng and Quail, 1992). We have noticed that light-grown cop9-1 plants also develop greenish roots, which are distinct from the roots of dark-grown mutant or light-grown wild-type plants (data not shown). This observation suggests that the COP9 locus is also involved in the control of tissue-specific plastid differentiation.
Phenotype of the cop9 Mutants Overlaps with That of the cop1 Mutants

All of the cop9 mutant characteristics examined thus far closely resemble those caused by the cop1 and det1 mutations. Because the det1 and cop1 mutations have different effects on two light-regulated processes, phytochrome control of seed germination and dark adaptation of light-grown plants, we further examined the effect of the cop9 mutation on these two developmental processes.

The initial seed germination process in Arabidopsis is thought to be under phytochrome control because far-red light treatment, which reduces active phytochrome, greatly reduces the germination rate of wild-type seeds and because red light, which converts the inactive phytochrome to the active form, reverses far-red light inhibition (Chory et al., 1989; Deng et al., 1991). To test the effect of the cop9-1 mutation on this phytochrome-controlled process, germination rates of cop9-1 seeds after different light treatments (Deng et al., 1991) were determined. The results showed that a 5-sec far-red light pulse reduced the rate of cop9-1 seed germination from 80 to 20%. A red light pulse following the far-red pulse reversed this effect (data not shown). Therefore, as it is for cop1 mutants, the germination of cop9-1 seeds is still under phytochrome control.

To examine whether the mutation in the COP9 locus also affects repression of light-inducible genes during the dark-adaptive process of light-grown plants, expression of representative light-regulated genes in light-grown and dark-adapted (for 2 days) wild-type and mutant plants was analyzed. As shown in Figure 7, the mRNA levels of all three genes (rbcS, fedA, and cab) examined decreased extensively upon 2-day dark adaptation in wild-type plants. In cop9-1 mutant plants, however, the expression of all three genes remained at a constant level after dark adaptation. This property of the cop9 mutants is also found in cop1 (Deng et al., 1991), but not det1 mutants (Chory et al., 1989). Note again that cab gene expression was severely suppressed in both light-grown and dark-adapted mutant plants (Figure 7, section cab).

Expression of the COP1 Gene in the cop9 Mutant

Collectively, our results establish that the cop9 and cop1 mutations have parallel phenotypes, and therefore their gene products may have closely related roles during light-regulated development of Arabidopsis. As a first step in analyzing possible interactions between COP1 and COP9 genes at the molecular level, we examined the effect of the cop9-1 mutation on the accumulation of COP1 mRNA in both dark- and light-grown seedlings. As illustrated in Figure 8, the cop9 mutation leads to approximately a threefold to fivefold increase in COP1 mRNA. However, as it is for wild-type plants, the difference in COP1 expression between light- and dark-grown mutant seedlings was very little. This suggests that the COP9 gene is involved in the suppression of COP1 gene expression in a
lings exhibit a wide variety of traits normally associated with light-grown plants, including open and enlarged cotyledons, short hypocotyls, advanced cell-type differentiation, initiation of chloroplast differentiation, and high-level expression of light-inducible genes. This phenotype implies that the mutation in the COP9 locus uncouples the perception of light signals from the commitment to the photomorphogenic program in early seedling development of Arabidopsis. In addition, light-grown cop9 plants are unable to complete their life cycle and display many abnormalities including lack of dark/light regulation of photosynthetic gene expression during dark adaptation and chloroplast differentiation in root tissue. These characteristics indicate that COP9 has a fundamental role during adult plant development as well.

Mutations in three other Arabidopsis loci that lead to a similar phenotype have been described (det1 and det2, Chory et al., 1989a, 1991; cop1, Deng et al., 1991; Deng and Quail, 1992). Phenotypic comparison of cop9 with these mutants is summarized in Table 2. Although most of the morphological characteristics of dark-grown seedlings are similar among those mutants, there are some major differences. For instance, cop1 and cop9 do not affect the phytochrome-controlled seed germination process, whereas det1 does. This suggests that the relevant phytochrome and the transduction pathway

light-independent manner, although further studies are necessary to understand its functional implication.

**DISCUSSION**

We report here the identification and characterization of a new Arabidopsis locus, COP9. A recessive mutation in the COP9 locus leads to a constitutive photomorphogenic phenotype in the absence of light. Specifically, the dark-grown cop9-1 seed-

**Figure 7.** Gel Blot Analyses of Steady State RNA Levels of Light-Inducible Genes from Light-Grown and Dark-Adapted Plants.

Wild-type (WT) or cop9-1 mutant plants were grown in continuous light for 2 weeks (L), and plants grown in the same light conditions followed by 48 hr of dark adaptation (DA) were sampled. The hybridization probes are as given in the legend to Figure 5. Equal amounts of total RNA were loaded in each lane (2 μg for rbcS, cab, and the 18S rRNA; 5 μg for fedA).

**Figure 8.** RNA Gel Blot Analysis of COPI Expression in Wild-Type and cop9-1 Mutant Seedlings.

Twelve-day-old wild-type (WT) and cop9-1 mutant seedlings grown in the dark (D) or light (L) were used for RNA extraction. Total RNA of 30 μg was loaded in each lane. The blot was hybridized with the antisense RNA riboprobe as described in Methods.
leading to this response are not affected by cop1 or cop9 mutations. Therefore, seed germination and photomorphogenesis during seedling development may involve two independent developmental commitments. Moreover, cop9, cop1, and det2 mutants, but not det1, are defective in light/dark regulation of photosynthetic gene expression in dark-adapted adult plants. This suggests that distinct signaling pathways may be responsible for photomorphogenesis of seedling development and light-dependent processes in adult plants, although both processes share common components (such as cop1 and cop9). Further, the det2 mutant does not exhibit any chloroplast differentiation in dark-grown cotyledons and light-grown root tissue as do the three other mutants. This suggests that the control of plastid differentiation and other photomorphogenic traits requires distinct sets of regulatory components.

Cop9 and cop1 are the only two photomorphogenic mutants sharing the same range of phenotypes so far examined (Table 2), suggesting that the gene products of COP9 and COP1 control the same range of physiological functions. It is therefore possible that the two gene products may be closely associated, physically as a complex or indirectly along the same signaling pathway, to control the developmental switch between photomorphogenesis and skotomorphogenesis. Several lines of evidence support this idea. First, the cop9-1 mutant not only has a phenotype identical to that of cop1 mutants (especially the T-DNA–tagged allele), but also modulates expression of the cab1 gene through the same promoter region. Second, the presence in the COP1 protein of a domain homologous to the β subunit of trimeric G-proteins in addition to a Zn binding motif (Deng et al., 1992) fits in well with the notion that COP1 may be an integral component of the molecular master switch that turns on or off the photomorphogenic pathway. Recent studies of Gβ domain–containing proteins from other systems (Frankel, 1991; Simon et al., 1991; Williams et al., 1991; Deng et al., 1992) all suggest the involvement of the G-protein domains in protein–protein interactions. It is reasonable to assume that the COP1 protein is also able to interact or complex with other protein components, and mutations in their genes would lead to the same phenotype as the cop1 mutants. The COP9 gene could encode such a COP1–interactive component that is essential for the COP1 function. Third, the increased mRNA level of the COP1 gene in the cop9-1 mutant plants would suggest that the COP9 gene product has an effect on the expression of the COP1 gene. Thus, an indirect interaction between COP1 and COP9 loci is implicated. To address the relationship between COP1 and COP9 at the molecular level, knowledge of the molecular identity of the COP9 gene will be required.

### METHODS

#### Plant Materials and Growth Conditions

The wild-type and cop9 mutants of Arabidopsis thaliana are in an ecotype Wassilewskija (WS) background. The cop9-1 mutants were recovered from screening of the Du Pont T-DNA mutagenized lines (Feldmann, 1991). Seeds from plants heterozygous for cop9-1 mutations were used in all experiments. From this heterozygous population, wild-type and mutant plants were harvested individually and pooled separately to assure the same growth conditions. For germination, seeds were surface sterilized for ~15 min in 30% bleach (Clorox), rinsed at least five times, and plated in Petri plates (100 x 25 mm) containing growth medium (GM; Valvekens et al., 1988). After cold treatment at 4°C for 7 to 10 days in the dark, the plates were incubated in a growth chamber at 22°C in complete darkness or in a cycle of 16-hr light/8-hr darkness, or in continuous light for RNA and β-glucuronidase (GUS) activity analyses. The light source for Arabidopsis plant growth was a combination of fluorescent and incandescent lights, ranging from

<table>
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<th>Wild Type</th>
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<td>Opened, enlarged</td>
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a The table is compiled from the following references: Chory et al. (1989a; det1), Chory and Peto (1990; det1), Chory et al. (1991; det2), Deng et al. (1991; cop1), Deng and Quail (1992; cop1), and this work (cop9).

b NA indicates data not available.
50 to 100 μE m⁻² sec⁻¹. In the seed germination experiments, light sources of specific wavelengths (red, far-red, green safelight) were used as described previously (Deng et al., 1991).

Light and Electron Microscopy

The fixation and embedding of Arabidopsis seedlings for light and transmission electron microscopy were performed according to a published procedure (Deng and Gruissem, 1987). The embedded material was sectioned using an ultramicrotome. The staining procedure has also been described previously (Deng et al., 1991).

For scanning electron microscopy, seedlings were fixed in 4% glutaraldehyde in 100 mM sodium phosphate buffer, pH 6.8, at room temperature for 2 hr. The seedlings were then rinsed eight times in the same buffer without glutaraldehyde and dehydrated in a graded ethanol series. Dehydrated material was then critical point dried in liquid CO₂. Individual seedlings were mounted on the stubs and sputter-coated with gold-palladium in an SPI sputter coater. Specimens were examined in an ISI SS40 scanning electron microscope.

RNA Analysis

Wild-type or cop9 seedlings grown under dark or light conditions for 10 to 12 days were used for RNA analysis. The dark-grown seedlings and dark-adapted plants were harvested under a dim green safelight. Isolation of total RNA, electrophoresis and blotting, and hybridization with radioactively labeled DNA probes were performed as described by Sharrock and Quail (1989). Hybridization probes for rbcS, fedα, cab, chs, and the 18S rRNA were made from the purified DNA fragment as described by Deng et al. (1991). Probes were labeled with ³²P-dCTP using a random priming DNA labeling kit (U.S. Biochemicals). To detect the COP1 mRNA shown in Figure 8, an antisense riboprobe corresponding to an entire COP1 cDNA clone was used following a published protocol (Deng et al., 1992).

Transgenetic Plants and GUS Activity Assay

Promoter–GUS fusion constructs and plant transformation were described by Deng et al. (1991). The transgenic lines were crossed with heterozygous cop9-1 plants. The F1 plants heterozygous for both the cop9-1 and promoter–GUS fusion were self-pollinated. The F2 seeds, which consisted of one-quarter mutant and three-quarters wild type, were used for the GUS assay. The ratio of plants carrying promoter–GUS constructs among F2 wild-type and mutant populations was determined according to Jefferson (1987) by measuring the fluorescence of 4-methylumbelliflorone produced by GUS cleavage of 4-methylumbelliferylβ-D-glucuronide. Total protein concentration was determined by the Bio-Rad protein assay according to the manufacturer's suggested procedure.

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REFERENCES


N Wei and X W Deng
Plant Cell 1992;4:1507-1518
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