

Light-induced chromophore activity and signal transduction in phytochromes observed by ^{13}C and ^{15}N magic-angle spinning NMR

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Both thermally stable states of phytochrome, Pr and Pfr, have been studied by ^{13}C and ^{15}N cross-polarization (CP) magic-angle spinning (MAS) NMR using cyanobacterial (Cph1) and plant (*phyA*) phytochrome sensory modules containing uniformly ^{13}C - and ^{15}N -labeled bilin chromophores. Two-dimensional homo- and heteronuclear experiments allowed most of the ^{13}C chemical shifts to be assigned in both states. Chemical shift differences reflect changes of the electronic structure of the cofactor at the atomic level as well as its interactions with the chromophore-binding pocket. The chromophore in cyanobacterial and plant phytochromes shows very similar features in the respective Pr and Pfr states. The data are interpreted in terms of a strengthened hydrogen bond at the ring D carbonyl. The red shift in the Pfr state is explained by the increasing length of the conjugation network beyond ring C including the entire ring D. Enhanced conjugation within the π -system stabilizes the more tensed chromophore in the Pfr state. Concomitant changes at the ring C propionate carboxylate and the ring D carbonyl are explained by a loss of hydrogen bonding to Cph1-His-290 and transmittance of conformational changes to the ring C propionate via a water network. These and other conformational changes may lead to modified surface interactions, e.g., along the tongue region contacting the bilin chromophore.

photomorphogenesis | photoreceptors | chromophore-protein interaction | phycocyanobilin | solid-state NMR

Phytochrome photoreceptors were first characterized in plants, where they mediate many photomorphogenetic processes (for reviews see refs. 1 and 2). More recently, this family of photoreceptors has been enlarged by the discovery of homologous proteins in cyanobacteria (3, 4) and nonphotosynthetic bacteria (5, 6). A characteristic feature of all phytochromes is the photoreversibility between two states: The absorption of red light initiates photochemical activity of the thermally stable Pr state ($\lambda_{\text{max}} \approx 660$ nm), which travels through a series of intermediates (7) and eventually generates the far-red-absorbing Pfr state. The Pfr state, with a moderate thermal stability of several hours to days, is converted back to Pr upon absorption of a far-red photon ($\lambda_{\text{max}} \approx 710$ nm). The origin of this red shift is not known. All phytochromes bind an open-chain tetrapyrrole (bilin) as a chromophore, whose photochemistry triggers the conversion between the Pr and Pfr states. The x-ray structures of the chromophore-binding PAS-GAF bidomain of *Deinococcus radiodurans* (8) and *Rhodospseudomonas palustris* (9), both assembled with biliverdin, have been reported. The recently solved structure of a complete PAS-GAF-PHY sensory module of Cph1 from *Synechocystis* sp. PCC 6803 phytochrome in its Pr state demonstrated that the phycocyanobilin (PCB) cofactor is completely sealed from access to bulk solvent (10). Although a comparison between these 3D structures reveals some differences of the chromophore-binding pocket, most of the chromophore-protein interactions are conserved. In all crystal structures, the open-chain tetrapyrrole chromophore has been

reported to adopt a ZZZ_{ssa} geometry [5-Z, 10-Z, 15-Z, 5-syn, 10-syn, 15-anti, see supporting information (SI) Fig. S1] of the three methine bridges. The chromophore in different phytochromes has been intensively studied by various spectroscopic methods. It is commonly accepted that the conversion from Pr to Pfr is initiated by a Z \rightarrow E photoisomerization of the methine bridge between rings C and D (11–14). However, the exact geometry of the chromophore in the Pfr state and the role of the chromophore-binding pocket in the phototransformation have yet to be established. Moreover, slight rotations around single bonds that are hardly reflected by the crystal structures may cause a more distorted chromophore, a scenario that is supported by a recent investigation using vibrational spectroscopy and density functional theory calculations (15).

Only little is known about the details of the photochemical machinery allowing for intramolecular signal transduction from the chromophore onto the protein surface. Mutational studies on Cph1 (16) have demonstrated the crucial role of Asp-207 (Cph1 numbering of residues is used throughout the article) for intramolecular signal transduction (Fig. S2). It has been proposed that in Cph1 Tyr-176, whose side chain is close to ring D, acts as a molecular gate in the decay of the photochemically excited Pr (17). Moreover, in bacteriophytochrome RpBphP2, two tyrosine residues, Tyr-207 and Tyr-272 (equivalent to Tyr-198 and Tyr-263 in Cph1, respectively), play likewise an important role during the Pr \rightarrow Pfr photoconversion (9).

Cross-polarization (CP) magic-angle spinning (MAS) NMR has evolved into a uniquely versatile tool for the structure elucidation in systems of high-molecular-mass and solid materials. In conjunction with selective isotope labeling, CP/MAS NMR allows for the study of large protein complexes down to the atomic level (18). In this work, the N-terminal sensory modules of the cyanobacterial phytochrome Cph1 (Cph1 Δ 2) and the 65-kDa fragment of oat phytochrome A (*phyA*65) have been studied by ^{13}C and ^{15}N CP/MAS NMR. Holoproteins of these phytochromes were generated by *in vitro* assembly with uniformly ^{13}C - and ^{15}N -labeled PCB cofactor (u -[^{13}C , ^{15}N]-PCB), thus selective observation of the chromophore in the protein matrix has been achieved. The quality of the ^{15}N data is significantly improved compared with previous work (19), allowing for 2D spectroscopy. Here, we show a full NMR analysis of the cofactor in both states, Pr and Pfr. Dramatic changes

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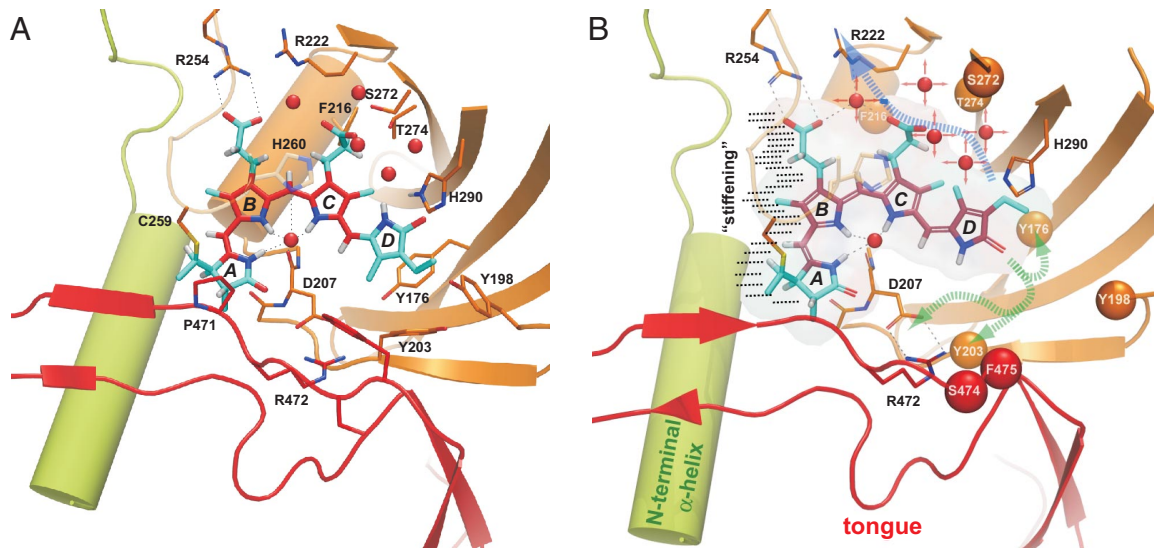


Fig. 5. The PCB-binding site of Cph1Δ2. (A) Structural view on the protein environment of the PCB-chromophore in the Pr state (10) highlighting the H-bonding network. (B) Overview of putative structural changes caused by Pfr state formation. Blue and green dotted arrows indicate potential paths of signal transmission within the chromophore-binding site. The observed loss of conformational freedom along rings A and B is highlighted by dotted lines. This figure was made by using PyMol (32).

the Pfr/Pr mixture (ratio $\approx 1:1$) of *phyA65* (see Fig. S6) lead to the ^{13}C assignment in both Pr and Pfr states (Table S1). The change in chemical shift accompanying the Pr \rightarrow Pfr conversion is shown in Fig. 2B. Also, the comparison of Fig. 2A and B demonstrates that the phototransformation affects the chromophore in Cph1Δ2 and *phyA65* in a similar manner. In *phyA65*, however, the positions 13 and 13¹ show a bigger change in chemical shift than in Cph1Δ2. This explains the difference observed at 125 ppm between the difference spectra (Fig. 4B and D) and may suggest a different torsion angle around the 14–15 single bond in Cph1Δ2 and *phyA65* phytochrome.

As shown by vibrational techniques, the conformations of the bilin chromophore in the Pr and Pfr states in native plant phytochrome, a dimer of two 124 kDa units (*phyA124*), resemble that in the photosensory modules *phyA65* of oat phytochrome (28, 29) and Cph1 of *Synechocystis* (30). Furthermore, our NMR data add clear evidence that the chromophore and its interactions with the protein are conserved in both states throughout the Cph1/plant phytochrome family. Homology modeling of *phyA65* and a comparison of its electrostatic surface properties with Cph1Δ2 (see Fig. S7) indicate that the sensory modules of both phytochromes provide a common electrostatic environment for the PCB chromophore despite significant differences along their solvent-exposed molecular surfaces. These striking similarities justify the following conclusions that may be drawn for the whole Cph1/plant phytochrome family.

Discussion

Chromophore Photoconversion. As shown in Fig. 2A and B, the photoconversion of PCB mostly affects rings C and D. The striking change in chemical shifts at the positions 13–19 is in line with photoisomerization occurring along the C15=C16 double bond. During this process, the chromophore is involved throughout its entire structure; hence, the photoisomerization is not a local event but modifies the chromophore–protein interaction dramatically. A significant effect is also seen at the 10-methine carbon that is situated between the almost coplanar rings B and C. In contrast, no major effect occurs around methine carbon 5 that links rings A and B. The observed pattern can be rationalized by the assumption of five effects: (i) The chromophore is tensely fixed in the Pfr state, (ii) the conjugation increases in the Pfr

state, (iii) the hydrogen bonding interaction of the ring D carbonyl increases in the Pfr state, (iv) a local change of the electronic structure around ring C is identified, and (v) a significant change of the protein interacting with the ring C carboxylate group takes place.

(i) The loss of conformational heterogeneity at the ring B propionate side chain implies an increase of local tension. Several cross-peaks at rings A and B become sharper in the Pfr spectrum, e.g., carbons 4 and 6. The signal doubling observed for carbons 1 and 2 in the Pr state disappears in the Pfr state. These observations suggest an increase of mechanical tension occurring in the Pfr state, as is also observed by ^{15}N MAS NMR (19) and vibrational spectroscopy (13). Such tension would also explain the change at the 3¹ carbon atom that links the chromophore via a thioether covalently to Cys-259.

(ii) The entire conjugation pattern undergoes a significant modification. In Fig. 2 on the left side of ring C, even-numbered carbons are marked for a downfield shift (blue), whereas odd-numbered carbons are up-shifted (red). On the right side of ring C, however, the opposite pattern appears. Such pattern change, involving the entire conjugated chain, implies a change in bond order. Assuming enhanced tension in the Pfr state, we would propose an increase of bond order for single bonds, increasing their rotational energy and providing the required stiffness, concomitant with a decrease in bond order for the double bonds.

(iii) There is a clear up-shift at the carbonyl of ring D associated with decreased electron density at carbons 17 and 19. This shift has not been observed in previous NMR studies (31); however, a clear change of this group has been shown by FTIR spectroscopy (14, 28). In the Pr state of Cph1 (Fig. 5A), only a weak hydrogen bond is formed between the ring D carbonyl and His-260 due to its energetically unfavorable angle of 102° (O-HE2-NE2) caused by the low tilt of ring D vs. ring C (26.3°). Therefore, an increase of hydrogen-bonding interactions takes place for the ring D carbonyl during Pfr state formation. Such an increased polarization at the terminal group may cause the increased conjugation throughout the entire chain of the chromophore and hence the red shift of Pfr absorption. Because no strong hydrogen bonding is observed for the protonated ring D nitrogen, in neither the Pr nor the Pfr state, it is reasonable to

assume that strong hydrogen bonding involving only the carbonyl of ring *D* stabilizes the chromophore in the Pfr state.

(iv) Whereas chemical shifts of carbons in rings *B* and *C* are almost mirror symmetrical in the Pr state, this symmetry is lost in the Pfr state. However, in the other rings, an alternating pattern along the conjugated chain occurs, only in ring *C* all carbons are labeled in red. This is indicative of an increase of electron density in the Pfr state at this ring. The interruption of the alternating pattern at ring *C* suggests that the origin of the change of the conjugation pattern is localized here. Conformational rearrangements of the nearby located residues His-260 or Tyr-176 (Fig. 5*A*) may contribute to a ring-current shift effect in the Pfr state; however, this alone cannot explain the interruption of the alternating pattern. It is possible that, in the Pr state, the conjugation is interrupted at or around ring *C* because of the interplanar tilt between rings *C* and *D* and that the observed alternating pattern is caused by the enlargement of the conjugated system extending beyond ring *C*. Such an effect could also explain the red-shift of the absorption spectrum upon generating the Pfr state. In any case, ring *C* appears to be the hotspot for the change of the electronic structure.

(v) At the propionate side chain of ring *C*, a significant change at the carboxyl group occurs. It can be assumed that this group faces strongly altered interactions with the protein environment. This change may correspond to a modification previously observed by FTIR spectroscopy (14, 28), which has been interpreted as an alteration of either a protein amide or a propionate carboxylate group. In contrast to the ring *B* propionate, the ring *C* propionate is well hydrated within a cluster of five water molecules and makes only an indirect interaction with the positive counter charge at Arg-222 via a water molecule (Fig. 5*A*). Interestingly, a structural comparison between Cph1 and the bacteriophytochromes shows that Arg-222 may either adopt an outward-oriented conformation toward the GAF-PAS interface or point into the core region of the GAF domain itself.

Hence, from our analysis, the following picture of the Pr → Pfr phototransformation emerges: The chromophore forms a strong hydrogen bond via its ring *D* carbonyl, increasing both the strength and length of the conjugation network and stabilizing the chromophore in a tensed shape (Fig. 5*B*). Observed changes in ¹⁵N chemical shifts in the terminal rings (ref. 19 and Fig. 3) may be explained by such tension linked to traction at the outer rings, leading to a banana-shaped cofactor in the Pfr state. In addition, these changes in ¹⁵N chemical shifts may also be linked to the modification of the conjugated system, leading to a flow of electron density from ring *A* to ring *D*.

Signal Transduction Pathway. The question arises at which positions the chromophore dynamics is coupled to the protein environment to allow signal transduction to the protein surface. Important information can be extracted from Fig. 2*A* and *B*. All changes occurring on the left side of the green line can be explained by a change of conjugation only. On the other hand, on the right side of the green line, multiple effects are overlaying, and two of them are clearly due to changed chromophore-protein interaction. There are significant changes localized at the carboxylate group of the propionate side chain of ring *C* as well as at the carbonyl group of ring *D*. The x-ray structures of Cph1 and the bacteriophytochromes show that His-290 (His-372 in *phyA65* and His-299 in DrBphP) is bridged via two conserved water molecules to the carboxylate group of ring *C* and forms a hydrogen bond to the carbonyl of ring *D* (8–10) (Fig. 5). Hence,

we assume that this highly conserved His-290 couples the photochemistry of the chromophore to the protein.

Because the ¹³C signal of the ring *A* carbonyl and the ¹H signal of the ring *A* nitrogen exhibit only minor changes during the Pr → Pfr photoconversion, only local conformational changes of the protein matrix surroundings are likely to occur. On the other hand, changes of the hydrogen-bonding network by ring *D* photoisomerization could alter the conserved salt bridge between Asp-207 and Arg-472 and thus transmit the signal to the protein surface, e.g., by rearrangement of the tongue region (Fig. 5*B*). As possible conserved partners for strong hydrogen bonding to the ring *D* carbonyl in the Pfr state, nearby H-bonding donors such as Asp-207, Tyr-198, Tyr-203, Tyr-263, and Ser-474 may be considered. Further MAS NMR experiments will be necessary to elucidate such changes of the hydrogen-bonding network within the chromophore-binding site. In particular, MAS NMR distance experiments and selective interface detection spectroscopy (SIDY) (33) will be useful.

Materials and Methods

Sample Preparation for MAS NMR Spectroscopy. The u-[¹³C, ¹⁵N]-PCB was prepared following published methods (27). Preparation of Cph1Δ2 and *phyA65* apo- and holoproteins were performed as described (34, 35). For the measurements of the Pr state, samples were irradiated with light filtered through a far-red cut-off filter ($\lambda_{\text{max}} = 730$ nm). Pfr/Pr mixture was produced by saturating irradiation at 660 nm by using appropriate LED (Roithner Lasertechnik, Vienna, Austria). Cph1Δ2 phytochrome in its pure Pfr state was obtained by size-exclusion chromatography using Superdex 200 (Amersham Pharmacia/GE) (36).

MAS NMR Spectroscopy. The 1D ¹³C CP/MAS spectra were recorded by using a DMX-400 spectrometer, equipped with 4-mm CP/MAS probe. All data were recorded at 243 K with a spinning frequency of 10 kHz. The proton 90° pulse was set to 3.6 μs. The ¹H power was ramped 80–100% during CP. During the data acquisition, the protons were decoupled from the carbons by use of the two-pulse phase-modulation (TPPM) decoupling scheme (37). For u-[¹³C, ¹⁵N]-PCB-Cph1Δ2 measurements in the Pr and Pfr states, ≈15 mg of protein were placed in a 4-mm zirconia rotor. Approximately 12 mg of u-[¹³C, ¹⁵N]-PCB-*phyA65* was used for the measurements of the Pr state and Pfr/Pr (1:1) mixture.

All 2D ¹³C-¹³C DARR experiments were performed at a field of 17.6 T on an Avance-750 WB spectrometer, equipped with a 4-mm triple-resonance CP/MAS probe (Bruker). Typical ¹H 90° and ¹³C 180° pulse lengths were set at 3.1 and 5.0 μs, respectively. Mixing times of 5 and 50 ms were used to maximize homonuclear recoupling between ¹³C nucleus. The ¹³C-¹H dipolar interaction has been recovered by continuous wave irradiation on ¹H radio frequency field intensity to satisfy the $n = 1$ condition (20). The ¹H power was ramped 80–100% during CP. The ¹H decoupling was ≈80 kHz TPPM during acquisition. The 2D ¹³C-¹³C spectra of Cph1Δ2 were recorded with 1,536 scans and with 8-ms evolution in the indirect dimension, leading to experimental times of 80 h. The spectra of the *phyA65* protein were recorded with 2,048 scans in 2.5 days. The data were processed with the Topspin software version 2.0 (Bruker) and subsequently analyzed by using the program Sparky version 3.100 (T. D. Goddard and D. G. Kneller, University of California, San Francisco).

The 1D ¹⁵N CP/MAS spectra were recorded by using an AV-750 spectrometer, equipped with 4-mm CP/MAS probe. The proton 90° pulse was set to 3.1 μs, temperature was 243 K, and the spinning frequency was 8 kHz. The ¹H-¹³C and ¹H-¹⁵N heteronuclear experiments were performed at the DMX-400 and Avance-750 WB spectrometer, respectively, by using a frequency-switched Lee-Goldburg pulse sequence (38).

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