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Published in:
Biophysical Journal

DOI:
10.1016/j.bpj.2011.06.065

Citation for published version (APA):

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On the Involvement of Single-Bond Rotation in the Primary Photochemistry of Photoactive Yellow Protein

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ABSTRACT Prior experimental observations, as well as theoretical considerations, have led to the proposal that C₅-C₇ single-bond rotation may play an important role in the primary photochemistry of photoactive yellow protein (PYP). We therefore synthesized an analog of this protein’s 4-hydroxy-cinnamic acid chromophore, (5-hydroxy indan-(1E)-ylidene)acetic acid, in which rotation across the C₄-C₇ single bond has been locked with an ethane bridge, and we reconstituted the chromophore with this analog. In PYP reconstituted with the rotation-locked chromophore, 1), absorption spectra of ground and intermediate states are slightly blue-shifted; 2), the excited-state dynamics of the chromophore are accelerated; and 3), the quantum yield of photochemistry is ~60% reduced. These effects imply that C₄-C₇ single-bond rotation in PYP is affected by the charge of the amino acid residue at position 52, which was varied by 1), varying the pH of the sample between 5 and 10; and 2), site-directed mutagenesis to construct R52A. These results imply that C₄-C₇ single-bond rotation in PYP is an alternative to C₇-C₈ double-bond rotation, in case the nearby positive charge of R52 is absent, but rather facilitates, presumably with a compensatory movement, the physiological Z/E isomerization of the blue-light-absorbing chromophore.

INTRODUCTION

In addition to reproduction, and its inherent errors, which are cornerstones of evolution, the ability to perceive environmental signals and adjust accordingly is a key characteristic of cellular life. It is therefore of prime importance to understand the molecular basis of the elementary steps of such signal transduction processes and when necessary to repair or improve these processes. Photosensory receptors, i.e., proteins that can generate a biological signal upon the absorption of a photon of visible electromagnetic radiation, have traditionally played a key role as model systems for such studies (1). The accuracy with which these proteins can be activated in time and space is unrivalled.

Several different families of these photosensory receptors have been characterized, each with their own specific (chromophore) structure and mechanism of primary photochemistry. Best known are the rhodopsins, in which the absorption of green light leads to Z/E isomerization of the retinal chromophore, and the LOV domains, which show absorption of green light leads to Z/E isomerization of the flavin chromophore and a nearby cysteine. Here, however, we have chosen yet another model system for such studies, photoactive yellow protein (PYP (2)), which functions as a photosensory receptor for a photophobic response in Halorhodospira halophila (3).

Submitted March 24, 2011, and accepted for publication June 17, 2011.

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Editor: Leonid S. Brown.
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0006-3495/11/09/1184/9 $2.00

doi: 10.1016/j.bpj.2011.06.065
then rapidly (i.e., with a half-life of 6 ps) thermally relaxes back to the stable GSI.

The \( I_0 \) intermediate converts with \( \sim100\% \) efficiency to \( I_1 \) (also denoted \( pR_1 \)), and subsequently to the \( pR_2 \) intermediate, presumably by additional configurational relaxation of the \( cis \) chromophore. Next, a proton is transferred from E46 to the chromophore (15,20) at a rate of \( \sim10^3 \) s\(^{-1} \) to form the first of a series of blue-shifted intermediates (i.e., \( pB' \)) in this photocycle, which leads to (partial) unfolding of the protein (21) to form the signaling state \( pB \). A complex thermal recovery process, which involves the \( pG' \) intermediate, leads to re-formation of the ground state within 1 s (22–26).

Formation of the electronically excited singlet state through absorption of a blue photon is accompanied by a profound charge redistribution in the cinnamyl chromophore of PYP, as demonstrated with Stark spectroscopy (27). It is significant that in several polar organic dyes with a similar characteristic, based on a pronounced donor/acceptor asymmetry across their ethylenic bond, light absorption leads to formation of a so-called twisted-intramolecular charge transfer (TICT) state (28). However, the structural transition that underlies formation of a TICT state may well be a rotation (TICT) state (28). Nevertheless, rotational flexibility of the \( C_4-C_7 \) bond does contribute to an increase in the quantum yield of signaling state formation in PYP: restriction of this flexibility decreases the quantum yield of product formation in PYP and dramatically increases the yield of the GSI.

**MATERIALS AND METHODS**

**Set-up for ultrafast visible spectroscopy**

The ultrafast transient absorption experiments in the visible spectral range were performed with a setup described in more detail in Groot et al. (33). Briefly, the output of a Ti:Sapphire regenerative-amplified laser system operating at 1 kHz (Hurricane; SpectraPhysics, Mountain View, CA) is divided into two beams. One beam is sent to a BBO crystal to generate the excitation pulse at the desired center wavelength of 400 nm by

FIGURE 1 Schematic representation of the structure of the chromophore binding pocket of wild-type PYP before (A) and after (B) the two modifications characterized in this study, namely, the R52A mutation and replacement of the coumaryl chromophore by a rotation-locked derivative, (5-hydroxy indan-(1E)-ylidene)acetic acid.

The results obtained reveal that neither the net charge of R52 nor \( C_4-C_7 \) single-bond rotation is critically required for the primary photochemistry of PYP. Nevertheless, rotational flexibility of the \( C_4-C_7 \) bond does contribute to an increase in the quantum yield of signaling state formation in PYP: restriction of this flexibility decreases the quantum yield of product formation in PYP and dramatically increases the yield of the GSI.
frequency doubling. With the second beam, a white light continuum was generated by focusing it on a 2-mm quartz plate. The excitation pulse from the BBO crystal was focused in the sample to a diameter of ~130 μm and spatially overlapped with the smaller probe beam. The overlap between pump beam and probe beam was carefully checked to be homogeneous by means of spectral shape comparison on variation of the pump spot size. The absorption changes in the visible were recorded after dispersion in a spectrograph, with a 256-element diode array (S4801-256Q; Hamamatsu, Hamamatsu City, Japan). The pump beam was polarized at the magic-angle orientation (54.7°) with respect to the probe beam using a Berek polarizer. The sample was moved during the measurement in a Lissajous scanner to ensure a fresh spot for every excitation pulse. A phase-locked chopper operating at 500 Hz was used to ensure that on every other shot the sample was excited and the changes in transmission, and hence optical density, could be measured. The time delay between the pump and probe beam was controlled by sending the pump beam over a moveable delay line. The instrument response function, determined via the cross correlation of pump and probe, was ~150 fs. For each experiment, ~100 time-gated spectra were recorded between ~10 ps and 2.5 ns relative to the maximum of the instrument response function. All experiments were performed at room temperature.

Set-up for μs/ms time-resolved visible spectroscopy

An Edinburgh Instruments LP900 spectrometer (Livingston, West Lothian, United Kingdom) equipped with a photomultiplier, in combination with a Continuum Surelite OPO laser (for further details, see Hendriks et al. (34)) was used for μs/ms time-resolved visible spectroscopy. PYP samples were excited with 446-nm laser flashes of ~5–6 mJ/pulse (pulse duration 6 ns). Time traces were recorded for the four proteins at 360 nm, ~446 nm, and between 484 and 503 nm (dependent on the χ2 of the particular protein), with the slow-board option of the photomultiplier (time resolution ~2 μs). Optical interference filters were used before the sample to minimize measurement artifacts induced by probe light.

Transient ms/s UV-vis spectroscopy

UV-vis spectra were recorded using an HP8453 UV-vis spectrophotometer (Hewlett Packard, Palo Alto, CA). Time-resolved spectra were recorded from 250 to 600 nm, using an integration time of 0.1 s. A Kratkyhof cuvette was used to thermostat the sample at 25°C, with simultaneous pH recording. A Schott KL1500 LCD lamp was used to illuminate the samples with wild-type or R52A protein. For the rotation-locked proteins, a microsecond flash lamp was used.

Steady-state fluorescence

Steady-state fluorescence spectra were recorded on a Fluorolog 3 spectrometer (Spex, Metuchen, NJ) with a 450-W Xe lamp as the excitation light source. The excitation wavelength was set at the absorption maximum of the respective protein (see Fig. 2 below), and emission was recorded from 450 to 600 nm for the two rotation-locked derivatives (i.e., the wild-type (WTRL) and R52ARL) and from 455 to 600 nm (with a slit width of 5 nm) for the two proteins reconstituted with p-coumaric acid (i.e., wild-type and R52A). The slit width for the excitation and emission light was set at 0.5 and 5 μm, respectively, for all four samples.

Synthesis of (5-hydroxy indan-(1E)-ylidene)acetic acid (rotation-locked chromophore)

After protection of its phenolic hydroxy group with tert-butyl-dimethylsilanyloxyl chloride, ~300 mg of (5-hydroxy-indan-(1E)-ylidene)acetic acid (190.20 mol wt) was synthesized from 5-hydroxy-1-indanone through coupling with diethylphosphonoacetate. The phenolic hydroxyl group was deprotected with tetra-n-butyl-ammonium fluoride. For this synthesis, reagents were purchased at the highest commercial quality available and used without further purification. Flash chromatography was carried out with ACROS silica gel (particle size 35–70 μm). Infrared spectra were recorded using an IFS 28 spectrophotometer (Bruker, Billerica, MA), NMR spectra were obtained using a Bruker ARX 400 spectrometer (400 MHz), and accurate mass values of intermediates and the final product were recorded on a JMS SX/SX102A four-sector mass spectrometer (JEOL, Tokyo, Japan), coupled to a JEOL MS-MP7000 data system or a TSQ7000 mass spectrometer (Thermo Finnigan, San Jose, CA) using Xcaliber 1.2 software for acquisition and data processing.

Site-directed mutagenesis

Site-directed mutagenesis was performed using the QuikChange kit (Stratagene, La Jolla, CA) and confirmed by DNA sequencing, as described previously (35).

Sample preparation

Wild-type PYP and its R52A mutant derivative were produced and isolated as described previously for wild-type PYP (36). Apo-PYP was reconstituted with the 1,1’-carbonyldiimidazole derivative of p-coumaric acid or rotation-locked chromophore, as described by Hendriks et al. (37). The reconstituted holoproteins were purified in two subsequent steps, with Ni-affinity and anion-exchange chromatography, respectively (37). The purified holoproteins were used without removing the genetically introduced N-terminal hexahistidine-containing tag, in a buffer containing 20 mM Tris-HCl.

FIGURE 2 Characterization of the static UV-vis absorbance and fluorescence emission of the four PYP derivatives. (A) Absorption spectra of wild-type PYP (black), WTRL (red), R52A (blue), and R52ARL (green) in 20 mM Tris buffer, pH 8.0. The absorption maxima are centered at 446, 443, 450, and 445 nm, respectively. (B) The corresponding emission spectra, with excitation of all samples at their respective absorbance maxima.
were characterized with static UV-vis spectroscopy (Fig. 2 of the structure of their chromophore-binding pocket), dene)acetic acid, respectively (see Fig. 1 for an overview hydroxy-cinnamic acid and (5-hydroxy indan-(1E)-yli
i.e., wild-type and R52A-PYP reconstituted with 4-
purification, the four proteins studied in this investigation,
<
\begin{align}
\text{Stokes shift in the fluorescence emission spectra of PYP. The decrease in the dynamic}
\text{electric transition of PYP. The decrease in the dynamic}
\text{smaller contribution of the vibronic sideband of the main}
\text{chromophore,}
\end{align}

Data analysis

The transient difference absorption spectra were subjected to global and
target analysis, as reviewed in van Stokkum et al. (38). Briefly, the basis
of global analysis is the superposition principle, which states that the
measured $\psi(t,\lambda)$ data result from a superposition of the spectral properties, $\epsilon(\lambda)$, of the components present in the system of interest weighted by their concentration $c_j(t)$.

$\psi(t,\lambda) = \sum_{j=1}^{n_{\text{comp}}} c_j(t) \epsilon_j(\lambda)$

The $c_j(t)$ of all $n_{\text{comp}}$ components are described by a compartmental model that consists of first-order differential equations, with sums of exponential decays as solution. We will consider two types of compartmental model: 1), a sequential model with increasing lifetimes, also called an unbranched unidirectional model, which results in evolution-associated difference spectra (EADS); and 2), a full compartmental scheme, possibly including branchings and equilibria, which yields species-associated difference spectra (SADS). The latter is most often referred to as target analysis, where the target is the proposed kinetic scheme, including specific spectral assumptions.

With ultrafast spectroscopy, the instrument response function can usually adequately be modeled with a Gaussian with parameters for location and full width at half-maximum (typically 100–250 fs). The dispersion of this location parameter is described by a polynomial. All exponential decays from the above models have to be convolved with this instrument response function.

RESULTS

After heterologous overexpression in *Escherichia coli* and
purification, the four proteins studied in this investigation, i.e., wild-type and R52A-PYP reconstituted with 4-
hydroxy-cinnamic acid and (5-hydroxy indan-(1E)-yli
dene)acetic acid, respectively (see Fig. 1 for an overview of the structure of their chromophore-binding pocket), were characterized with static UV-vis spectroscopy (Fig. 2 A). The results show that whereas the R52A mutation causes a slight red shift (4 nm for samples containing the $p$-coumaryl chromophore), the two rotation-lock PYPs show a modest blue shift. The full width at half-maximum of the latter spectra, however, is significantly smaller than that of the two samples reconstituted with the endogenous chromophore, $p$-coumaric acid, presumably due to a much smaller contribution of the vibronic sideband of the main electronic transition of PYP. The decrease in the dynamic Stokes shift in the fluorescence emission spectra of the two rotation-locked PYPs is even more pronounced, shifting from >500 nm for the endogenous chromophore to <475 nm (Fig. 2 B) for the rotation-locked derivatives.

This figure also reveals that the already low fluorescence quantum yield of PYP is even lower (~50%) in the rotation-locked derivatives, whereas substitution of R52 by an alanine results in an almost threefold increase of this yield.

Next, time-resolved visible pump/visible probe measurements in the 100 fs to 2 ns time domain were performed on all four samples, using 400-nm excitation. All four samples show rich dynamics in which some trends are immediately apparent, like the more extensive ultrafast relaxation in the rotation-lock PYPs leading to a significantly shorter-lived signal than in wild-type PYP (see Fig. S1 in the Supporting Material for a set of transients of all four samples collected at 446 nm, derived from the time-gated spectra). However, much more detail is visible in the analysis of the corresponding EADS (Fig. S2). An optimal fit to the data requires four lifetimes for each sample plus a component that does not decay on the timescale of our experiment (i.e., $\gg 2.7$ ns).

These EADS clearly show that the two rotation-locked proteins have 1), a smaller red-shifted stimulated emission with respect to the 510-nm position at which the stimulated-emission band of the coumaryl derivatives is centered, consistent with their fluorescence characteristics (Fig. 2 B); 2), significantly faster and monoexponential excited-state decay (decay in 0.5 and 0.6 ps, respectively, versus the 0.7–7 ps in wild-type), as can be concluded from the disappearance of the contribution of stimulated emission from the subsequent spectra in each series of EADS; 3), both rotation-locked proteins form decreased amounts of the primary photoproducts (the blue and green spectra can be assigned to the states $I_0$ and $I_1$, with product absorption bands at ~485 and 475 nm, respectively). Note that the product bands of the rotation-locked proteins appear to be slightly blue-shifted, which may result in partial cancellation of their absorbance with the bleached ground-state absorption, thus making a reliable estimate of the amount of these products formed difficult; and finally, 4), the rotation-locked proteins display an intermediate spectrum with a 3-ps lifetime that resembles the spectrum of the GSI of wild-type PYP resolved in pump-dump-probe experiments (18,39) and target analysis (A. Rupenyan and M. L. Groot, unpublished).

However, to be able to characterize in more detail these initial photocycle steps and the distinct spectral characteristics of the various intermediates formed upon photoactivation in these four proteins, a target analysis of the data is required. A complication in this analysis is the multiplicity of the excited state of each sample: the decay of the excited state has to be fitted by up to three time constants, and in a similar way, the appearance of $I_0$ can be described with two to three time constants. From these excited states, the yield of $I_0$ formation is largest for the shorter-lived excited states, in agreement with previous observations (see, e.g., works by Larsen and colleagues (18,32)). However, the target analysis of the spectral data of the two rotation-locked proteins already provides satisfactory results using a single
excited state. Therefore, to facilitate comparison between the four samples here, we have fitted the datasets obtained with the two proteins reconstituted with the \( p \)-coumaryl chromophore (i.e., wild-type PYP and R52A) with a single component for the excited-state decay as well, at the cost of a small decrease in root-mean-squared value.

The results of this target analysis (see Fig. 3) and the corresponding table with rate constants (see Table S1) provide more quantitative information on the systems dynamics in the four proteins and give information beyond that derived from the global analysis (e.g., the quantum yields). From this target analysis, it is clear that rotation-locking of the chromophore causes not only much faster excited-state decay but also an almost twofold lower quantum yield of photochemistry. We were surprised to find that in the latter two samples this is accompanied by the absence of internal conversion directly to the ground state, presumably because the free-energy barrier for the transition that leads to the GSI is even lower. The result is that in these two samples, the quantum yield of formation of the GSI state reaches values that approach unity (i.e., 83%). The spectral characteristics of these intermediates are consistent with the above observations (Fig. 4): the stimulated emission of the rotation-locking of the target analysis, it is clear that rotation-locking of the chromophore causes not only much faster excited-state decay but also a smaller molar extinction coefficient. For the GSI, it is difficult to estimate the \( \lambda_{\text{max}} \) because of the extensive overlap with ground-state depletion. The \( I_1 \) intermediates show the expected blue shift relative to their corresponding \( I_0 \) states, except in the case of the \( I_1 \) state of the R52A protein, which is almost isoennergic with its \( I_0 \).

The results obtained to date have revealed that within this set of four proteins, R52A is the most similar to wild-type PYP. One would expect the rotation-locked samples to be more similar to wild-type PYP, but different from R52A PYP if the charge on R52 were steering the primary photochemistry of PYP toward single-bond rotation (see above).

As this observation is clearly different from what has been predicted by theory (17,30), we tested a second approach in which the charge on R52 is varied. By varying the pH of the buffer in the range 5–10, we modulated the net charge of the side chain of R52 (see Discussion) and, by consequence, the environmental electrostatics of the \( p \)-coumaryl chromophore. The results presented in Fig. 5 reveal that the primary photochemistry in PYP is totally invariant with pH in this pH range. This applies to both the observed lifetimes and the shape of the difference spectra.

Locking the rotation around the C4-C7 bond not only has consequences for the ultrafast photochemistry of PYP but might also affect the slower processes that occur in the photocycle of PYP. We therefore also analyzed the \( \mu \)s/ms time-resolved visible absorption changes at three different wavelengths: 360 nm, at which the main contribution is from \( pB \) intermediates; in the range 484–503 nm, to record the contribution of the red-shifted intermediates (i.e., \( pR \)) (see also Table S2); and \( \approx \)446 nm, the absorbance maximum of the four proteins, at which bleaching of \( pG \) and absorption of \( pR \) contribute to the dynamics of the changes in UV-vis absorbance. The absorbance traces at 360 nm are of particular interest, because at this wavelength

![Figure 3](image-url)
both the decay of the $I_1/pR$ state (which coincides with formation of $pB'$ (20)) and the thermal recovery of the ground state can be observed. The results obtained (Fig. 6) clearly reveal that the R52A mutation accelerates $pB'$ formation (in combination with the $p$-coumaryl chromophore) and retards ground-state recovery. This is similar to the effect observed by others (e.g., Hellingwerf et al. (4) and Cusanovich and Meyer (5)) in R52Q and several other mutant proteins. A global analysis of these data (Table S2, Fig. S3, and Fig. S4) furthermore shows that the effect of replacing the $p$-coumaryl chromophore with the rotation-locked chromophore is an approximately five- and ninefold retardation of the rate of formation of the first blue-shifted state for wild-type PYP and R52A, respectively, whereas the recovery reaction (i.e., the re-formation of $pG$) for these proteins is accelerated 8- and 16-fold, respectively. However, the data for the two rotation-locked proteins in this time domain are well-fitted with a sum of two exponentials (Table S2), whereas for the wild-type protein, at least three exponentials are required (26). We therefore carried out a target analysis of this same data set based on the photocycle scheme $pR \rightarrow pB' \rightarrow pB \rightarrow pG$. For the wild-type protein, the results obtained confirm previous observations (5,24,26), whereas the data obtained with the R52A protein show that this mutation particularly accelerates proton transfer from E46 to the chromophore (i.e., $pR \rightarrow pB'$) and also decelerates $pG$ recovery (Table 1). We therefore tentatively conclude that single-bond rotation around the C4-C7 bond contributes to both of these processes. The slower part of the photocycle of the two rotation-locked proteins is well described by the sequential model $pR \rightarrow pB \rightarrow pG$, in which a single exponent suffices to describe the $pR$ to $pB$ transition. The estimated SADS (see Fig. S5) are consistent with the expected shapes for $pR$ and $pB$, establishing the suitability of these two photocycle schemes for the two sets of proteins (i.e., wild-type and R52A on the one hand and WTRL and R52ARL on the other).

**DISCUSSION**

In the past, the use of various rotation-locked chromophores has provided important information on the primary photophysics in the two largest and most diverse families of photosensory receptors that use E/Z/E isomerization of their chromophore to initiate the biological signaling process, i.e., the rhodopsins (40,41) and the phytochromes (42). For the xanthopsin family also, chromophore derivatives with the C7=C8 ethylenic bond of the chromophore locked in the *trans* and *cis* states, respectively, have been exploited to better understand the molecular basis of functioning of this family (43,44).

Here, we have made use of yet another rotation-locked chromophore, i.e., one in which rotation of the C4-C7 single bond is prevented by making it part of a cyclopentane ring. This restricts the flexibility within this chromophore even more than it does within derivatives in which a cyclohexane ring is used instead (45). This rotation-locked analog has been used to reconstitute wild-type PYP and a mutant

![FIGURE 6](image)

**TABLE 1** Target analysis of the transitions between the intermediates of the photocycle of PYP in the microsecond-to-second time domain

<table>
<thead>
<tr>
<th>PYP derivative</th>
<th>$pR \rightarrow pB'$</th>
<th>$pB' \rightarrow pR$</th>
<th>$\Delta G$ (meV)*</th>
<th>$pB' \rightarrow pB$</th>
<th>$pB \rightarrow pG$</th>
</tr>
</thead>
<tbody>
<tr>
<td>Wild-type</td>
<td>3.65</td>
<td>1.72</td>
<td>19</td>
<td>2.02</td>
<td>0.00366</td>
</tr>
<tr>
<td>R52A</td>
<td>15.2</td>
<td>0.97</td>
<td>71</td>
<td>2.71</td>
<td>0.00049</td>
</tr>
<tr>
<td>WTRL</td>
<td>1.37</td>
<td>0.0276</td>
<td>0.0076</td>
<td></td>
<td></td>
</tr>
<tr>
<td>R52ARL</td>
<td>1.76</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

* $\Delta G$ of the reaction between $pR$ and $pB'$. Kinetic scheme for WTRL and R52ARL: $pR \rightarrow pB' \rightarrow pB \rightarrow pG$. Estimated rate constants (ms$^{-1}$) of the transitions between intermediates.
with an altered amino acid at position 52, R52A. Although studies were available in the literature on the nanosecond- to-microsecond spectroscopic characterization of the R52Q mutant of PYP, here we have used the R52A mutant to have the arginine substituted by the even less polar amino acid alanine, and we have characterized this protein at higher time resolution. Nevertheless, with respect to the quantum yield, absorbance maxima, and dynamics characteristics, the two mutants are quite similar (31,46,47).

The results of the ultrafast spectroscopy have been shown to be very similar between the two rotation-locked samples on the one hand and the two PYP derivatives reconstituted with p-coumaryl chromophore on the other. If the charged R52 had been decisive for the occurrence of C=O double-bond isomerization (17), one would have predicted a much larger difference between the wild-type and R52A PYP isomerization. It seems to us that in this aspect, the computational description of Z/E isomerization in PYP has to be refined. Conversely, the two rotation-locked proteins are similar in their spectroscopic properties and their dynamics, and show a reduced, but not blocked, product formation. Therefore, we conclude that the flexibility to rotate around the C2=C3 bond is necessary for maximal yields of photochemistry in PYP. We think that it will be revealing in future computational analyses of PYP to include studies of protein reconstituted with this single-bond rotation-locked chromophore, to provide a firm theoretical basis for our observations. It is relevant to note that considering the mechanism of isomerization of the C7=C8 ethylenic bond in PYP, which is followed by a rotary movement of the carbonyl group around the long axis of the p-coumaryl chromophore, single-bond rotation around the C-S bond and/or around single bonds within C69 may also be part of the primary photochemistry in PYP. Several additional features reported in this study form a challenge for future calculations based on first principles. A relevant example is the relatively blue peak position of the rotation-locked derivatives in the I0 state (Fig. 4).

For the rotation-locked proteins, just a single excited-state (ES) compartment was sufficient to fit the ultrafast transient absorption data. This suggests that the multiphasic nature of the decay of the ES, which for wild-type PYP needs to be fitted with up to three ES compartments (18) (A. Rupenyan and M. L. Groot, unpublished results), is an inherent property of the chromophore and is absent in the rotation-locked samples. Furthermore, the increased rigidity of the locked chromophore abolishes internal conversion (Fig. 3), which is according to expectation based on theory set forth by others (e.g., Seidner and Domcke (48) and Abbruzzetti et al. (49)), and approximately halves the quantum yields of photochemistry and fluorescence in the two rotation-locked proteins. As a result, the contribution of decay of the ES through the channel for GSI formation has increased, up to 0.83 in rotation-locked R52A PYP. This latter observation will aid in the further characterization of the precise configuration of this GSI intermediate with time-resolved infrared spectroscopy (14,19).

Although biochemistry textbooks generally quote a value of ~12.5 for the pK of the side chain of an arginine (see, e.g., Berg et al. (50)), the value for R52 in PYP must be much lower. First, in the neutron diffraction study of PYP that revealed the existence of the low-barrier hydrogen bond between E46 and the chromophore, it was observed that even at pH 7.5 (the pH of the mother liquor), R52 was fully uncharged (11). This result implies that the pK of R52 is <7.5, although this pK might be tuned slightly because R52 is a surface residue. In this respect, it is relevant to note that a recent study in which an NMR titration of all amino acids of PYP was presented revealed that R52 has a pK of 8.7 (F. A. A. Mulder, unpublished). Hence, one can safely assume that the net charge of R52 will change from positive to neutral when one increases the pH from 5 to 10. As in this transition the primary photochemistry of PYP remains unaltered (Fig. 5), this provides independent evidence that the charge on R52 does not have a profound effect on the outcome of the isomerization process in the chromophore of PYP that follows (blue) light absorption.

Restriction of the rotation across the C4-C7 bond also significantly affects the kinetics in the intermediate and slower parts of the photocycle of PYP. Two effects are distinguishable: the rate of formation of the blue-shifted intermediate is decreased, and its rate of decay is accelerated (Table 1). Both effects are compatible with the interpretation that the pB state of the rotation-locked proteins represents an incompletely unfolded signaling state, leading to the prediction that its absorbance maximum is slightly red-shifted compared to the corresponding intermediate of wild-type PYP (26,51). Apparently, hindering C4-C7 single-bond rotation increases the time it takes to bring E46 and the chromophore into a position that allows unidirectional proton transfer, which in turn leads to a less stable signaling state.

Comparing wild-type PYP with R52A shows that this mutation stabilizes the pB state with respect to pR (Table 1, column 4). Considering the recovery rates of the two proteins, it may well be that this is due to stabilization of pB in the R52A protein, but a strained chromophore may of course also destabilize pR. It has been reported that R52 in the pB state hydrogen-bonds to the chromophore (52). However, as this observation was made on a pB state confined in a crystal lattice, whereas the pB states in solution appear to be quite different (53,54), we do not think that such direct hydrogen-bonding is involved.

The effects of the restricted single-bond rotation, and the R52A mutation, on the photocycle kinetics turn out to be additive, so that in the R52ARL protein, the recovery rate is close to that of wild-type PYP.

A comparison of the maximal increase in absorbance at 360 nm and the maximal decrease at 446 nm (Fig. 6 and
Fig. S5) using the microsecond/millisecond data from wild-type PYP as a reference also allows an independent estimate of the quantum yield of these PYP derivatives. Considering the accuracy with which such data can be measured, the data obtained are consistent with the results displayed in Fig. 3: An approximately twofold decrease is caused by the rotation-locked chromophore.

It will be of interest to test this and other chromophore analogs on the phototactic capabilities of *H.* *halophila,* similar to the way they were exploited in *Idiomarina halophila* (44).

CONCLUSIONS

We have studied the isomerization pathway of PYP and the role of the charge of the side chain of amino acid R52 therein by selectively locking one of the single bonds of the chromophore. Preventing rotation of the C4-C7 chromophore bond enhances the rate of formation of a nonproductive intermediate state, GSI, and leads to reduction of the physiological Z/E isomerization of the chromophore. These results confirm that C4-C7 single-bond rotation in PYP is not an alternative to C7=C8 double-bond rotation but appears to optimize double-bond isomerization (e.g., with a compensatory movement). The initial photocycle dynamics of PYP were observed to be not significantly affected by the charge of the amino acid residue at position 52, which was varied by 1), varying the pH of the sample between 5 and 10; and 2), site-directed mutagenesis to construct R52A.

SUPPORTING MATERIAL

Two tables and five figures are available at http://www.biophysj.org/biophysj/supplemental/S0006-3495(11)00836-8.

REFERENCES


Biophysical Journal 101(5) 1184–1192