

Impact of copper stress on environmental bacteria *Shewanella oneidensis*

Rikhia Majumdar¹, Marianne Ilbert²

¹ Department of Genetic Engineering, SRM Institute of Science and Technology, Potheri, SRM Nagar, Kattankulathur, Tamil Nadu-603203

² UMR7281, CNRS Laboratoire de Bioenergetique et d'Ingenierie des Protéines, 31 Chemin Joseph Aiguier, 13400 Marseille, France

ABSTRACT

Although copper-proteins are vital for the health of living organisms, free copper in the cell is highly toxic as it generates reactive oxygen species (ROS), which are known to have damaging effects on all cellular macromolecules. The study of microorganisms that can be continuously stressed in their natural habitats is expected to give access to new resistant pathways. Here we describe the effect of copper on environmental bacteria, *Shewanella oneidensis* and the potential role of Hsp33, a molecular chaperone under copper stress. Comparison of W. T and $\Delta hsp33$ showed a significant difference where the wild type survived better than the mutant at 38°C. Complementation of $\Delta hsp33$ with the expression *in trans* of hsp33 lead to a better survival. In presence of copper a slight difference between the two strains could be observed *in vivo*. *In vitro* we could clearly show that copper induces *S. oneidensis* proteins aggregation on a model protein (citrate synthase) as well as on several proteins using cellular extract. Some aggregation was prevented in presence of Hsp33 which allow us to demonstrate that, at least *in vitro*; Hsp33 is able to prevent copper induced aggregation of several client proteins. This study highlights a potential role played by molecular chaperones upon metal stress. Targeted proteins need to be clearly identified and the mechanism further studied.

Keywords: Copper stress, Hsp33, Growth curve, Aggregation

