Structure of the MntC Protein: Mn^{2+} Import in Cyanobacteria is Redox Controlled

Noam Adir, Valeria Rukhman, Meira Melamed-Frank, Rina Anati, *Department of Chemistry, Technion Haifa Israel.* E-mail: nadir@tx.technion.ac.il

Cyanobacteria have unique Mn requirements due to the essential role of Mn in Photosystem II and the low concentrations of Mn^{2+} in fresh and sea water. We have determined the crystal structure of the MntC solute binding protein (SBP) component of the high-affinity manganese ABC-type transport system from the cyanobacterium *Synechocystis* sp. PCC 6803 to 2.9Å using a combination of MAD phasing and molecular replacement. The trimeric structure was refined to an R/R_{free} of 0.23/0.29, and anomalous difference diffraction maps show the presence of Mn^{2+} in the binding site, the first SBP structure containing bound Mn^{2+}. The Mn^{2+} binding site has a distorted tetrahedral geometry, with E220 and D295 situated closer to the ion than H89 and H154. This geometry may be due to a disulfide bond between C219 and C268. Reduction of the disulfide bond *in vitro* and *in crystal* releases bound Mn^{2+}. Sequence homology comparisons show that only cyanobacterial Mn SBPs contain conserved cysteine residues, and we thus propose that reduction of the disulfide bond by a redox active protein alters the position of E220 thereby modifying the affinity towards the bound metal. To more fully understand the import of Mn, we have cloned both the MntC and MntB permease from the thermophilic cyanobacterium *T. vulcanus*. The *T. vulcanus* MntC contains the conserved cysteines and binds Mn^{2+} *in vitro*. The protein was crystallized and structure determination is in progress. Expression experiments of the transmembrane MntB are under way.

Keywords: ABC transporter system, photosynthesis, redox