**Folding of complex redox proteins by dedicated molecular chaperones**

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Chlorinated compounds (so-called organohalides) are widespread soil and groundwater pollutants. Only few bacteria have the ability to degrade these compounds via organohalide respiration (OHR). Reductive dehalogenases (RDases) are complex redox enzymes involved in the reduction of organohalides, and contribute to the biodegradation of these pollutants. RDases need to be folded and loaded with iron-sulfur centers and a corrinoid cofactor prior to their transport across the cytoplasmic membrane via the Twin-arginine translocation (Tat) pathway. A new family of Tat molecular chaperones, named RdhT, was recently shown to participate in the maturation of RDases (1-2), and successfully applied for heterologous production of these complex redox enzymes (3).

The present study focuses on the interaction of RdhT molecular chaperones with their cognate RDases. PceT (the paradigmatic member of the RdhT family) interacts as a dimer with the Tat signal peptide of PceA, its cognate RDase, as shown by isothermal titration calorimetry. When recombinant *pceT* and *pceAHis* genes are heterologously expressed in *E. coli*, both proteins co-purify on Ni-NTA chromatography which indicates that PceT binds to PceA also *in vivo*. Although recombinant PceA is not functional in *E. coli*, it is produced in a soluble form when *pceT* is co-expressed and represent the basis for reconstitution experiments.

Currently, *in vivo* strategies are developed in *E. coli* to allow a rapid screening of interacting RdhT chaperones with the Tat signal peptides of RDases. This will further help evaluating the cross-reactivity of RdhT chaperones towards Tat signal peptides, and help identifying specific amino acids of the chaperones that are involved in the interaction event.

References:

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