

Light perception in higher plants

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Abstract. Photosynthetic plants depend on sunlight as their energy source. Thus, they need to detect the intensity, quality and direction of this critical environmental factor and to respond properly by optimizing their growth and development. Perception of light is accomplished by several photoreceptors including phytochromes, blue/ultraviolet (UV)-A and UV-B light photoreceptors. In recent years, genetic, molecular ge-

netic and cell biological approaches have significantly increased our knowledge about the structure and function of the photoreceptors, and allowed the identification of several light signal transduction components. Furthermore, this research led to fruitful interaction between different disciplines, such as molecular biology and ecology. It is safe to assume that we can expect more milestones in this research field in the upcoming years.

Key words. Phytochrome; blue light receptor; signal transduction; *Arabidopsis* mutants.

Introduction

Plants are able to detect the quality, quantity and direction of light and to use it as an external signal to optimize their growth and development. The majority of developmental processes throughout the entire life cycle of plants are influenced by light: seed germination, seedling development, sensing neighboring plants, phototropism (the bending response in relation to the direction of the light) and induction of flowering. Light is perceived by several photoreceptors, which detect different facets of the solar spectrum. These photoreceptors include the phytochromes (Phy), which are responsible for the detection of far-red (FR) and red (R) light. The blue/UV-A photoreceptors sense the blue and UV-A part of the spectrum and some of them have recently been molecularly cloned [1–5]. Essentially nothing is known yet about the molecular nature of the UV-B photoreceptors, which, for example, regulate the formation of UV-shielding pigments [6–8].

Our knowledge about plant photoreceptors, their function and signal transduction was significantly extended by recent progress in the identification of photoreceptor and signal transduction mutants. Most of these studies were done with the model plant *Arabidopsis thaliana*. Thus, here I focus mostly on results obtained with this species. Several excellent reviews on the same topic have

been published recently, and I refer the reader to these for additional information or other points of view [6, 9–24].

The phytochromes

Phytochromes are the best-characterized plant photoreceptors. They are encoded by gene families consisting of five members (*PHY A-E*) in the model plant *Arabidopsis* [16, 25–27]. The phytochromes are responsible for the detection of R and FR. Phytochromes are polypeptides of about 125 kDa carrying a chromophore, the phytychromobilin, which is a linear tetrapyrrole covalently bound to a conserved cysteine residue in the N-terminal region (fig. 1). Phytochromes exist in two forms, the red light absorbing P_r ($\lambda_{\max} = 660$ nm) and the far-red light absorbing P_{fr} ($\lambda_{\max} = 730$ nm). Upon absorption of red light P_r is converted to P_{fr} , and P_{fr} is converted back to P_r upon absorption of far-red light. The photoreversibility of phytochrome, which persists *in vitro*, was an ideal feature for its purification and identification as a photoreceptor. Phytochrome is synthesized in the P_r form [28]. Although the two forms of phytochrome have different spectral absorption ranges, these overlap. Due to this overlap, the photoequilibrium of P_{fr}/P_{tot} depends on the wavelength and is about 80%

in red (660 nm), 3% in far-red (730 nm) and about 40% in blue (450 nm) light (fig. 1). Due to the activation of phytochrome by blue light, a photoresponse induced by blue can therefore be caused by phytochrome or specific blue light receptors. P_{fr} is the active form of phytochrome, although some studies with phytochrome mutants also indicate a physiological function for P_r [29–31]. Phytochromes are dimers, and there is so far only evidence that a phytochrome monomer dimerizes with another identical phytochrome monomer, such as

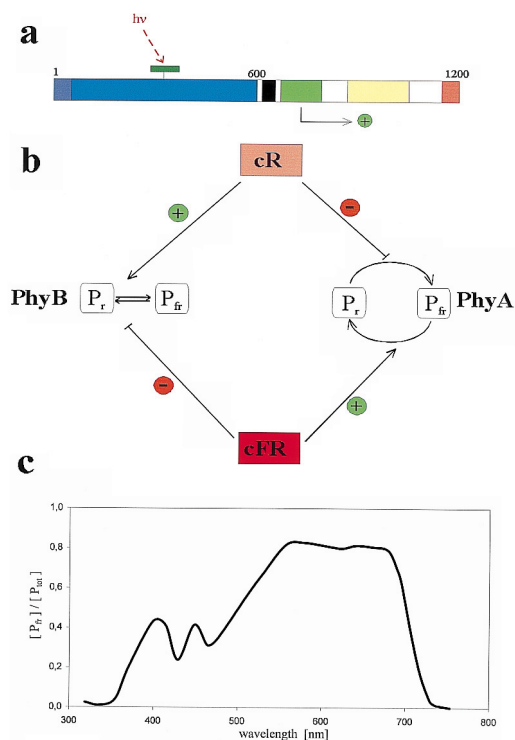


Figure 1. Scheme of the phytochrome domains, the antagonistic effects of PhyA and PhyB in the deetiolation process and the ratio of P_{fr}/P_{tot} under different light regimes. (a) The figure highlights the various functional domains of phytochrome. The linear tetrapyrrole chromophore is indicated by a green rectangle. The N-terminal 600-amino acid region (blue) determines the photosensory specificity of phytochrome. The region necessary for signal transduction (green) is separated from the photosensory domain by the protease-sensitive hinge region (black). The C-terminal part contains also the dimerization domain (yellow). Regions affecting the biological activity at the N-terminal and C-terminal end are indicated in violet and red (adapted from [16, 24]). (b) Model of the antagonistic effects of PhyA and PhyB in continuous red light (cR) and continuous far-red light (cFR) on the deetiolation process. High-intensity cR promotes the deetiolation (\oplus) via PhyB, and high-intensity cFR promotes deetiolation via PhyA (FR-HIR). In contrast, deetiolation is suppressed (\ominus) by high fluence rates of cFR (absorbed by PhyB) or by high fluence rates of cR (absorbed by PhyA). (c) Shown is the ratio of the FR-absorbing form of phytochrome (P_{fr}) to the total amount of phytochrome (P_{tot}) as a function of wavelength in photostationary equilibrium (adapted from [101, 104]).

PhyA with PhyA or PhyB with PhyB [19]. The localization of phytochrome has been analyzed with different methods. Most studies support the view that phytochrome is a soluble protein localized in the cytosol [16, 19]. However, recent work by Nagatani and co-workers demonstrated that PhyB is localized in the nucleus, and that the translocation between the cytosol and the nucleus is light-regulated [32]. Besides the localization in different compartments and other differences to be discussed below, the stability of the P_{fr} form of PhyA is about 100-fold less than the stability of other phytochromes. Classical photobiological studies and the use of monoclonal antibodies against different phytochromes had already demonstrated that there are two distinct pools of phytochrome, which had been named type I and type II. Type I phytochrome is much more abundant in dark-grown seedlings than type II. After transfer to light, type I phytochrome rapidly decays, resulting in an about 100-fold decrease of type I phytochrome in green plants compared with dark-grown seedlings, whereas the pool of type II phytochrome is relatively unaffected [9, 15, 16, 19]. Degradation of type I phytochrome is mediated by the ubiquitin system [33]. As a result of this degradation, not is only the total amount of phytochrome reduced but the ratio between the different pools is also changed. It has been demonstrated that PhyA is a type I phytochrome, whereas PhyB–E are light-stable in *Arabidopsis* and very likely constitute the pool of type II phytochrome [27, 34]. Due to the dramatic decrease in the amount of PhyA during deetiolation, phytochrome responses in green plants are dominated by PhyB (and other light-stable phytochromes), whereas phytochrome responses in etiolated seedlings are dominated by PhyA.

The molecular cloning of phytochromes and the construction or isolation of modified versions allowed the identification of regions and amino acids critical for proper function. For example, recombinant PhyA, PhyB and PhyC were expressed in *Escherichia coli* and yeast cells. Addition of phycocyanobilin (a chromophore very similar in structure to the authentic chromophore) to the purified apoprotein or yeast cells expressing phytochrome, resulted in the formation of photoreversible phytochrome, demonstrating that the chromophore is autocatalytically attached to the target cysteine [35–44]. Subdomains located within the N-terminal 600 amino acids are important for chromophore assembly and spectral integrity [45, 46]. Similarly, subdomains were identified which are necessary for dimerization and located at the center and close to the C terminus of the polypeptide (fig. 1) [47–49].

Phytochrome function

The primary mechanism of phytochrome action is still not known. The discovery of a phytochrome gene in the

moss *Ceratodon purpureus* having a C-terminal extension with similarity to serine-threonine and tyrosine protein kinases [50] led to the hypothesis that the *Ceratodon* phytochrome is a light-regulated kinase [51, 52], and that higher plant phytochromes might also have kinase activity. Nevertheless, kinase activity of the plant phytochromes has not yet been demonstrated. Based on sequence alignments, Schneider-Poetsch and co-workers found similarities to bacterial histidine kinases in the C-terminal region of phytochromes [53, 54]. Recently, a model in which phytochrome has kinase activity has received much support from the discovery that the cyanobacterium *Synechocystis* sp. PCC6803, whose genome has been completely sequenced, contains a gene coding for a protein with about 30% identity to the N-terminal region of plant phytochrome including the chromophore attachment site. The C-terminal part of this *Synechocystis* gene has striking sequence similarity to the two component sensor histidine kinases. It has also been shown that the recombinant *Synechocystis* protein attaches the chromophore (a linear tetrapyrrol) autocatalytically and is photoreversible [55–58]. In addition, the recombinant chromoprotein is able to autophosphorylate and to transfer the phosphate to another protein encoded in the same operon [56]. Thus the *Synechocystis* phytochrome-like protein has all the characteristics of a two-component sensory system. Plant hormone receptors related to two-component systems have been identified before [59–62]. It is therefore attractive to speculate that the plant phytochromes also belong to this class of sensor proteins. So far there is no definite proof for that, and the similarity to histidine kinase could just be a relic of the evolutionary origin of phytochrome.

As already mentioned, the classical criterion for a phytochrome response is reversibility (a response activated by a single R pulse can be suppressed by giving an FR pulse after the R pulse). There are other phytochrome responses, which are induced by such low intensities of (R) light that the P_{fr}/P_{tot} ratio is within the same range as when a saturating FR pulse alone is given. Such a response can therefore not be reversed by FR treatment. The response to such low light intensities is called very low fluence response (VLFR) [15, 19, 21, 63]. VLFR can be induced by R in the range between 10^{-10} and 10^{-7} mol m⁻². In addition, there are phytochrome responses which depend on prolonged exposure to relatively high light intensities, the so-called high irradiance response (HIR). Like the VLFR, the HIR is not photoreversible. The ‘classical’ HIR described by Hartmann [64] operates in continuous FR, but there is also an HIR in R and other light qualities [19, 65]. Since HIRs depend on prolonged light exposure, the reciprocity law is not valid for these

response modes. The low fluence response (LFR, 10^{-6} – 10^{-3} mol m⁻² of R) can be reversed by FR treatment. Based on mutant studies (see below) and theoretical calculations it is assumed that the PhyA_rPhyA_{fr} heterodimer can induce a response, whereas PhyB is only active in the PhyB_{fr}PhyB_{fr} homodimeric form [19].

Due to the identification of mutants deficient in defined phytochromes and overexpression of different phytochromes in wild-type and (phytochrome) mutant backgrounds, it was possible to assign specific responses to individual phytochromes. PhyA-deficient *Arabidopsis* do not germinate in high-intensity FR and poorly in very-low intensity light over the whole range from UV-A to FR [66]. The VLFR seen for the expression of the gene encoding the chlorophyll a/b-binding protein (CAB) is missing in the *Arabidopsis phyA* mutant but is present in the *phyB* mutant [67]. Inhibition of the extension growth of the hypocotyl under high-intensity FR is not observed for the *phyA* mutant [25, 26, 68, 69], whereas *phyB* mutants are not affected in these responses. On the other hand, *Arabidopsis phyB* mutants fail to inhibit extension growth of the hypocotyl [26, 68, 70] and to germinate [31, 71] under continuous low to high fluence R. These examples demonstrate that different phytochromes have distinct functions, namely PhyA mediates responses under FR-HIR and VLFR conditions and PhyB under LFR and R-HIR conditions.

Although, PhyA and PhyB are the most prominent phytochromes in *Arabidopsis*, *phyA/phyB* double mutants still show phytochrome responses. For example, seed germination in the *phyA/phyB* double mutant is still R/FR-reversible, indicating that the involved phytochrome belongs to the LFR type, but shows a fluence rate dependency similar to PhyA [66, 72]. PhyC function has been studied by overexpression. Transgenic tobacco and *Arabidopsis* lines overexpressing PhyC both show an R-dependent increase in leaf expansion [73, 74]. Since neither PhyA nor PhyB overexpression affects leaf expansion, regulation of leaf expansion seems to be a specific function of PhyC. In contrast to the *phyA* and *phyB* mutants which have been identified in mutant screens, PhyD is lacking in a ‘normal’ ecotype of *Arabidopsis*, the ecotype Wassilewskija [75], indicating that PhyD function is not essential under natural conditions. Nevertheless, the *phyD* mutant shows slight defects in R responses especially when combined with the *phyB* mutation [75]. Little is known so far about the role of PhyE.

In deetiolation and some other processes as well, the different phytochromes can act not only additionally but also antagonistically, depending on the ratio of R to FR (fig. 1). Continuous high-intensity FR induces deeti-

olation via PhyA action (FR-HIR); continuous R induces deetiolation via PhyB action. Conversely, enrichment of the incident light with FR suppresses PhyB, and enrichment of incident light with R suppresses PhyA. Thus, the ratio between R and FR, which alters dramatically under natural conditions (e.g. FR enrichment under the canopy due to absorbance of R by chlorophyll), is the determinant of the relative influence of different phytochromes to mediate a response [15, 16]. Although PhyA plays only a minor role in green *Arabidopsis* plants, it is essential when seeds germinate under the canopy but has almost no effect when seeds germinate in open sunlight [69, 76]. In green plants PhyB (and other light-stable phytochromes) dominates and exhibits among other responses the shade-avoidance response under FR enrichment [15, 77].

As outlined above, different phytochromes have different response modes: PhyA mediates VLFR and FR-HIR; PhyB mediates the LFR. The different response modes of phytochromes may suggest that different phytochromes use different signaling pathways. But domain-swapping experiments performed by Quail and co-workers argue against it. In these experiments, the coding regions for the N-terminal domain (carrying the chromophore binding sites) of *Arabidopsis* PhyA and PhyB were fused to the coding region of the C-terminal domain of PhyB and PhyA, respectively. Overexpression of these constructs in transgenic *Arabidopsis* has demonstrated that the N-terminal domains contain the photosensory specificities, since overexpression of PhyA-PhyB fusion results in the same phenotype as overexpression of PhyA, whereas overexpressors of PhyB-PhyA fusion have the same phenotype as PhyB-overexpressing lines [78]. Since the N-terminal domains of both PhyA and PhyB alone lack biological activity [49, 79, 80], the C-terminal domain is important for signal transduction. As demonstrated by the domain-swapping experiments, the C-terminal domain is exchangeable between the two phytochromes, thus indicating that the primary mechanism of PhyA and PhyB action is the same. In the same line are the observations that overexpression of full-length *Arabidopsis* PhyB as well as either its C- or N-terminal domain interferes with PhyA activity [32, 81]. In addition to the domain-swapping experiments, mutant alleles of *PHYA* and *PHYB* were identified which affect signal transduction. All of the *phyB* and the majority of the *phyA* mutations detected in this screen reside within a 160-amino acid-long region, especially in the stretch between positions 776 and 793 [16, 82]. One can conclude that the 160-residue-long region of both PhyA and PhyB is directly involved in the interaction with a downstream component and, as already concluded from the domain-swapping experiments, that the primary

partner could well be the same for both PhyA and PhyB. However, since mutants specific for either PhyA or PhyB signal transduction were identified (see below), it is difficult to understand how a common partner for PhyA and PhyB could channel signals into pathways specific for PhyA or PhyB. Besides the domains necessary for chromophore binding, photoreversibility and signal transduction, further functional domains of phytochrome were identified by overexpression of deletion derivatives of phytochrome. Deletion of the N-terminal 52 amino acids of oat PhyA resulted in a loss of FR sensing and signaling [79, 83]. Exchanges of several serine residues in this region to alanine or deletion of the N-terminal serine-rich region results in an enhanced biological activity of the overexpressed phytochrome [49, 84, 85]. It has also been shown that one specific serine residue in this region is phosphorylated [86]. Taken together, mutant studies and analysis of transgenic plants overexpressing different phytochromes have provided detailed knowledge about the function of the different phytochromes and about domains involved in phytochrome function.

Blue light photoreceptors

Blue light affects several processes such as growth of the hypocotyl, stem, cotyledons and the leaves, stomata opening, phototropism, flowering and gene expression [12, 13, 22, 23, 87–89]. Although phytochromes affect most of these processes and are also activated by blue and UV light, several lines of evidence demonstrated the involvement of specific blue/UV-A photoreceptors. Action spectroscopy indicated that either flavins, pterins or carotenoids could act as chromophores of blue light receptors [90–93]. Very recent studies on the chromophore composition of cloned blue light receptors (see below) support the flavin and pterin models for blue light receptors presented in the past [90, 91]. Up to now, three blue light receptors or likely blue light receptor candidates have been cloned from *Arabidopsis* (fig. 2), and mutants have been identified for each. Koornneef and co-workers isolated several mutants, which in contrast to wild type have a long hypocotyl when grown in the light (*hy* mutants). One of these mutants (*hy4*) is affected in blue light-dependent inhibition of hypocotyl elongation [94]. Besides hypocotyl elongation, *hy4* mutants are also affected in blue light-regulated formation of anthocyanin and expression of the first enzyme in anthocyanin biosynthesis, chalcone synthase (CHS) [1, 94–96]. A transfer DNA (T-DNA)-tagged *Arabidopsis* line was used to isolate the *HY4* gene [1]. The *HY4* gene encodes a protein with about 30% identity within the first 500 amino acids to the enzyme DNA photolyase from *E. coli*. The remaining C-terminal part, which is

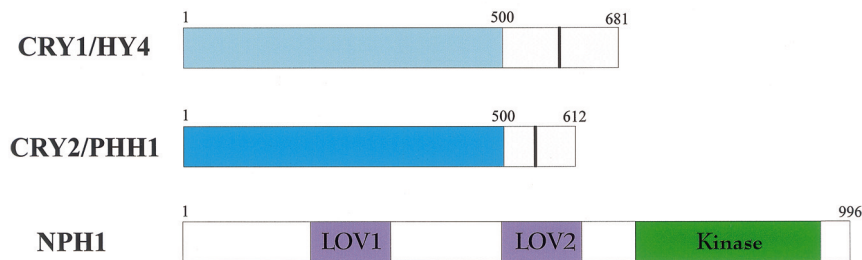


Figure 2. Scheme of the three cloned blue light receptors of *A. thaliana*. CRY1/HY4 and CRY2/PHH1 share significant similarity with class I DNA photolyases in the region between amino acid residues 1–500 (indicated in blue). As far as tested, this region binds the chromophores FAD and MTHF. CRY1/HY4 and CRY2/PHH1 are 54% identical in the N-terminal 500-amino acid region, but are very divergent in the C-terminal extensions except sharing a short serine-rich stretch (indicated in black). In the N-terminal region of NPH1 are two domains of about 100 amino acids (LOV1 and LOV2), sharing 43% identity and thought to be involved in sensing the light signal. The C-terminal part of NPH1 contains 11 sequence motifs typical of serine-threonine kinases (shown in green) (adapted from [101]).

lacking in DNA photolyases but is essential for HY4 function shares some similarity with tropomyosin A of rat smooth muscle [1]. The *E. coli* DNA photolyase belongs to the so-called class I DNA photolyases present in many microbial organisms, which repair the cis-syn cyclobutane pyrimidine dimers of UV-B-damaged DNA. Light energy in the blue/UV-A region is used for the catalysis [97]. Screening for further mutant alleles of *hy4* led to the identification of residues essential for HY4 function. These studies demonstrated that amino acid changes in the HY4 protein which affect the growth response of the hypocotyl in blue light also affect the accumulation of anthocyanin [96]. Despite the significant similarity of the HY4 protein, which was named cryptochrome 1 (CRY1) [17], with DNA photolyase, CRY1 has no photolyase activity when expressed in *E. coli* or insect cells [98, 99]. Heterologous expression of CRY1 enabled the identification of the chromophores bound to CRY1. Whereas only flavosemiquinone (FADH) could be identified as a non-covalently bound chromophore of CRY1 in extracts of insect cells [98], *E. coli*-expressed CRY1 contains both FADH₂ and the pterin-type chromophore 5,10-methenyltetrahydrofolate (MTHF) noncovalently attached to the apoprotein [99]. The same chromophores are present in DNA photolyase from several species such as *E. coli* and *Saccharomyces cerevisiae*. Photoreduction experiments with CRY1 expressed in insect cells resulted in the semireduced form of FAD (FADH), shifting the absorption spectrum to green light [98]. The presence of a semireduced form of CRY1 in the plant would be consistent with the fact that, in contrast to wild type, the extension growth of the hypocotyl in green light is not inhibited in the *hy4* mutant [98]. Further studies are needed to identify the authentic chromophores bound to the blue light receptors in the

plant cell. Besides the lack of photolyase activity of CRY1, all the evidence obtained from studies with the *hy4* mutant and transgenic lines overexpressing CRY1 points to a blue light photoreceptor function of CRY1 [96, 100]. The *hy4* mutant is affected only in some blue/UV-A light responses, indicating that more blue/UV-A photoreceptors exist in higher plants (see also fig. 3). Indeed, in a complementary DNA (cDNA) screen with degenerate oligonucleotides representing conserved regions of class I DNA photolyases, another photolyase-related gene from white mustard (*Sinapis alba* L.) was isolated [2] that shares 54% identity in the deduced amino acid sequence with CRY1 (fig. 2). Expression of this cDNA in photolyase-deficient *E. coli* cells resulted in weak photoreactivation [2], but later studies demonstrated that the *E. coli*-expressed protein has no photolyase activity in vitro, although it binds FADH₂ and MTHF as chromophores [99]. cDNA and genomic clones encoding a protein with 89% identity to the white mustard protein were isolated thereafter from *A. thaliana*. The gene was named *AT-PHH1* [3] or *CRY2* [4]. The highest similarity of PHH1/CRY2 with CRY1 is in the region between amino acids 1–500 (fig. 2). Like CRY1, PHH1/CRY2 has an extension at the C terminus which differs in size and sequence from the CRY1 extension, except sharing a short stretch of several serine residues and a few other conserved amino acids [3]. The function of this serine stretch has not been analyzed so far. Antisense expression of part of *PHH1/CRY2* not related to *CRY1* affected blue light-regulated expression of the *CHS* gene (U. Grüne and A. Batschauer, unpublished data), suggesting a blue light receptor function for PHH1/CRY2. Further support for a blue light receptor function for PHH1/CRY2 was provided very recently by the identification of *Arabidopsis* mutants defective in the *PHH1/CRY2* gene

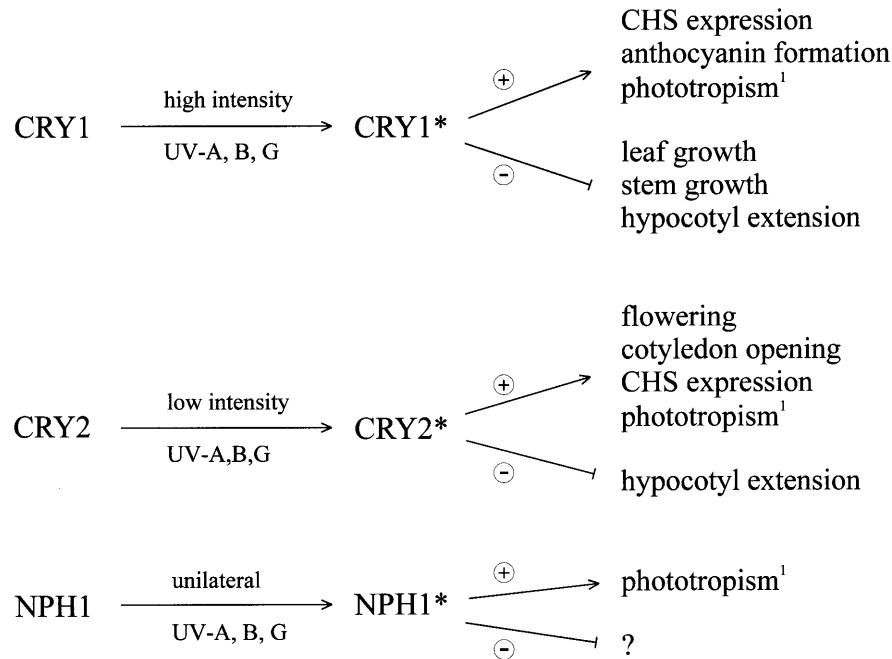


Figure 3. Physiological processes regulated by *A. thaliana* blue light receptors. CRY1 and CRY2 have multiple, partially overlapping functions, whereas NPH1 seems to be specific for phototropism. (¹) First and second positive curvature in phototropism is lacking in the *nph1* mutant; the *cry1/cry2* double mutant is lacking the first positive curvature but is normal in the second one. Mutations in either *CRY1* or *CRY2* alone have no effect on phototropism. Indicated is which process is promoted (\oplus) or inhibited (\ominus).

[102]. The *Arabidopsis* mutant *pha-1* [103] and additional *Arabidopsis* mutants created by fast-neutron bombardment having mutations or deletions in the *CRY2* gene are late flowering and show an increase in the number of leaves under long-day (LD) but not under short-day (SD) conditions [102]. Transgenic lines overexpressing *CRY2* show the opposite effect—slightly earlier flowering than the wild type in SD but not affected in LD [102]. Studies on the LD plant *Sinapis alba*, like *Arabidopsis* a crucifer plant, have shown that the efficiency of blue light in night break experiments is much higher than the efficiency of R [104], suggesting involvement of a blue light receptor in flower induction. Surprisingly, in continuous blue light the *cry2* mutant flowers as early as wild-type plants. Only when blue and red light are given together does the *cry2* mutant show a late flowering phenotype compared with wild type [102]. Since the mutation of *phyB* results in earlier flowering when R is given continuously, *PhyB* seems to repress flowering. However, it is not clear why the *phyB* mutant flowers as early as wild type, when blue light and red light are given simultaneously. A simple model in which *PhyB* would just repress and *CRY2* promote flowering is not consistent with these data. In addition, the role of phytochromes other than *PhyB* in the regulation of flowering time

have to be analyzed in further detail. For example, the *Arabidopsis phyA* mutant is less able to detect light treatments in the middle of the dark period [31], and overexpression of oat *PhyA* in tobacco affects flowering time [73]. The molecular mechanism by which *CRY2* regulates flowering time is even more complicated, owing to the amount of *CRY2* protein is itself light-regulated. In blue light the *CRY2* protein is rapidly degraded [105, 106]. Downregulation of *PHH1/CRY2* is not affected in *hy4* [105] and nonphototropic *nph1* mutants (U. Grüne and A. Batschauer, unpublished data), indicating that the downregulation is an autoregulatory process. It has also been demonstrated that under low-intensity blue light the amount of *CRY2* is virtually unaffected and that *CRY1* and *CRY2* both affect the extension growth of the hypocotyl but operate under different light intensities [106]. It will be very important to learn in further studies how blue light receptors and phytochromes interact and how downregulation of *PHH1/CRY2* in blue light fits with a model in which *PHH1/CRY2* is a major player in sensing the photoperiod.

Phototropism (the bending response in relation to the direction of the light) is one of the best-studied blue light responses in plants. Recently, a putative photoreceptor involved in phototropism was identified.

Winslow Briggs and co-workers have characterized in maize coleoptiles and etiolated pea seedlings a plasma membrane-associated protein of about 120 kDa which is rapidly phosphorylated upon blue light treatment in an intensity-dependent fashion [107–110]. In vitro studies indicated that the 120-kDa protein autophosphorylates after blue light treatment [12]. Unilateral irradiation of coleoptiles results in a gradient of protein phosphorylation, demonstrating that the phosphorylated protein is directly involved in the phototropic response [111–113]. The identification of *Arabidopsis* mutants, impaired in phototropism [114, 115], was the starting point for the successful molecular cloning of a putative photoreceptor for phototropism. The *nph1* (nonphototropic hypocotyl 1) mutant does not show first and second positive curvature and lacks the 120-kDa protein mentioned above [115]. This mutant was used to isolate the corresponding gene. The *NPH1* gene encodes a protein of 996 amino acids (112 kDa) and complements the *nph1* mutant phenotype [5]. The C-terminal region of *NPH1* has high similarity with the PVPK1 family of serine-threonine protein kinases, and the N-terminal part of *NPH1* has two similar regions of about 100 amino acids related in sequence to motifs present in proteins from archaea, eubacteria and eukaryotes—proteins which are known to be regulated by environmental signals, such as light, oxygen and voltage (LOV), that change their redox state. As far as we know, the change in redox state is mediated by a flavin. As outlined above, flavin would also be a likely prosthetic group for a blue light receptor in phototropism. The conserved domain (LOV domain) in the different proteins including *NPH1* could act as a flavin-binding site. However, very recent data show that the *cry1/cry2* double mutant is deficient in the first positive curvature [116], indicating that the two cryptochromes together could act as photoreceptors for phototropism and that *NPH1* could be a component in the signal transduction pathway. Alternatively, *NPH1* could still be the photoreceptor for both first and second positive curvature. Phototropism would then depend on three blue light receptors (as well as on *PhyA* and *PhyB*), and the activity of *NPH1* would just be modulated by the cryptochromes.

In summary, recent work on blue light receptors in higher plants led to the identification of two different classes of proteins, the photolyase-related cryptochromes and the kinase and LOV domain containing *NPH1*, the likely photoreceptor for phototropism. Although the determination of the chromophore composition of these blue light receptors is not complete, there is good evidence that all the plant blue light receptors and blue light receptor candidates known so far are flavoproteins (O. Kleiner and A. Batschauer, unpublished data; W. R. Briggs, personal communication).

Whereas the molecular cloning of the phytochrome photoreceptor family of *Arabidopsis* is complete, it is still not clear whether the same is true for the blue light receptors, or whether further ones (e.g. regulating stomatal opening) await identification.

Light-signaling molecules

As outlined above, most of the plant photoreceptors have been characterized in recent years. Less is known about the components of the light signal transduction pathways, and we can expect a very complicated network consisting of a great number of signaling molecules which are not only affected by light but also by additional factors such as other environmental stimuli or endogenous signals like phytohormones [18]. In principal two different strategies have been used to characterize light signal transduction: the genetic approach and the biochemical/cell biological approach [6, 14, 16, 18, 21, 117–120].

Genetic approach

The genetic approach was, and is currently, very fruitful in identifying genes involved in light signal transduction (fig. 4). Screening for signal transduction mutants was done essentially in two ways: first to identify mutants which show a kind of etiolated phenotype in the light [94], and second to identify mutants which show a light-grown phenotype in darkness [121–124]. Among the *hy* mutants (long hypocotyl of light-grown plants) isolated by Koornneef and co-workers most proved to be affected in photoreceptor genes (*hy3* = *phyB*, *hy8* = *phyA*, *hy4* = *cry1*) [1, 25, 26, 31, 68, 69, 71] or to be impaired in the synthesis of the phytochrome chromophore (*hy1*, *hy2*) [125]. However, the mutant *hy5* is impaired in responsiveness to different wavelengths and thus appears to be a downstream element of both phytochrome and blue light receptor transduction pathways [94]. Indeed, the *HY5* gene was cloned and encodes a bZIP transcription factor [126] which binds to the light-responsive element of the *CHS* gene leading to transcriptional activation [127]. *HY5* interacts directly with another protein, *COPI* [127–129], previously identified as a repressor of photomorphogenesis (see below). Screening for mutants having a dark-grown phenotype in the light has the advantage that the screens can be done with different light regimes allowing the isolation of mutants affected specifically in the signal transduction pathway of one photoreceptor. The *Arabidopsis* mutants *fhy1* and *fhy3*, for example, differ from wild-type plants under FR-HIR conditions [11, 69, 130, 131] but have normal levels of *PhyA*. Thus *FHY1* and *FHY3* most likely encode for components specific for the

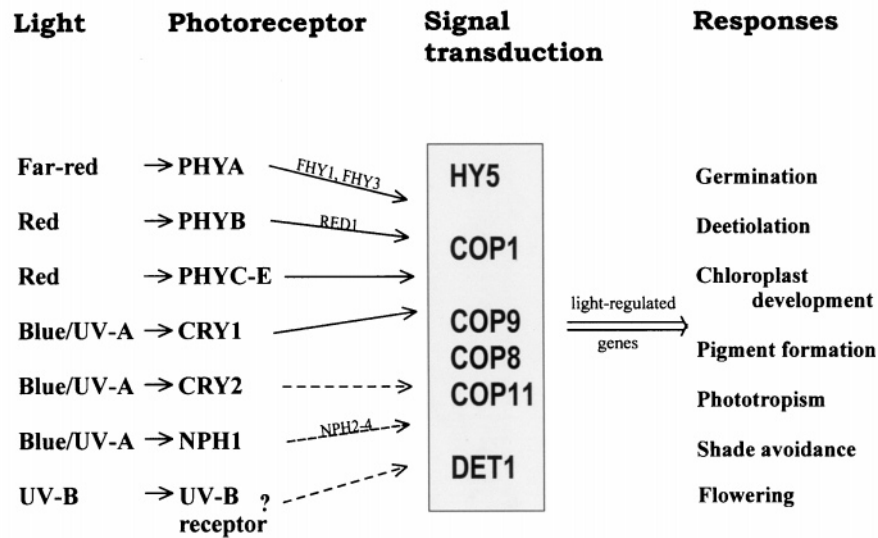
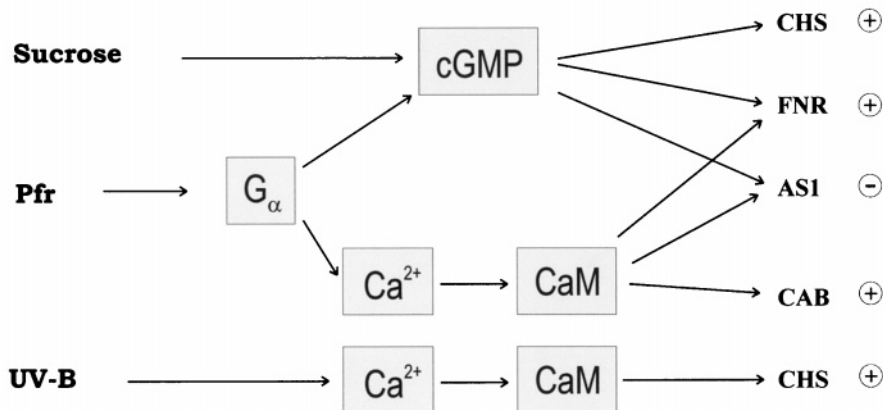
a**b**

Figure 4. Scheme of components involved in light perception and signal transduction. (a) All the genes of the indicated photoreceptors (except for UV-B) and the signaling components (HY5, COP1, COP9, COP11/FUS6, DET1) have been cloned from *A. thaliana*. Genetic studies indicate the involvement of FHY1 and FHY3 in the signal transduction of PhyA, of RED1 in the signal transduction of PhyB and of NPH2-4 in the signal transduction of NPH1. (b) The function of G proteins, cGMP and Ca^{2+} /calmodulin as second messengers of the light signal transduction pathway is implicated by inhibitor studies with cell cultures and microinjection experiments with the phytochrome-deficient *aurea* mutant of tomato. The indicated genes regulated by cGMP and/or Ca^{2+} /CaM encode for chalcone synthase (CHS), the chlorophyll a/b-binding protein (CAB), ferredoxin-NADP⁺ oxidoreductase (FNR) and asparagine synthetase (ASI). Further signaling molecules not indicated have already been characterized and more can be expected. The schemes, however, cannot explain how the light signals transduced by the different photoreceptors result in specific responses by using common signal transduction components (adapted from [6, 21, 101]).

PhyA signal transduction pathway. Another mutant, *red1*, seems to be affected in PhyB but not PhyA signal transduction [132], whereas *pef1*, a mutant identified in a screen for early-flowering mutants [133], is altered in

the signaling pathway of both PhyA and PhyB. All mutants in light signal transduction identified so far are recessive except *shy1* and *shy2* [134, 135]. *Shy1* and *shy2* were isolated in a screen for suppressors of the *hy2*

mutation. Like *cop/det/fus* mutants (see below), dark-grown *shy* seedlings undergo most of the developmental processes of light-grown wild-type seedlings [134, 135].

Mutant screens performed in darkness led to the identification of *cop* (constitutive photomorphogenesis) and *det* (deetiolated phenotype) mutants with phenotypes similar to that of light-grown seedlings (for review see [14, 18, 21, 118, 129]). The *COP/DET* loci are identical to previously identified *FUS* (*fusca*) loci. The *fus* mutants show enhanced accumulation of anthocyanin, and strong alleles are lethal during seedling development [136]. The recessive nature of the *cop/det/fus* mutations together with their phenotypes indicate that *COP/DET/FUS* are repressors of photomorphogenesis and that these repressors are inactivated by the light signals perceived by the photoreceptors. Indeed, genetic interaction studies of photoreceptor mutants with *cop/det/fus* mutants indicate that *cop/det/fus* are epistatic to photoreceptor mutations and that *COP/DET/FUS* are localized downstream of the photoreceptors [123, 137], although this is difficult to conclude from such experiments. Some of the *COP/DET/FUS* genes have been cloned. *COP1/FUS1* encodes a protein with three well-characterized domains: a WD-40 domain typical for the β -subunit of heterotrimeric G proteins, a ring-finger zinc binding domain and a coiled-coil domain, which could act in protein-protein interactions [138–140]. Except for the zinc binding domain, *COP1* shares significant homology with d-TAF_{II}80 from *Drosophila*, a component of the RNA polymerase II complex, suggesting that *COP1* acts in the dark as a repressor of transcription by interacting with the RNA polymerase complex in a nonproductive manner. It has been demonstrated for a fusion of *COP1* with the reporter β -glucuronidase (*COP1-GUS*) that *COP1* is enriched in the nucleus in darkness and excluded from the nucleus in light [141]. The translocation of *COP1* is a relatively slow process, requiring several hours at least in the cells tested thus far [141]. Most deetiolation processes are much faster. The translocation of *COP1* could therefore act in maintaining the light program rather than as a molecular switch of photomorphogenesis. The nuclear localization of *COP1* in the dark is impaired in mutants defective in other *COP* genes, *COP8*, *COP9*, *COP11* [142]. *COP9/FUS7* and *COP11/FUS6* have been cloned [124, 143]. *COP9* is exclusively localized in a large protein complex consisting of several proteins including *COP11* [124, 142, 144]. The *COP9* complex is nuclear-localized, but in contrast to *COP1*, light has no effect on its localization [144, 145]. It has been hypothesized that the *COP9* complex is directly involved in the nuclear localization of *COP1*, although *COP1* is not part of the *COP9* complex [129]. Another repressor of photomorphogenesis which has been cloned is *DET1* [146].

DET1 has no obvious homology with any other protein in the databases, but is like *COP1* localized in the nucleus. In contrast to *COP1*, the nuclear localization of *DET1* is not light-regulated [146]. Despite the localization of *DET1* in the nucleus, the protein does not bind DNA [18]. It is therefore likely that the action of *DET1* and *COP1* requires protein-protein interaction, probably with components of the basal transcription machinery. This interaction could result in the repression of genes that are required for photomorphogenesis.

Biochemical and cell biological approach

Besides the genetic approach, a variety of biochemical approaches have been used to identify signaling molecules downstream of the photoreceptors. Signal transduction in pulvinar movement and guard cell swelling, processes which are regulated by blue light, is beyond the scope of this review, and I refer the reader to recent reviews on this topic [23, 147]. Phytochrome-mediated phosphorylation of a number of mostly unidentified proteins has been demonstrated [148–151]. Phosphorylation and translocation between the cytosol and the nucleus of the bZIP transcription factor CPRF2 from parsley [152–154] and import of the bZIP factor GBF2 from *Arabidopsis* into the nucleus [155] is also light-regulated. In the case of CPRF2 it has been demonstrated that the light response is mediated by phytochrome. Since these processes are faster than the expulsion of *COP1* from the nucleus, phosphorylation and translocation of CPRF2 and GBF2 into the nucleus could therefore be a molecular switch in the deetiolation process, as is the release of the bZIP factor HY5 from the *COP1/HY5* complex [127]. Studies with cholera and pertussis toxin suggest that heterotrimeric guanosine-triphosphate (GTP)-binding proteins are part of the phytochrome signaling pathway [156]. The aurea mutant of tomato, a mutant affected in the biosynthesis of phytochromobilin [157], was used in microinjection experiments to define components of the phytochrome signal transduction chain (fig. 4). Microinjected purified oat phytochrome into single cells of the hypocotyl resulted in chloroplast development, anthocyanin formation and expression of light-regulated genes [158, 159], processes normally not seen in the mutant. Chloroplast development and anthocyanin formation were induced only in the injected cell, indicating that the phytochrome signal transduction pathway is cell-autonomous. In contrast, microbeam irradiation experiments indicate that the signals which induce the transcription of the *CAB* gene are generated in the irradiated cells but are also transmitted to neighboring cells [160]. Activators of heterotrimeric G proteins (GTP γ S, cholera toxin) had the same effect as microinjected PhyA, whereas inhibitors of heterotrimeric G proteins (GDP β S, pertussis toxin) inhibited the action

of coinjected PhyA [158, 159]. Yeast-expressed PhyB injected into aurea cells could stimulate chloroplast development but in contrast to injected PhyA could not stimulate anthocyanin formation [42]. This is consistent with the observation that continuous R treatment of *Arabidopsis* seedlings, which stimulates PhyB, is very inefficient for anthocyanin accumulation and *CHS* expression [42, 161]. Microinjection experiments identified further signaling molecules located downstream of the G proteins, namely cyclic guanosine-monophosphate (cGMP) and calcium/calmodulin [158, 162]. cGMP alone could stimulate anthocyanin accumulation and *CHS* expression, whereas calcium/calmodulin alone could stimulate *CAB* expression and allow partial development of the chloroplast. Full development of the chloroplast and expression of further chloroplast genes required both cGMP and calcium/calmodulin. Light-responsive cis-elements fused to truncated 35S promoters respond also to these signaling molecules [163]. Repression of genes which are downregulated by light (such as asparagine synthetase) is controlled by the same calcium and cGMP pathways [164]. Surprisingly, the signaling pathway of UV-B leading to the activation of *CHS* in parsley protoplasts and *Arabidopsis* cell suspension cultures involves calcium and is therefore different from the cGMP-dependent phytochrome signal transduction that regulates *CHS* expression [8, 165].

Conclusion

In recent years, progress in the characterization of plant photoreceptors and components of light signal transduction chains has been immense. This progress was made possible by the interaction of different disciplines such as genetics, molecular biology, physiology, biochemistry and cell biology. Although most of this research has focused on molecular aspects of photoreceptor function and signal transduction, the results obtained have also had a significant impact on our understanding of how plants adapt to changing light conditions in the natural environment. We have learned that multiple phytochromes exist which have partially antagonistic functions, and it will be interesting to see whether the same is true for blue light receptors. Despite profound knowledge of the components of the light signal transduction chain, we are far from understanding in detail how light signals are transduced. We must expect further complexity, since other external and internal signals such as hormones, carbohydrates and so on (not discussed here) interfere with light signals. A major challenge in the near future is to understand in greater detail how different photoreceptors interact, to elucidate the structures of photoreceptors and to identify their primary interacting partners.

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