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Substrate water exchange in photosystem II core complexes of the extremophilic red alga *Cyanidioschyzon merolae* $^{\!\!\!\!\!\!\!\!\!\!\!\!/}$



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ARTICLE INFO

Article history:
Received 22 February 2014
Received in revised form 31 March 2014
Accepted 1 April 2014
Available online 12 April 2014

Keywords:
Cyanidioschyzon merolae
Photosystem II
Water oxidation
Oxygen evolution
Substrate—water exchange
Membrane-inlet mass spectrometry

ABSTRACT

The binding affinity of the two substrate–water molecules to the water-oxidizing M_4CaO_5 catalyst in photosystem II core complexes of the extremophilic red alga *Cyanidioschyzon merolae* was studied in the S_2 and S_3 states by the exchange of bound ^{16}O -substrate against ^{18}O -labeled water. The rate of this exchange was detected via the membrane-inlet mass spectrometric analysis of flash-induced oxygen evolution. For both redox states a fast and slow phase of water–exchange was resolved at the mixed labeled m/z 34 mass peak: $k_f = 52 \pm 8 \text{ s}^{-1}$ and $k_s = 1.9 \pm 0.3 \text{ s}^{-1}$ in the S_2 state, and $k_f = 42 \pm 2 \text{ s}^{-1}$ and $k_{slow} = 1.2 \pm 0.3 \text{ s}^{-1}$ in S_3 , respectively. Overall these exchange rates are similar to those observed previously with preparations of other organisms. The most remarkable finding is a significantly slower exchange at the fast substrate–water site in the S_2 state, which confirms beyond doubt that both substrate–water molecules are already bound in the S_2 state. This leads to a very small change of the affinity for both the fast and the slowly exchanging substrates during the $S_2 \rightarrow S_3$ transition. Implications for recent models for water-oxidation are briefly discussed.

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1. Introduction

The molecular oxygen we breathe is produced by cyanobacteria, algae and higher plants via light-induced water oxidation in photosystem II (PSII). This reaction occurs within the oxygen evolving complex (OEC) that catalyzes the oxidation of two water molecules into molecular oxygen, four protons and four electrons. This complex is comprised of four manganese atoms and one calcium atom, which are connected by five μ -oxo bridges. These atoms are arranged in a chair-like structure with a distorted cubane base (Mn₄CaO₅ cluster) [1–6]. Four consecutive flashes lead via sequential charge separations in the chlorophyll-containing reaction center of PSII to the accumulation of four oxidizing

Abbreviations: C. merolae, Cyanidioschyzon merolae; PSII, photosystem II; PSIIcc, photosystem II core complexes; OEC, oxygen evolving complex; S states (S_i) , oxidation states of the OEC; W_b fast exchanging substrate—water; W_s , slowly exchanging substrate—water; k_s , rate constant of slow water exchange; k_b , rate constant of fast water exchange; TR-MIMS, time resolved membrane inlet mass spectrometry; FIOPs, flash induced oxygen evolution pattern

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equivalents in the OEC, which subsequently liberates O_2 . To describe this reaction cycle, which was deduced from flash-induced oxygen evolution patterns [7], Kok and coworkers introduced the S state model, also known as the Kok cycle, with five different oxidation states of the OEC [8]. The S state model denotes the number of stored oxidizing equivalents in a particular S state by the index i (S_i : S_0 – S_4). The molecular mechanism captured by this elegant kinetic scheme is presently not fully understood and different mechanisms have been proposed [3,9–16].

Cvanidioschyzon merolae is an extremophilic red microalga that naturally grows at extremely low pH (pH 0.2-4) and moderately high temperatures (40–56 °C) [17,18]. The composition of the extrinsic lumenal proteins of PSII stabilizing the OEC differs somewhat from that of higher plants, green algae and prokaryotic cyanobacteria [19]. Higher plants and green algae both contain PsbO, PsbP, and PsbQ (and possibly PsbR), whereas red algae contain PsbO, PsbP, PsbQ' (CyanoQ homologue), PsbU and PsbV. Cyanobacteria contain PsbO, PsbU, PsbV and the cyanobacterial homologues of PsbP and PsbQ: CyanoP and CyanoQ. Notable is the intermediate composition of extrinsic proteins in red algae compared to prokaryotes and eukaryotes. A 17 Å electron density map derived from electron microscopy and single particle analysis of the C. merolae dimeric PSII particles has recently been published together with a functional study of this complex under extreme conditions [20]. In the same study it was found that C. merolae PSII retained significant photosynthetic activity in an unusually broad range of pH, temperatures and light intensities. Since the mechanism of wateroxidation is known to be highly dependent on the prompt release of

This paper is dedicated to the memory of Warwick Hillier (18.10.1967–10.01.2014). Using membrane-inlet mass spectrometry and FTIR spectroscopy Warwick made many important discoveries regarding substrate—water binding to the OEC and the mechanism of water-oxidation. He was a very good scientist and friend who was highly appreciated throughout the photosynthesis community. In 2007 he was awarded the Robin-Hill Award of the International Society for Photosynthesis Research (ISPR).

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protons produced during water-oxidation [21], it is highly interesting to study if this greater pH stability of PSII is related only to the above-described differences in the protein composition, or if the kinetic parameters of the OEC may also be changed, such as the binding affinity of the Mn_4CaO_5 catalyst for the two substrate–water molecules.

The time resolved membrane inlet mass spectrometry (TR-MIMS) approach used in this study gives information on how the affinity of the manganese catalyst for water substrate changes during the S state transitions [22]. The affinity can be directly probed by exchanging already bound $H_n^{16}O$ substrates (n=0,1,2) with bulk $H_2^{18}O$. This exchange can be then probed by photo-generating oxygen release after various incubation times followed by the analysis of the isotopic composition of thus produced O_2 by isotope ratio mass spectrometry [13, 22–30]. Here, we present for the first time substrate—water exchange rates in the highly stable dimeric PSII core complexes isolated from the extremophilic red alga *C. merolae* [17]. We discuss the mechanistic implications of these data in the context of the substrate—water exchange rates obtained previously for the purified spinach and cyanobacterial PSII core complexes [23,25].

2. Materials and methods

2.1. Purification of C. merolae PSII dimers

Cell culturing, isolation of thylakoids and purification of dimeric PSII particles were performed essentially as described in [20]. Following solubilization of thylakoids (1 mg/mL Chla) with 1% (w/v) dodecyl- β -D-maltoside, dimeric PSII core complexes were purified by anion exchange chromatography on DEAE Toyopearl 650M and DEAE Toyopearl 650S media, using a continuous NaCl gradient (0.05–0.15 M NaCl), as described in detail in [20]. The purity of dimeric PSII core complexes (PSIIcc) was assessed by SDS-PAGE, size exclusion chromatography (SEC) and spectrophotometrically, according to the procedures described in [20].

2.2. PSII activity measurement

The oxygen evolving activity of purified dimeric PSIIcc was measured using a Clark-type oxygen electrode (Hansatech). Measurements were performed at 30 °C in a buffer composed of 40 mM MES-KOH pH 6.1, 10 mM CaCl₂, 5 mM MgCl₂, 25% (w/v) glycerol in the presence of 0.125 mM 2,6-dichloro-p-benzoquinone (Sigma, Germany) and 2.5 mM potassium ferricyanide (POCH, Poland) as the exogenous electron acceptors. Samples (1 μ g/mL Chl) were illuminated with a white light intensity of 5000 μ E/m²/s, using a KL 2500 LCD white light source (Schott, Germany). Activities were calculated from initial rates of oxygen evolution curves. Each measurement was repeated 3 times. The average activity of dimeric PSII was 4500 μ mol O₂/mg Chl/h, and was consistent across multiple preparations.

2.3. Membrane-inlet mass spectrometry

An isotope ratio mass spectrometer (ThermoFinnigan Delta plus XP) connected to a membrane inlet sample chamber (165 μ L) via a cooling trap (dry ice) was used for the time-resolved membrane inlet mass spectrometry measurements (TR-MIMS) described in this study. TR-MIMS measurements were performed at m/z 32, m/z 34 and m/z 36 to quantify the flash-induced oxygen production from PSII samples as described previously [22,31]. The samples were stored at -80 °C. Prior to measurements, the sample aliquots were thawed on ice and diluted in measuring buffer (pH 6.1, 10 mM CaCl₂, 5 mM MgCl₂, 40 mM Mes, 1 M betaine) to a chlorophyll concentration of 0.3 mg/mL. Synchronization in the S₁Y_D^{ox} state was achieved by pre-flashing each sample aliquot (300 μ L, Chl [0.3 mg/mL]) once with a Xenon flash lamp (~5 μ S FWHM), followed by dark adaptation for 1 h at 20 °C. After 40 min dark-adaptation the sample aliquot (165 μ L) was loaded into the

membrane inlet sample chamber. After 20 min of degasification under continuous stirring at 20 °C, the sample was advanced to the S₂ state with one flash (or two flashes at 2 Hz to attain the S₃ state) (~6 µs FWHM). Rapid injection ($t_{1/2} = 3$ ms) of $H_2^{18}O$ (97.7%) with a gas tight syringe (Hamilton CR-700-50) into the cuvette enriched the sample with $H_2^{18}O$ (24% final). The dissolved oxygen in the $H_2^{18}O$ aliquot was removed prior to injection by adding glucose, glucose oxidase and catalase. The rapid H₂¹⁸O injection was initiated with a computer (LabView software), which triggered the release of 8 bars N₂ from a fast switching valve (FESTO MHE2-MS1H 3/2G-M7-K) that pushed a pneumatic piston (Festo AEVC-12-10-A-P) connected to the syringe plunger [22]. The same computer also controlled the timing of the subsequent flashes that initiate the O₂ release after defined incubation times. The time for subtrate-water exchange was varied between 0 s and 10 s by injecting $H_2^{18}O$ at various time points before giving two turnover flashes at 100 Hz (S₂ state exchange) or one turnover flash (S₃ state). The oxygen yields of the substrate-water exchange measurements were corrected for flash-induced double hits and injection artifacts as described in [22,23], and normalized by giving 4 flashes at 2 Hz 5 min after the third turnover flash. At very short incubation/exchange times corrections were also made to account for the isotopic enrichment and chlorophyll concentration present in the sample at the time of illumination [23].

2.4. Rate of H_2^{18} O injection and mixing

The rate of $H_2^{18}O$ injection into the cuvette and the time for complete mixing with a sample was determined in separate experiments by measuring fluorescence as a function of time after fluorescein injection. The fluorescein solution (30 μ M, 40 μ L) was injected into the cuvette prefilled with a buffer solution (0.1 M Tris pH 8.0, 165 μ L). The fluorescein was excited by a LED lamp (Luxeon V-Star blue, 1 W) via a band pass filter (Newport 470 nm–495 nm) and fiber optic tube. The resulting fluorescence (fluorescein — λ_{ex} 490 nm; λ_{em} 525 nm) was guided via a bifurcated optical fiber and a second band pass filter (Newport 520 nm–547 nm). A photodiode (Hamamatsu S-2281/C9329) converted the fluorescence into an electrical signal that was measured with an oscilloscope.

2.5. Flash-induced oxygen-evolution pattern

The flash-induced oxygen-evolution pattern (FIOP) was obtained using TR-MIMS by giving 16 flashes separated by dark times of 25 s (Xenon flash lamp, ~5 μ s FWHM). The experiments were performed at 20 °C and pH 6.1 (CaCl $_2$ 10 mM, MgCl $_2$ 5 mM, Mes 40 mM, betaine 1 M) at a chlorophyll concentration of 0.33 mg Chl/mL. Prior to loading into the MIMS cell, the sample was pre-flashed once and mixed with $H_2^{18}O$ (10% v/v), followed by dark adaptation for 1 h at 20 °C. An Excel spreadsheet program that was based on the extended Kok model was used to fit the FIOP.

3. Results

3.1. Flash-induced oxygen pattern (FIOP)

Fig. 1 shows the flash induced oxygen yield pattern (FIOP) of the *C. merolae* dimeric PSII core particles that was obtained at m/z 34 in the absence of artificial electron acceptors. The O_2 oscillation pattern shows the characteristic features of the Kok model, with a maximum of oxygen yield after the third flash. As typical for core preparations, only a very small second oscillation is observed due to the limited plastoquinone pool. The oscillation can be fit with a miss parameter $\alpha=19$, a double hit parameter $\beta=4$, and 100% S_1 state population in the darkadapted sample [8,32]. The slightly high miss parameter is likely due to the long dark-times of 25 s that are required for resolving the oxygen yields after each flash individually.

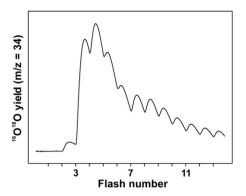


Fig. 1. Flash-induced oxygen evolution pattern (FIOP) of *C. merolae* PSIIcc. Evolution of $^{16}O^{18}O$ was induced by 16 saturating Xe-flashes and detected by membrane-inlet mass spectrometry. The dark-times between flashes were 25 s. Other parameters: 20 °C, pH 6.1, 10% (v/v) $H_2^{18}O$.

3.2. Substrate-water exchange rates

This good oscillation allows for the determination of the substrate—water exchange rates via time-resolved isotope-labeling MIMS. Fig. 2 shows the rise of the m/z 34 and m/z 36 signals as a function of substrate—water exchange time at 20 °C and pH 6.1. The fast phase of the characteristic biphasic rise of the m/z 34 signal is attributed to the exchange of the fast exchanging H_2O (W_f), whereas the slower phase represents the slowly exchanging substrate—water (W_s) [22]. Notably, the fast exchange in the S_2 state is very well resolved compared to all earlier studies with PSII from other organisms. At m/z 36 the exchange of W_s is rate limiting and thus only a mono exponential rise is observed [22,23].

Table 1 Substrate–water $H_2^{18}O/H_2^{16}O$ exchange rate constants for *C. merolae* PSIIcc. $H_2^{18}O/H_2^{16}O$ exchange was measured in the S_2 and S_3 states at 20 °C, pH 6.1. The rates for the fast (k_f) and slow (k_s) were obtained by fitting the rise of the labeled $^{16,18}O_2$ and $^{18,18}O_2$ oxygen products with $H_2^{18}O$ incubation time (Fig. 1) with Eqs. (1) and (2), respectively.

| S state | $k_{\rm f}$, s ⁻¹ | $k_{\rm s}$, s ⁻¹ |
|----------------------------------|-------------------------------|---|
| S ₃ S ₂ | $42 \pm 2 \\ 52 \pm 8$ | $\begin{array}{c} 1.2\pm0.3 \\ 1.9\pm0.3 \end{array}$ |

The exchange rates (Table 1) were obtained by fitting (solid line) the data with the sum of two exponential functions for m/z 34:

$$^{34}\mathrm{Y} = 0.66 \cdot \left(1 - \exp\!\left(-^{34}k_{\mathrm{f}} \cdot t\right)\right) + 0.34 \cdot \left(1 - \exp\!\left(-^{34}k_{\mathrm{s}} \cdot t\right)\right) \tag{1}$$

where the pre-exponential factors are dependent on the final $H_2^{18}O$ concentration, as explained in references [22,23].

The time course at m/z 36 was fit by the single exponential function:

36
Y = 1 - exp $\left(-^{36}k \cdot t\right)$. (2)

The values of the slow components measured at m/z 34 ($^{34}k_s$) and m/z 36 (^{36}k) were forced to be identical during the fits, and therefore only k_f and k_s are given in Table 1.

The data in Table 1 show that the substrate–water exchange rates slow down during the $S_2 \rightarrow S_3$ transition by a factor of 1.6 for W_s and 1.2-fold for W_f . These findings signify a small increase in the substrate affinity for both W_s and W_f during the $S_2 \rightarrow S_3$ transition.

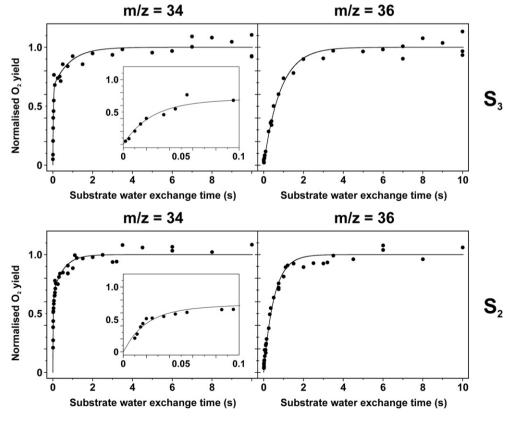


Fig. 2. Substrate—water exchange in the S_3 (top panels) and S_2 (bottom panels) states of *C. merolae* PSIlcc. The normalized O_2 yield (symbols) as a function of the time after $H_2^{18}O$ injection (final enrichment, 24%) is plotted. The solid lines are kinetic fits to the biphasic exchange at m/z 34 and the monophasic exchange at m/z 36 according to Eqs. (1) and (2), respectively. The rate constants to the fits are given in Table 1. The measurements were performed at 20 °C and pH 6.1.

4. Discussion

4.1. Both substrate-waters are bound in the S2 state

More and more details are presently revealed about the mechanism of photosynthetic water oxidation [33–35]. One important aspect for fully understanding this mechanism is the elucidation of the two substrate–water-binding sites, and how the protonation, oxidation and binding states of the two substrate–waters change during the S state cycle. The slowly exchanging water has been suggested to be an oxo-bridge between Ca and Mn, and specifically the bridge known presently as O5 [15,28,29]. This notion is based on the observed increase in the exchange rate of W_s if Ca is replaced by Sr [28] and the S state dependent differences of its exchange rate [13,15]. Strong support for this possibility came from DFT calculations [36] and, recently, from EPR/ESEEM and 17 O-exchange ELDOR-detected NMR studies at W-band that demonstrated that the oxo-bridge O5 can incorporate the 17 O label from the bulk within 15 s [30,37].

Two different structures of the Mn_4CaO_5 cluster have been proposed to be in equilibrium in the S_2 state, and it is not clear at this point which structure the cluster attains in the S_3 and S_4 states [38–41]. The two S_2 state structures differ in the position of the central O5 oxo-bridge, which may be either bound between Ca, Mn_{B3} and Mn_{A4} (open cube structure; outer position), or between Ca, Mn_{B3} and Mn_{D1} (closed cube configuration; inner position, see Fig. 3). Depending on which structure is favored for the higher S states, three different binding sites for the fast exchanging water were put forward: Mn_{A4} , Ca and Mn_{D1} [15,40,42–44]. Accordingly, W2, W3 or a water molecule (WX) postulated to bind to Mn_{D1} during the $S_2 \rightarrow S_3$ state transition would be in 'striking' distance to O5, the suspected slowly exchanging substrate W₅.

It is therefore mechanistically important that in this study the fast substrate-water exchange was clearly resolved in the S2 state, where the structure of the Mn₄CaO₅ cluster is relatively well established. Previously, only two other studies detected the fast exchange in S₂ [26, 27]. In spinach thylakoids the fast exchange in S2 was resolved at $10~^{\circ}$ C ($120~\text{s}^{-1}$), but not at $20~^{\circ}$ C [26]. A similar rate was reported earlier for spinach BBY preps, which were depleted of the extrinsic 16 and 23 kDa protein by salt washing [27]. Since this rate is very close to the time-resolution of the instrumentation, which is determined by the speed of mixing of the sample with $H_2^{18}O$ (175 s⁻¹ in the cited work), some doubts remained whether W_f was indeed bound to the catalyst in the S2 state. These were increased by the FTIR finding that one water molecule binds to the OEC during the $S_2 \rightarrow S_3$ transition [45, 46]. Moreover, the mechanism derived by Siegbahn by DFT calculations [16,44] also suggests that the fast substrate–water is not, or only very weakly bound to the Mn₄CaO₅ cluster in the S₂ state.

The rate of fast substrate exchange, $k_{\rm f}$, measured here for the S_2 state is very similar to that in the S_3 state, and therefore well resolved. If we exclude a diffusion limitation for the fast exchange in the S_2 state (NMRD experiments and theoretical calculations suggest much faster diffusion rates for water in proteins [47,48]), this finding demonstrates that in *C. merolae* PSII the fast water is bound in a similar way to the

 Mn_4CaO_5 cluster in the S_2 and S_3 states. Therefore, if a water binds during the $S_2 \rightarrow S_3$ transition, it cannot be the substrate during the present reaction cycle; it may rather be the 'next substrate', *i.e.* it will be oxidized during the next turnover of PSII [42,46].

4.2. Binding site for the fast exchanging substrate

The only 30 times faster exchange rate of W_f compared to W_s in the S_2 and S_3 states makes it rather unlikely that W_f is bound to Ca. Not only because such a slow exchange of a terminal water ligand of Ca would be to our knowledge unprecedented [28,36], but also because the significant slowing of the rate of W_f exchange — from the exchange rate being beyond resolution in the S_1 state to being rather similar to the rate of exchange of W_s in the S_2 state — is hard to rationalize for a Cabound water. In contrast, binding to a Mn ion that is being oxidized from Mn^{III} to Mn^{IV} during the $S_1 \rightarrow S_2$ transition would provide a direct explanation for this finding.

Most recent DFT-based models of the catalytic cycle suggest that in the S_2 state the open cube structure is dominant and that in this configuration Mn_{D1} is the last Mn^{III} in the S_2 state, and that Mn^{III}_{A4} is oxidized in the $S_1 \rightarrow S_2$ transition [16,49–51]. As such, Mn_{A4} is the most likely binding site for W_f . Of the two waters bound in the crystal structure to Mn_{A4} [6], only W2 is in a suitable position for O – O bond formation with O5. In addition, exchange experiments with ammonia have excluded W1 from being a substrate [30]. We therefore tentatively assign W2 to be the fast exchanging substrate W_f [15,42].

4.3. Deceleration of the slow exchanging substrate in the $S_2 \rightarrow S_3$ transition

The third important information derived from this study is the deceleration of the slow water exchange in the $S_2 \rightarrow S_3$ transition. The slow exchange in the S₃ state of C. merolae PSII core particles is calculated to be 1.2 \pm 0.3 s⁻¹ at 20 °C. This rate is ~2-fold slower than the slow rate previously determined for the S₃ state of spinach thylakoid membranes $(2.2 \pm 0.1 \text{ s}^{-1}; 10 \text{ °C and } 4.9 \pm 0.3 \text{ s}^{-1}; 20 \text{ °C})$ [23], but similar to those measured at 10 °C in core particles of spinach ($k_s = 1.1 \text{ s}^{-1}$) and Thermosynechococcus elongatus ($k_s = 0.5 \text{ s}^{-1}$), as well as Synechocystis PCC 6803 ($k_s = 0.9 \text{ s}^{-1}$) [25]. While in spinach the slow exchange rate was previously found to be identical in the S_2 and S_3 states, the k_s rate determined here for the C. merolae PSIIcc clearly slows down during the $S_2 \rightarrow S_3$ transition. This deceleration can be caused by the structural change of the Mn_4CaO_5 catalyst that occurs upon the $S_2 \rightarrow S_3$ transition and/or by the additional oxidation of the OEC [13,52,53]. DFT calculations suggest that the exchange of Mn-bound water ligands is impossible in the Mn^{IV} oxidation state. It was therefore proposed that water exchange in the S_3 state requires the equilibrium $S_3Y_7 \leftrightarrow S_2Y_7^{\bullet}$ [36]. In such a situation an overall slowing of the exchange rates would be expected to occur during the $S_2 \rightarrow S_3$ transition, since the state in which water can exchange is available only for transient periods. As such, this exchange model would be qualitatively consistent with the present data, but in conflict with the exchange rates previously obtained for spinach samples. However, an alternative proposal involving the equilibrium between the above-

Fig. 3. Possible mechanism of O_2 formation during the $S_4 o `S_2(H_2O_2)` o S_0$ transition. This suggestion [15,42,43,54] is based on the closed cube configuration of the S_2 state, and thus suggests that it is this configuration that proceeds to S_3 via water binding (WX) to Mn_{A4} .

described open and closed cube forms of the Mn_4CaO_5 cluster is also able to account for the present findings [42]. Species dependent changes may reflect a slight shift in the respective equilibria.

4.4. Implications for the mechanism of O − O bond formation

While more research is required to elucidate the mechanism of photosynthetic water oxidation, the strong binding of W_f in the S_2 state described in this study provides further evidence for O-O bond formation between two Mn-bound substrates. The data thus favor direct coupling over nucleophilic attack mechanisms. Specifically, our present analysis points to W2 as being the fast exchanging substrate, W_f . Assuming that the Mn_4CaO_5 cluster attains in the S_4 state a structure that is similar to either the open or closed cube conformation reported for S_2 [38], the O-O bond could be formed with O5 being either in the outer, open cube position (geminal coupling) or, in our opinion more likely, it may couple with O5 while O5 is part of the distorted heteronuclear $CaMn_3O_4$ cube (closed cube) [15]. This latter option is presented schematically in Fig. 3.

Acknowledgements

This work was supported by The Strong Research Environment Solar Fuels (Umeå University), the Artificial Leaf Project Umeå (K&A Wallenberg Foundation (grant KAW 2011.0055)), Energimyndigheten (grant 2012-005968-36648-1 to JM) and the Polish Ministry of Science and Higher Education/European Science Foundation (grant 844/N-ESFEuroSolarFuels/10/2011/0 to JK).

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