Biomolecular Aspects of Mercury Transformations

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Bacteria participate significantly in mercury transformation in natural and industrial environments. Previous studies have shown that bacterial mercury resistance is mediated by the *mer* operon, typically located on transposons or plasmids. It encodes specific genes that facilitate uptake of mercury species, cleavage of organomercurials, and reduction of Hg(II) to Hg(0). Expression of *mer* operon genes is regulated by MerR, a metal-responsive regulator protein on the level of transcription. In vitro studies have shown that MerR forms a non-transcribing pre-initiation complex with RNA polymerase and the promoter DNA. Binding of Hg(II) induces conformational changes in MerR and other components of the complex resulting in the transcription of *mer* operon genes. As part of ongoing investigations on allosteric conformational changes induced by Hg(II) in dimeric MerR, and the implications on the binding of RNA polymerase to the promoter of the *mer* operon, we applied small angle scattering to study the regulatory mechanism of MerR in the presence and absence of Hg(II). Our results show that in the presence of Hg(II) the MerR dimer undergoes a significant reorientation from a compact state to a conformation revealing two distinct domains. Bacterial reduction of Hg(II) can also occur at concentrations too low to induce *mer* operon functions. Dissimilatory metal reducing bacteria, such as *Shewanella* and *Geobacter* are able to reduce Hg(II) in the presence of mineral oxides. This process has been linked to the activity of outer membrane multiheme cytochromes. We isolated and purified a decaheme outer membrane cytochrome OmcA from *Shewanella oneidensis* MR-1 and characterized its envelope shape in solution by small angle x-ray scattering. Structural features were identified and compared to homology models. These results show that OmcA is an elongated macromolecule consisting of separate modules, which may be connected by flexible linkers.