Resonance Raman evidence that the thioester-linked 4-hydroxycinnamoyl chromophore of photoactive yellow protein is deprotonated in the dark state.

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Resonance Raman Evidence That the Thioester-Linked 4-Hydroxycinnamyl Chromophore of Photoactive Yellow Protein Is Deprotonated

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ABSTRACT: Resonance Raman spectra of the ground state of photoactive yellow protein (PYP), a photoactive pigment found in Ectothiorhodospira halophila, have been obtained with excitation at 413.1 nm using a microspinning sample cell. The resonance Raman spectra of the thioester-linked 4-hydroxycinnamyl chromophore in the protein are compared with the preresonance Raman spectra of the 4-hydroxycinnamyl phenyl thioester and 4-hydroxycinnamic acid model compounds at various pH values. Bands at 1568, 1542, 1500, 1434, and 1166 cm⁻¹ in the Raman spectrum of the anionic form of the 4-hydroxycinnamyl phenyl thioester are shown to be characteristic for the deprotonation of the chromophore. The observation of bands in PYP exhibiting very similar frequency and intensity patterns provides strong evidence that the chromophore in PYP is stabilized as a phenolate anion at pH 7.4, in support of conclusions from crystallographic studies. Furthermore, the insensitivity of the PYP Raman spectrum to placement of the protein in D₂O buffer is consistent with the absence of the exchangeable phenolic proton on the cinnamyl chromophore. These results establish the feasibility of elucidating the molecular mechanism of light-to-information transduction by this new photosensory pigment with resonance Raman spectroscopy.

Photoactive yellow protein (PYP),† a water-soluble yellow-colored protein with a visible absorption maximum at 446 nm, is found in several halophilic phototrophic bacteria including Ectothiorhodospira halophila (Meyer, 1985; Meyer et al., 1990; Hoff et al., 1994a). E. halophila exhibits a negative phototactic reaction or repellent response to physiological intensities of blue light (Sprenger et al., 1993). The wavelength dependence of this phototaxis matches the absorption spectrum of PYP, leading to the hypothesis that PYP functions as the photoreceptor in E. halophila (Sprenger et al., 1993). Absorption of a photon by PYP initiates a cyclic photochemical reaction with at least two photointermediates (Meyer et al., 1987; Hoff et al., 1994a). The photocycle of PYP is similar to those of membrane-bound rhodopsins isolated from Halobacterium salinarium (Meyer et al., 1987; Hoff et al., 1994a). However, the protein structure of PYP is very different from that of bacteriorhodopsin (McRee et al., 1989; Van Beeumen et al., 1993); PYP has an α/β-fold characterized by a central, twisted, six-stranded, antiparallel β-sheet flanked on both sides by loops and helices (Borgstahl et al., 1995), while bacteriorhodopsin contains seven closely packed α-helices (Henderson et al., 1990). In addition, while the chromophore of PYP is a 4-hydroxycinnamyl group covalently bound to a cysteine via a thioester linkage (Hoff et al., 1994b; Baca et al., 1994), all rhodopsins contain a Schiff base-linked retinal chromophore. PYP therefore exemplifies a new class of photoreceptor proteins whose protein structure is now well known (Hoff et al., 1994b; Baca et al., 1994; Borgstahl et al., 1995). However, little is known about the structure of the chromophore and especially the light-induced structural changes in the chromoprotein that lead to the signaling state of this photoreceptor.

We report here the first resonance Raman vibrational spectra of PYP. Resonance Raman spectroscopy provides a sensitive and selective probe for monitoring the structure and structural changes of chromophores embedded in proteins (for example, see Mathies et al. (1987)). Interestingly, X-ray crystallographic data suggest that the chromophore in the ground state of PYP is stabilized within the folded protein as a phenolate anion (Baca et al., 1994; Borgstahl et al., 1995). This suggestion encouraged us to examine the ionization state of the chromophore using resonance Raman spectroscopy. To interpret the basic vibrational characteristics of the PYP chromophore, preresonance Raman spectra of the 4-hydroxycinnamyl phenyl thioester and 4-hydroxy-cinnamic acid model compounds were also obtained at various pH values. Comparison of PYP and model compound Raman data provides strong evidence that the chromophore in native PYP is deprotonated at the phenolic hydroxyl group at pH 7.4 and also gives new insight into how the chromophore interacts with the encompassing protein. This work establishes the feasibility of studying the various PYP photointermediates to elucidate its mechanism of phototransduction.

MATERIALS AND METHODS

Photoactive yellow protein from E. halophila was isolated by a modification of Meyer's method (1985) as described by Hoff et al. (1992). Typically, 200 µg of freeze-dried
The model compound, 4-hydroxycinnamyl phenyl thioester (HCPT), was prepared by the reaction of thiophenol with acetylpyridinium salt formed from free 4-hydroxycinnamic acid and 2-fluoro-1-methylpyridinium p-toluenesulfonate, as described previously (Duran et al., 1987). The final purification of the model compound was performed with a Rainin HPLC, which was equipped with a C18 reverse phase column (25 mm x 500 mm) run with a linear gradient from 60% acetonitrile in water to 100% acetonitrile over 40 min at 4.0 mL min⁻¹. The eluted solution was then vacuum evaporated.

A microspinning sampling system, consisting of a thin (150-μm) circular cover glass (18 mm diameter) and a 360-μm Teflon spacer, was developed for resonance Raman studies on PYP. The sample spinning system, which is shown in Figure 1, allows us to record resonance Raman spectra from as little as 80 μL of colored-protein solution at any rotation speed from 1 to 30 Hz. This minimized the contamination of spectra with scattering from photoproducts that might build up using stationary cell formats. For resonance Raman spectroscopy, typically ~80 μL of aqueous protein solution was secured into a shallow circular chamber (18 mm diameter) in a stainless steel block that was formed by clamping a thin circular cover glass (18 mm diameter, 150 μm thick) on a 360 μm thick Teflon spacer using a threaded ring. The resonance Raman scattering was collected at about 90° to the incident laser beam. The protein was dissolved in 180 μL of 10 mM Tris-HCl (pH 7.4) buffer, and then the solution was centrifuged at ~4000 rpm in a microcentrifuge tube for 1 min to remove insoluble particles.

Normal coordinate analysis was performed using the semiempirical PM3 Hamiltonian running under HyperChem version 4.0 (Hypercube Inc.) on a NEC Image P90 with Intel 90-MHz Pentium microprocessor.

**RESULTS AND DISCUSSION**

The 413.1-nm excited resonance Raman spectra of PYP in H₂O and D₂O in the 1750–1000 cm⁻¹ region are compared in Figure 2 with the 488.0-nm excited resonance Raman spectrum of the neutral form of HCPT at pH 9.5. At a glance, the resonance Raman spectrum of PYP in H₂O in Figure 2A is more similar to the Raman spectrum of the anionic form of HCPT at pH 9.5. A comparison of the resonance Raman spectra of PYP in H₂O and D₂O in the 1750–1000 cm⁻¹ region are compared in Figure 2 with the 488.0-nm excited resonance Raman spectrum of the neutral form of HCPT at pH 9.5. At a glance, the resonance Raman spectrum of PYP in H₂O in Figure 2A is more similar to the Raman spectrum of the anionic form of HCPT at pH 9.5. A comparison of the resonance Raman spectra of PYP in H₂O and D₂O in the 1750–1000 cm⁻¹ region are compared in Figure 2 with the 488.0-nm excited resonance Raman spectrum of the neutral form of HCPT at pH 9.5. At a glance, the resonance Raman spectrum of PYP in H₂O in Figure 2A is more similar to the Raman spectrum of the anionic form of HCPT at pH 9.5. At a glance, the resonance Raman spectrum of PYP in H₂O in Figure 2A is more similar to the Raman spectrum of the anionic form of HCPT at pH 9.5. At a glance, the resonance Raman spectrum of PYP in H₂O in Figure 2A is more similar to the Raman spectrum of the anionic form of HCPT at pH 9.5.

Before examining the details of the protein spectra, the effect of deprotonation on the molecular vibrations of HCPT...
must be examined to determine the proper chemical structure to be discussed. Upon deprotonation, the most intense doublet band centered at 1600/1587 cm\(^{-1}\) in Figure 2C downshifts to 1568/1542 cm\(^{-1}\). The two bands at 1600 and 1587 cm\(^{-1}\) are analogous to the Y8a and Y8b modes of tyrosine, respectively ([for review, see Harada and Takeuchi (1986)]. The deprotonation of tyrosine to form tyrosinate is known to shift the Y8a and Y8b modes from 1617 to 1603 cm\(^{-1}\) and from 1601 to 1558 cm\(^{-1}\), respectively. The latter large 43-cm\(^{-1}\) downshift is partially due to the involvement of phenolic hydrogen motions in the corresponding mode of tyrosine (Harada & Takeuchi, 1986). Thus, it is reasonable that the bands at 1600 and 1587 cm\(^{-1}\) for the neutral form of HCPT would be very sensitive to deprotonation. Second, in the spectrum of the anionic form, two distinctive bands show up at 1500 and 1434 cm\(^{-1}\), that can be ascribed to the Y19a and Y19b modes of tyrosine, respectively. Third, the band at 1176 cm\(^{-1}\) in Figure 2C downshifts by 10 cm\(^{-1}\) to 1166 cm\(^{-1}\) in Figure 2D. Thus, there are a variety of distinctive marker bands for the deprotonation of the PYP chromophore.

The above three spectral characteristics accompanying deprotonation are also confirmed in the protein spectrum in Figure 2A. In particular, the low frequencies of the 1558/1534-cm\(^{-1}\) doublet, the presence of the characteristic modes at 1498 and 1439 cm\(^{-1}\), and the excellent frequency correspondence of the 1165-cm\(^{-1}\) mode all argue that the chromophore in the ground state of PYP is deprotonated. Thus, the resonance Raman spectrum of PYP at pH 7.4 can be understood in terms of the deprotonation of the 4-hydroxycinnamyl chromophore at the hydroxyl group.

An additional line of evidence that the chromophore in PYP is deprotonated is obtained by examining spectra in D\(_2\)O. Solvent replacement by D\(_2\)O does not cause any significant change in the spectrum of the protein, as shown in panels A and B of Figure 2. There is only a small difference in peak position and relative intensity between the protein spectra in H\(_2\)O and D\(_2\)O. For example, the prominent bands at 1558, 1498, 1439, and 1165 cm\(^{-1}\) in H\(_2\)O shift by only 3-4 cm\(^{-1}\), and the band near 1290 cm\(^{-1}\) is somewhat weaker in D\(_2\)O than in H\(_2\)O. The slight spectral differences between H\(_2\)O and D\(_2\)O might suggest that some perturbation is imposed on the deprotonated chromophore, e.g., by hydrogen-bonding donors in the protein and/or internal water molecules vibrationally coupled to the chromophore. It is important to note that the spectrum of neutral HCPT is sensitive to D\(_2\)O exchange as expected, while that of anionic HCPT is not (data not shown).

Two broad bands are seen near 1670 and 1720 cm\(^{-1}\) in the protein spectrum of Figure 2A. The intensity of these bands increases when the spinning speed of the Raman sample cell is slowed from 20 to 1 Hz (data not shown). Upon speeding up the rotation rate, the intensity of both bands immediately drop, demonstrating that they are due to transient intermediates rather than permanent photodegradation. A more detailed characterization of these intermediate spectra and comparison with model compounds will be presented elsewhere.

There are two other interesting features to be noted in the resonance Raman spectrum of PYP. First, there is an intense band at 1288 cm\(^{-1}\) that is probably due to stretching vibrations delocalized over the 4-hydroxycinnamyl skeleton, mainly ascribable to tyrosinate C=O and C–C stretching vibrations delocalized over the 4-hydroxycinnamyl skeleton. An atomic model compound of the acryloyl fragment –C=C–(–S–)=O. As shown in the model compound spectra in panels C and D of Figure 3, this band is seen near 1307 cm\(^{-1}\); no substantial change in the peak position is induced upon deprotonation, but the relative intensity of the band is considerably enhanced. The difference in wavenumber seen between PYP and 4-hydroxycinnamyl phenyl thioester might be associated with the conformation around the C–C single bond of the –C=C–C(–S–)=O fragment of the chromophore. An atomic model (Baca et al., 1994; Borgstahl et al., 1995), where the positions and bonding of the heavy (non-hydrogen) atoms in the 4-hydroxycinnamyl chromophore were crystallographically determined based on 1.4-Å diffraction data of PYP, provides insight into the conformation around the C–C single bond. The model clearly indicates that the chromophore takes up an s-cis conformation in the binding site of the protein. Although the conformation around the C–C single bond of the 4-hydroxycinnamyl phenyl thioester model compound in solution is not known, it is reasonable to assume that the model compound is found in the s-trans conformation. This suggests in turn that the wavenumber difference seen for the band near 1300 cm\(^{-1}\) between PYP and 4-hydroxycinnamyl phenyl thioester is due to alteration in the torsion angle about the C–C single bond for an s-cis form. Normal mode calculations on the thioester chromophore support the idea that the C–C mode frequencies are sensitive to conformational changes. The above results suggest that the band near 1300 cm\(^{-1}\) could be an important clue to determine the conformation of the chromophore in other photoinduced intermediates involved in the PYP photocycle.

The second feature to be noted is that a distinctive band is observed at 1633 cm\(^{-1}\) in the protein spectrum of Figure 2A but the corresponding band is seen at 1607 cm\(^{-1}\) in the HCPT spectrum of Figure 2D. Figure 3 shows that there are at least three bands near 1600 cm\(^{-1}\) for the 4-hydroxycinnamic acid model compound in the neutral and monoanionic forms. Further, there are at least two bands at 1630 cm\(^{-1}\)
and 1592 cm$^{-1}$ in this region for 4-hydroxycinnamic acid in the
dianionic form. Based on analogy with tyrosine (Harada & Takeuchi, 1986) and also with the HCPT results discussed
above, the bands near 1610 and 1594 cm$^{-1}$ seen in Figure 3,
panels A and B, are assigned to vibrational modes analogous to Y8a and Y8b of tyrosine, respectively; the bands at 1592 and 1546 cm$^{-1}$ in Figure 3C can be assigned
to vibrational modes equivalent to Y8a and Y8b of tyrosinate,
respectively. An important common feature for the above
three forms of 4-hydroxycinnamic acid is that a distinctive band is seen in the 1630–1640 cm$^{-1}$ range. A semiempirical
calculation for 4-hydroxycinnamic acid using PM3 indicates
that a stretching vibration of the central C=C double bond
makes a significant contribution to the 1635 cm$^{-1}$ mode.
Recently, D’Ordine et al. (1994) found drastic changes in the
Raman features for cinnamyl-coenzyme A, when the ligand binds to crotonase. The downshift of the acryloyl
C=C stretching vibration to 1563 cm$^{-1}$ was explained by
an electronic rearrangement of the π-electrons mainly in the
acryloyl portion of the cinnamyl chromophore upon binding
to crotonase. There is, however, no evidence that a similar
effect is occurring on the acryloyl portion of the chromophore
in PYP, since the C=C double bond stretching vibration of the
chromophore is seen at 1633 cm$^{-1}$ in the encompassing protein, close to the frequency observed in the model compounds.
The appearance of this band at 1633 cm$^{-1}$ in the protein spectrum of Figure 2A is quite interesting,
because it provides a way to probe the structure of the central
protein spectrum of Figure 2A is quite interesting,
photointermediates. Further experimental and theoretical
calculation for 4-hydroxycinnamic acid using PM3 indicates
an electronic rearrangement of the π-electrons mainly in the
acryloyl portion of the cinnamyl chromophore upon binding
to crotonase. There is, however, no evidence that a similar
effect is occurring on the acryloyl portion of the chromophore
in PYP, since the C=C double bond stretching vibration of the
chromophore is seen at 1633 cm$^{-1}$ in the encompassing protein, close to the frequency observed in the model compounds.

An important outcome of the present work is that comparative Raman studies on PYP in H$_2$O and D$_2$O and on its model compounds provide the unequivocal conclusion that the 4-hydroxycinnamyl chromophore in PYP at pH 7.4 is deprotonated in the ground state. The full crystallographic atomic model of PYP proposes that the deprotonated chromophore is stabilized by hydrogen bonds from the side chains of Tyr42 and Glu46 to the phenolic oxygen atom and by electrostatic complementarity with the positively charged Arg52. These three amino acids are interlocked by Thr50 through a network of hydrogen bonds (Borgstahl et al., 1995).

All structural information available now on PYP, including this Raman study, leads to a model of the binding pocket of PYP in the ground state, as shown in Figure 4. The 4-hydroxycinnamyl chromophore is deprotonated to form a phenolate anion. The three-center hydrogen-bonding interactions with the side chains of Tyr42 and Glu46, in concert with the positively charged side chain of Arg52, are presumably used to stabilize the phenolate anion, resulting in a lowering the pK$_a$ of the PYP chromophore by 2 or more units. It is estimated that the pK$_a$ of the chromophore in the unfolded holoprotein is 9.0 ± 0.5 (Baca et al., 1994). Resonance Raman studies on photointermediates of PYP are in progress and will provide dynamical information on the structure of the chromophore and its interactions with apoprotein during its progression through the photocycle. In particular, it will be important and interesting to determine if light absorption produces changes in C=C configuration, C–C conformation, and/or protonation state.

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REFERENCES

Baca, M., Borgstahl, G. E. O., Boissinot, M., Burke, P. M.,
Biochemistry 33, 14369–14377.
Biochemistry 34, 6278–6287.
D’Ordine, R., Tonge, P. J., Carey, P. R., & Anderson, V. E. (1994)
Biochemistry 33, 12635–12643.
Henderson, R., Baldwin, J. M., Cesa, T. A., Zemlin T. A.,
Hoff, W. D., Kwa, S. L. S., Van Grondelle, R., & Hellingwerf, K.
Hoff, W. D., Van Stokkum, I. H. M., Van Ramesdonk, H. J., Van
Bredereode, M. E., Brouwer, A. M., Fitch, J. C., Meyer, T. E.,
Van Grondelle, R., & Hellingwerf, K. J. (1994a) Biophys. J. 67,
1691–1705.
Hoff, W. D., Dux, P., Hard, K., Devreese, B., Nugteren-Roodzant,
I. M., Criaarda, W., Boelens, R., Kaptein, R., Van Bueemen,
Hoff, W. D., Sprunger, W. W., Postma, P. W., Meyer, T. E.,
Veenhuis, M., Leguith, T., & Hellingwerf, K. J. (1994c) J.
Biochemistry 26, 418–423.
Van Bueemen, J. J., Devreese, B. V., Van Jun, S. M., Hoff, W.
D., Hellingwerf, K. J., Meyer, T. E., Mccre, D. E., &
B1051306Z