Structure Determination of Proteins Involved in the Stability of Phycobilisomes during Environmental Stress

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The activities of the photosynthetic apparatus are highly controlled by the environment. Environmental parameters such as light quality, light intensity, temperature, water availability, and nutrient status play critical roles in photosynthetic complexes activities and the levels of pigments and proteins associated with those complexes.

An example of this modulation is the degradation of the light-harvesting pigment-protein complex, the phycobilisome (PBS), during starvation for sulphur and nitrogen.

The protein that appears to trigger PBS degradation during nutrient deprivation is nblA, a very small protein (6.5 kDa), whose level increases dramatically upon starvation of *cyanobactaria* for nitrogen or sulfur. This protein is apparently not a protease, and it may be a new class of proteins – a **dismantlease.** We are investigating the 3D structure of nblA from the *S. elongatus.* (a mesophilic cyanobaterium) and from the *T. vulcanus* (a thermophilic cyanobaterium). We have succeeded in cloning, expressing, purifying and crystallizing bough nblA proteins with and with out Se-methionine. Crystals of nblA from *S. elongates* were found to be amenable to be flash-frozen without addition of cryoprotectant, and X-ray diffraction was measured recently at the European Synchrotron Radiation Facility (ESRF-Grenoble) beamline ID14-I. The crystals diffracted to a resolution better than 2.5Å. Analysis of the diffraction pattern was performed using DENZO. The crystals belong to a P4 space group, with cell dimensions of a = 78Å, b = 78Å, c = 69Å, and four monomers in the asymmetric unit. We are now working on obtaining crystals that will enable collection of complete data sets with a better resolution and on structure determination.

Keywords: photosynthetic-related proteins, structural biology, stress