



Vibrational analysis on the revised potential energy curve of the low-barrier hydrogen bond in photoactive yellow protein

Yusuke Kanematsu^{a,b}, Hironari Kamikubo^c, Mikio Kataoka^c, Masanori Tachikawa^{b,*}

^a Graduate School of Information Science, Hiroshima City University, 3-4-1 Ozuka-Higashi, Asa-Minami-Ku, Hiroshima 731-3194, Japan

^b Quantum Chemistry Division, Yokohama City University, Seto 22-2, Kanazawa-ku, Yokohama 236-0027, Japan

^c Nara Institute of Science and Technology, 8916-5 Takayama, Ikoma, Nara 630-0192, Japan

ARTICLE INFO

Article history:

Received 18 August 2015

Received in revised form 15 October 2015

Accepted 23 October 2015

Available online 31 October 2015

Keywords:

Low-barrier hydrogen bond

Photoactive yellow protein

Vibrational analysis

ONIOM

PCM

ABSTRACT

Photoactive yellow protein (PYP) has a characteristic hydrogen bond (H bond) between *p*-coumaric acid chromophore and Glu46, whose OH bond length has been observed to be 1.21 Å by the neutron diffraction technique [Proc. Natl. Acad. Sci. 106, 440–4]. Although it has been expected that such a drastic elongation of the OH bond could be caused by the quantum effect of the hydrogen nucleus, previous theoretical computations including the nuclear quantum effect have so far underestimated the bond length by more than 0.07 Å. To elucidate the origin of the difference, we performed a vibrational analysis of the H bond on potential energy curve with O...O distance of 2.47 Å on the equilibrium structure, and that with O...O distance of 2.56 Å on the experimental crystal structure. While the vibrationally averaged OH bond length for equilibrium structure was underestimated, the corresponding value for crystal structure was in reasonable agreement with the corresponding experimental values. The elongation of the O...O distance by the quantum mechanical or thermal fluctuation would be indispensable for the formation of a low-barrier hydrogen bond in PYP.

© 2015 Kanematsu et al., Published by Elsevier B.V. on behalf of the Research Network of Computational and Structural Biotechnology. This is an open access article under the CC BY license (<http://creativecommons.org/licenses/by/4.0/>).

1. Introduction

Photoactive yellow protein (PYP) is a water-soluble photosensor protein found in halophilic photosynthetic bacteria. This protein is known to play an important role in the photocycle that regulates the negative phototaxis behavior of the bacteria [1]. PYP from *H. halophila* has especially drawn substantial attention due to the characteristic hydrogen bond (H bond) in the site. Yamaguchi et al. reported the detailed crystal structure of dark-state PYP with the coordinates of hydrogen atoms by the neutron diffraction technique [2]. The structure of PYP is shown in Fig. 1. They have assigned a hydrogen bond between Glu46 and *p*-coumaric acid (*p*CA) chromophore of PYP with significantly long O–H bond of 1.21 Å as low-barrier hydrogen bond (LBHB), which had never been directly observed in proteins until then. They have suggested the roles of LBHB in PYP to stabilize the negative charge around the chromophore in the protein interior, and to mediate the fast proton transfer during the photocycle. It has also been found that Arg52 located near the chromophore was deprotonated (neutral), whereas it had been believed to be protonated to act as counterion for the negative chromophore according to X-ray crystallography [3] and electronic structure calculation [4].

It was, however, claimed by Saito and Ishikita that Arg52 should be protonated and the H-bond between *p*CA and Glu46 was not LBHB but a normal H-bond according to the potential energy profile analysis with the conventional QM/MM calculation, and the comparison between the experimental chemical shifts in solution [5] and their computational values under the previously mentioned condition [6,7]. Hirano and Sato compared the potential energy profiles for systems with and without the protonation of Arg52 using the ONIOM method [8,9], which is an efficient method to calculate large systems such as proteins by dividing the system into several layers, and found the low barrier height for deprotonated Arg52 model with respect to hydrogen transfer coordinates in H-bond [10].

For the computation of the molecular geometry for H-bonded systems, we should pay careful attention to the protonic or deuteronic fluctuation in H-bonds due to nuclear quantum effect [11] and not only to the electrostatic contribution of the surrounding environment. Kita et al. calculated the isolated cluster model of H-bonding center in PYP by multicomponent quantum mechanics (MC_QM) method [12–14] and found that O–H bond length becomes longer due to the nuclear quantum effect [15]. Nadal-Ferret et al. showed that long O–H bonds could be experimentally observed by taking account of the nuclear quantum fluctuation of the hydrogen nuclei, and by local vibration analysis using QM/MM for PYP with deprotonated Arg52 [16]. By comparison of

* Corresponding author.

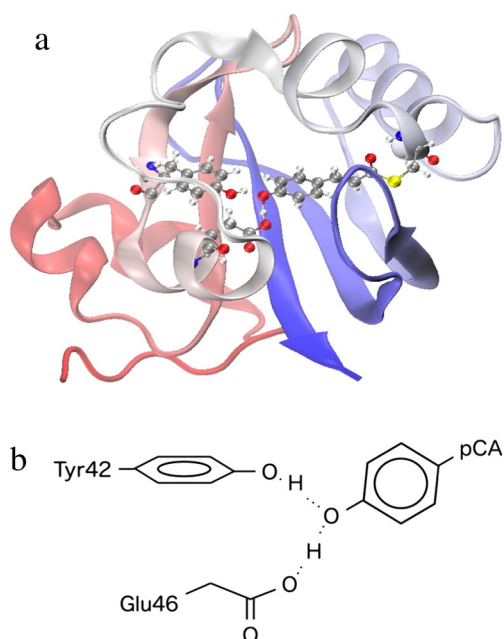


Fig. 1. (a) The entire structure and (b) the active center of photoactive yellow protein. OH bond focused on in the present work is also indicated.

the experimental and the computational geometrical parameters with and without the protonation of Arg52, they suggested that the formation of LBHB between pCA and Glu46 would be possible if Arg52 was deprotonated. Recently, we have also analyzed this geometry by the combination of ONIOM and MC_QM [ONIOM (MC_QM:MM)], and validated the above suggestion by comparison with the corresponding experimental values [17].

Table 1 lists the experimental and the computational OH bond lengths in various previous papers. Each computational work in Table 1 shows that the nuclear quantum effect of hydrogen nuclei elongates the OH bond length from the equilibrium structure. There, however, remains a difference between experimental and theoretical OH bond lengths of more than 0.07 Å, and the experimental observation was not yet fully supported by the computations.

In our previous work, we have examined several computational conditions for ONIOM calculations [17]. We found the expansion of the QM region can involve the degradation of the barrier height, which reasonably agreed with all electron ONIOM (QM:QM) calculations. It could be expected that the vibrational analysis on this potential energy curve would provide longer OH bonds than that of previous works. Therefore, the present paper will be devoted to the vibrational analysis for the model system of PYP with expanded QM region in order to elucidate the origin of the difference between the experimental measurement and the theoretical computation.

Table 1

The experimental and the computational OH bond lengths of Glu46 in the deuterated PYP from the previous works.

Experimental	(ref. [2])	R	1.21
Computational	(ref. [15])	R_{eq}	1.02
		$\langle R \rangle$	1.05
	(ref. [16])	R_{eq}	1.05
		$\langle R \rangle$	1.10
	(ref. [17])	R_{eq}	1.08
		$\langle R \rangle$	1.14

Units are in Å. For computational lengths, both the equilibrium (R_{eq}) and the vibrationally averaged ($\langle R \rangle$) values are shown.

2. Computational detail

We performed a numerical one-dimensional vibrational analysis by solving the nuclear Schrödinger equation on the basis of the Born–Oppenheimer approximation. The analyses dealt with two initial structures of PYP, one of which was the crystal structure (PDB ID: 2ZOI; temperature, 295 K; resolution, 1.50 Å) obtained by the neutron diffraction technique [2], and the latter was the equilibrium structure that has been optimized by conventional ONIOM calculation in our previous work [17]. The missing atoms in the crystal structure have been compensated for by AmberTools [18,19], resulting 1929 atoms with a total charge of 6– for the entire PYP. We utilized the ONIOM Electronic Embedding (ONIOM-EE) method [8,9] with the computational condition of “System 3-dp” of ref. [17], which includes Ile31, Tyr42, Glu46, Thr50, Cys69, pCA, and Arg52 in deprotonated form inside the QM region with CAM-B3LYP/6-31 + G(d,p) [20–22] level of calculation, and the other residues are in molecular mechanical level of calculation with AMBER ff99 and GAFF parameters [23]. As in ref. [16] and the Appendix in ref. [17], unrelaxed one-dimensional potential energy curves for the migration of the hydrogen nucleus along the direction vector q from Glu46 to pCA have been constructed for the vibrational analysis.

3. Results and discussion

3.1. The vibrational analysis on the equilibrium structure

At first, we would like to focus on the results of the vibration analysis on the equilibrium structure. Fig. 2 shows the potential energy curve and the corresponding vibrational distributions of the ground and the first excited states of a proton and a deuteron. The corresponding energy levels and the vibrationally averaged OH bond lengths are shown in

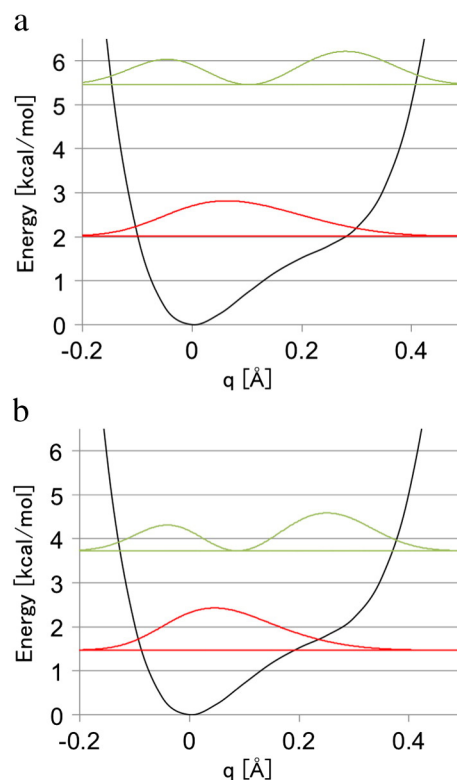


Fig. 2. The potential energy curve (black) and the corresponding vibrational distribution of the ground (red) and the first excited (green) states of (a) a proton and (b) a deuteron in the hydrogen bond between Glu46 and pCA of PYP at the equilibrium structure. The origin of the coordinate q was set on the equilibrium bond length (1.08 Å).

Download English Version:

<https://daneshyari.com/en/article/2079084>

Download Persian Version:

<https://daneshyari.com/article/2079084>

[Daneshyari.com](https://daneshyari.com)