m08.p01

Structure Analysis of Light Harvesting Complexes from the Dinoflagellate *Amphidinium carterae*

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Keywords: protein X-ray crystallography, protein complex, photosynthetic proteins

Dinoflagellates make use of a two component light harvesting system in order to increase energy inflow to the two photosystems. One is the membrane bound light harvesting complex LHC, which shows homology to higher plant CAB-proteins, but contains chl c instead of chl b [1]. The other complex is the unique, water soluble peridinin-chlorophyll *a*-protein (PCP) predicted to be located in the thylakoid luminal space [2, 3]. This complex occurs in different isoforms with the mainform showing a pI of 7.5 (MFPCP). Both complexes excessively utilize the carotenoid peridinin for light harvesting. The structure of the main form of PCP has been solved at a resolution of 2Å. We were able to produce a new crystal form of PCP with spacegroup $P4_22_12$. The structure has been solved by MR using the MFPCP as a search model and has been refined at a resolution of 2.9Å. While we observe a different packing arrangement in the crystal the protein still forms the trimer found in other spacegroups. The LHC of the dinoflagellate *A.carterae* has been extensively studied spectroscopically, but earlier attempts to determine its three dimensional structure by X-ray crystallography only yielded very small crystals too small for further characterization [4]. Here we report an optimized protein purification scheme, yielding reproducibly large amounts of protein for crystallization. We were able to identify new crystallization conditions, under which we could grow crystals of sizes up to $600x50x10\mu m^3$ in one to three month. Initial data have been collected to 3.5Å resolution. A preliminary crystallographic characterization will be presented.

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m08.p02

Toward the getting of photosystem II core complex crystals from *Pisum sativum*

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Keywords: membrane proteins, photosystem II, crystallization

The photosystem II (PSII) is a homodimeric multisubunit protein-cofactor complex consisting of membrane in-lying subunits, hydrophilic peripheral subunits and large number of cofactors (chlorophylls, pheophytins, carothenoids, plastoquinones, iron and manganese). Catalytic mechanism of PSII has been studied using a wide range of approaches [1-3], but particular molecular details of water oxidation catalyzed by the oxygen evolving center (OEC) remains unclear. Crystallographic studies of cyanobacterial OEC PSII from thermophilic cyanobacterium have provided several medium-resolution structures from resolution 3.8Å to 3.2Å [4-6]. Results of mentioned studies have given the first description of the structure of PSII, but present models are not absolutely complete as yet.
Crystallization experiments of monomeric and dimeric photosystem II core complex (OEC PSII) from *Pisum sativum* have been already described [7]. Here we report following experiments aimed at obtaining better-quality crystals suitable for diffraction analysis. We have studied the influence of additives ($MgCl_2$, $MgSO_4$, $MnCl_2$, $MnSO_4$, $(NH_4)_2SO_4$, $CdSO_4$) and detergents (DM, LDAO, CAPS and Zwittergent 3-12) on the crystallization behavior of protein complex. We expect to obtain typical photosystem II core complex crystals for initial crystallographic characterization.
This work is supported by the GA CR (206/03/D061), by the joint C.S.I.C. and AS CR project 2004CZ0003 - P2004CZ01, by the ME CR (MSM6007665808 and LC06010) AS CR (AVOZ60870520).

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