Bacterial mercury resistance : metal trafficking and regulation

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The proteins expressed by the canonic *mer* operon (*merRTPAD*) found in *Ralstonia metallidurans* CH34 have been used for a structure-function relationships study. The *merTPA* genes encodes the proteins responsible for the periplasmic sequestration of Hg(II) (MerP), the transport through the inner membrane of the metal into the cytoplasm (MerT), and the reduction of inorganic mercury to the less toxic elemental mercury (MerA, the cytosolic mercuric reductase). The products of the genes *merR* and *merD* play crucial roles at a regulatory level.

We have determined the following structures: oxidized MerP at 2Å resolution (1), both the reduced and the Hg-bound forms of the N-terminal extension of MerA (called MerAa) in solution (^{15}N-^{13}C-NMR) (2), the Hg-bound form of the peptide connecting the second and the third transmembrane segments of MerT (^{1}H-NMR) (3). Our data are consistent with a direct role of this cytoplasmic loop of MerT and MerAa in mercury exchange between these two proteins. In addition, we suggest that GSH is dispensable for the transfer of mercury from MerT to MerAa, although a donor thiol ligand such as a Hg(II)-diglutathione adduct is required to provide Hg(II) to the catalytic core of the mercuric reductase in good conditions for an efficient reduction.

In another hand, a specific role for MerD as a coregulator was proposed (4). MerD alone cannot bind to DNA but can form a ternary complex in association with merOP and MerR. Both the formation and the stability of this ternary complex are dependent on the relative concentration of the two proteins and modulated by the presence of mercury. We postulate that MerD could displace Hg-bound MerR from the *mer* operator to allow new synthesis of metal-free MerR able to switch off the induction of the *mer* genes when external mercury is exhausted. This could fully explain how MerD can be a co-regulator repressing the induction of the *mer* operon

References :

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