Structure of MntC from Cyanobacteria

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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 *Synechocytis* sp.PCC 6803 (*Syn*) to 2.9Å by combined MAD/molecular replacement. The metal ion binding site containing Mn^{2+} has a distorted tetrahedral geometry, with Glu220 and Asp295 situated closer to the ion than His89 and His154. This geometry may be due to a disulfide bond between Cys219 and Cys268.

Sequence homology comparisons show that only putative cyanobacterial manganese SBPs contain these conserved cysteines, suggesting the MntC has a special role in manganese mobilization into the photosynthetic apparatus. We show that reduction of the disulfide bond *in vitro* releases bound manganese. We propose that *in vivo* reduction of the disulfide bond by a redox active protein, alters the position of Glu220 thereby modifying the affinity towards the bound metal. We have identified a homologous gene from the thermophilic cyanobacterium *T. vulcanu*s. The final full length clone (GenBank accession code AAV65297) was sequenced and found to be 54% homologous with the *Syn mntC* and it contains the conserved cysteins. The gene was cloned into an expression vector and the expressed protein has been purified and crystallized. Preliminary ICP-MS measurements show that this protein binds Mn^{2+}, and we thus propose that this gene encodes for the MntC homolog in these species. We are now in the process of fine tuning the crystallizing conditions of this protein in order to determine its crystal structure.

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