

# Transcriptomics and functional analysis of copper stress response in the sulfate reducing bacteria *Desulfovibrio alaskensis* G20

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Copper (Cu) is an essential micronutrient required as a co-factor in the catalytic center of many enzymes in bacteria. However, excess Cu is hazardous and can generate pleiotropic effects. Cu has been the metal of choice for piping used in household water distribution systems. Due to its leaching from pipelines, Cu levels are present at elevated concentrations in ground water and in soils which is a matter of public health concern. Sulfate reducing bacteria (SRB) have been demonstrated to remove toxic levels of heavy metals including Cu. However, reports on toxicity of Cu towards SRB have primarily focused on degree of toxicity and subsequent elimination. In this study, we show in detail the Cu stress-related effects on a model sulfate reducing bacterium, *Desulfovibrio alaskensis* G20. Copper stress effects were measured at two different concentrations (5  $\mu\text{M}$  and 15  $\mu\text{M}$ ) as changes in the transcriptome through RNA-Seq. In the pairwise comparison of 5  $\mu\text{M}$  vs control (0  $\mu\text{M}$  Cu), 61.43% of genes were found to be downregulated and 38.57% genes were upregulated. In 15  $\mu\text{M}$  vs control, 49.51% genes were downregulated, and 50.5% genes were upregulated. The results indicated that the expression of inorganic ion transporters and translation machinery was massively modulated. Moreover, changes in the expression of critical biological processes such as DNA transcription and signal transduction were observed at high Cu(II) concentrations. These results will help us better understand the Cu(II) stress-response mechanism and provide avenues for future research.

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