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BRIEF COMMUNICATION

Force field development on pigments of photosystem 2 reaction centre

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Abstract

We developed new parameters for molecular dynamics (MD) simulations, namely partial atomic charges, equilibrium bond-lengths, angles, dihedrals, atom types, and force constants of chlorophyll *a* (Chl) and plastoquinone (PQ), and both reduced and neutral form of primary acceptor (PHO) molecule. These parameters are essential for MD simulations that can interpret various structure functional relationships during primary processes of charge separation and stabilization in photosystem 2 reaction centres.

Additional key words: chlorophyll; photosystem 2; plastoquinone.

Photosystem 2 (PS2) is a pigment-protein complex located in thylakoid membrane of cyanobacteria, algae, and higher plants. It performs series of light driven reactions, which result in a separation of charge and subsequently in a reduction of an electron-transport chain and water oxidation. Primary site of the energy conversion is located in so-called reaction centre (RC).

Recently, changes in excitonic interactions of PS2 RC pigments upon light-induced oxidation of primary donor (P680) or reduction of primary acceptor PHO were analyzed using absorption and circular dichroism (CD) spectra (Vácha *et al.* 2002). In contrast to the oxidation of primary donor, the light-induced change in the CD spectrum upon primary acceptor reduction was temperature-dependent. This suggests a hypothesis that at a room temperature the reduced PHO induces conformational changes of the RC protein environment, which affects the excitonic interaction of the RC chlorophylls (Chls).

Molecular modelling method such as MD (Allen and Tildesley 1987) coupled with quantum chemistry is a powerful tool for understanding and interpreting the upper mentioned optical spectra experiments (Vácha *et al.* 2005). Having chemically well defined three-dimensional (3D) molecular structure (Ferreira *et al.* 2004) and so-called force field (FF) parameters (MacKerell 2004), conformational study of the PS2 RC can be performed consequently by using MD technique.

Various calculations with different methods have been performed in order to obtain reliable collection of FF parameters for the cofactors of bacterial and higher plant RCs (Brooks *et al.* 1983, Kuczera *et al.* 1990, Foloppe *et al.* 1995, Ceccarelli *et al.* 2003, Tsai and Simpson 2003, Autenrieth *et al.* 2004). Currently, the most extensive bio-molecular FFs are the CHARMM22 (Chemistry at HARvard Molecular Mechanics, version *22*) (MacKerell *et al.* 1998) and CHARMM27. These include proteins, nucleic acids, lipids and, although limited, saccharides (MacKerell 2004). For the MD simulations on PS2 RC the present CHARMM22 and CHARM27 FF parameters are not fully applicable. Therefore, in this work we have focused on developing new CHARMM FF parameters, namely partial atomic charges, equilibrium bond-lengths, angles, dihedrals, atom types, and force constants of the PS2 RC pigments (Chl), plastoquinone (PQ), and both reduced and neutral forms of PHO molecule.

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First of the force field parameters, partial charges on atoms, were obtained by the method of Mulliken (1955) applied in CHARMM FF. Mulliken population analysis was performed *via* quantum chemical HF/6-31G* calculations (self-consistent Hartree-Fock method where 6-31G* is a set of functions for description of atomic orbitals; Roothan 1951) in Gaussian software package (Frisch *et al.* 1998. For an integrity of charge computations, also different charge fitting scheme according to restrained electrostatic potential (RESP) charge fitting method (Bayly *et al.* 1993) was performed.

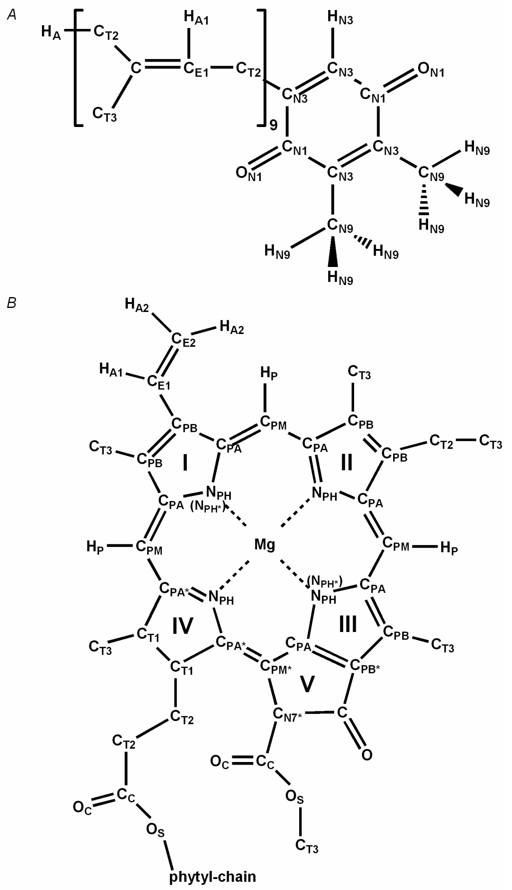

Fig. 1. Chemical structures of two photosynthetic molecules from the PS2 RC (Ferreira *et al.* 2004), (*A*) plastoquinone 9 (PQ) and (*B*) chlorophyll *a* (Chl) including force field atom types. Given the similarity between the molecular structure of Chl and pheophytin *a* (PHO), the same atom types are used for corresponding atoms in both chromophores. Only for the nitrogens on the pyrrole rings of PHO bound to hydrogens, different atom type was used to account for deviations of angle bendings (N_{PH*} for PHO instead of N_{PH} for Chl). Five new atom types added to CHARMM27 were named as follows, N_{PH*} (for PHO), C_{N7*} and three (porphyrin *α*, *β*, and *meso*) C_{PA*}, C_{PB*}, C_{PM*} carbons. The rest of atom types were fitted according to CHARMM27 developing scheme (MacKerell *et al.* 1998). Phytyl chain (consisting of four isoprene units, of which three are saturated) of Chl is not shown for clarity and no labels are given for hydrogen atoms attached to sp^3 carbons, their atom type is H_A.

Another force field parameters, atom types, were fitted according to CHARMM27 developing scheme (MacKerell *et al.* 1998). Although PS2 RC pigments are in part composed of some unique molecular fragments not fully included in the present force fields, CHARMM FF atom types for heme (Brooks *et al.* 1983, Kuczera *et al.* 1990) and purple bacterial pigments of *Rhodobacter capsulatus* (Foloppe *et al.* 1995) were used as the reference data to our newly developed FF parameters of PS2 RC pigments Chl, PHO, and PQ. Chemical structures of PS2 RC pigments including tabulated and also new atom types are described in Fig. 1. Details of development of the remaining FF parameters (bonds, angles, dihedrals, and force constants) for the PS2 RC pigments are shown in the following procedure. At first, initial 3D molecular structures of PS2 RC pigments were transferred from recent experimental crystal structure (Ferreira *et al.* 2004). Truncated fragments of different size of each pigment molecule were thoroughly constructed and these molecular structures pre-optimized with quantum chemical semi-empirical PM3 method (Parametric Model number 3; Stewart 1989) and further prepared for HF/6-31G* calculations in both *HyperChem* and *Gaussian 98* software packages. Potential energy profiles were calculated with reliable step size of 0.001 nm for bonds and 1.0° for angles and dihedral angles. New molecular structures of the truncated systems produced in each of HF/6-31G* calculation step were simultaneously optimized by relaxed potential energy surface scan, applied in *Gaussian 98*. *HyperChem* performs the same task, however, without updating the structure of the systems during the calculation process. The computed bond and angle potential energy profile near the minimum could be approximated with harmonic square function, following the convention used also in CHARMM. To reproduce potential energy barriers for torsional rotations one or more cosine functions were needed. The new equilibrium bond-lengths and bond force constants are presented in Table 1. Both used software packages applied for the FF calculations were capable to calculate appropriate parameters with negligible mutual discrepancies, but some parameters (see Table 1) were calculated only in *HyperChem*, due to the convergence criterion problem in *Gaussian 98*.

Table 1. Comparison of new bond parameters (equilibrium bond lengths and force constants) of three PS2 RC photosynthetic pigments: chlorophyll *a* (Chl), pheophytin *a* (PHO), and plastoquinone 9 (PQ) developed using RHF/6-31G* calculation in *HyperChem* with those developed in *Gaussian 98* at the same level of theory. All bond parameters listed are not involved in the current force fields including CHARMM27, AMBER99, and OPLS. Five new atom types named N_{PH*}, C_{N7*}, C_{PM*}, C_{PB*}, and C_{PA*} are closely related to original CHARMM27 atom types N_{PH}, C_{N7}, C_{PM}, C_{PB}, and C_{PA} originally defined for heme prosthetic group. The rest of atom types of PS2 RC pigments were fitted according to CHARMM27 developing scheme (MacKerell *et al.* 1998). (1) Bond parameters obtained from RHF/6-31G* potential energy surface scan (PES) calculation performed in *HyperChem* are listed in the first two columns. Bonds that are part of closed ring structures are not presented (parameterization not applicable in *HyperChem*, due to the necessity of ring disruption). (2) Bond parameters obtained from RHF/6-31G* relaxed PES calculation performed in *Gaussian 98* are listed in the last two columns. Parameters for two bonds N_{PH*}—H and N_{PH}—Mg were calculated only in *HyperChem* due to the convergence criterion problem in *Gaussian 98*. (3) Bond (C_{E2}—C) is involved in phytyl chain of Chl *a* and pheophytin *a* molecule. (4) Parameters for N_{PH}—Mg bond calculated at UHF/6-31G* in *HyperChem*.

Bond	Length(1) [nm]	Force constant(1) [MJ mol^{-1} nm^{-2}]	Length(2) [nm]	Force constant(2) [MJ mol^{-1} nm^{-2}]
C_{E2}—C(3)	0.133	241.24	0.1321	242.79
C_{N7*}—C_C	0.150	112.42	0.1513	101.94
C_{N7*}—C	–	–	0.1535	90.45
C_{N7*}—C_{PM}	–	–	0.1520	99.50
C_{N7*}—H_A	0.108	138.00	0.1081	136.33
C_{PB*}—C	–	–	0.1467	116.80
C_{PA}—C_{PB}	–	–	0.1360	197.11
C_{PA*}—C_{T1}	–	–	0.1520	98.62
C_{PA}—C_{PM*}	–	–	0.1460	125.12
C_{PB}—C_{PB*}	–	–	0.1434	132.57
N_{PH*}—H	0.099	212.00	–	–
N_{PH}—Mg(4)	0.210	29.54	–	–
O_S—C_C	0.132	196.68	0.1326	172.55
O_S—C_{T2}	0.142	141.56	0.1425	120.09
C_{N3}—C_{T2}	–	–	0.1505	105.93
C_{N3}—C_{N9}	–	–	0.1504	106.46

Completion of all missing FF parameters of PS2 RC pigments and calculations of charge distribution on reduced PHO molecule and its surrounding protein enable to run appropriate MD simulation of conformational changes of PS2 RC protein and subsequently better understand and interpret our recent optical spectra experiments.

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