

Epigenetics of Sulfate Reducing Bacteria Under Copper Stress

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Epigenetics is a mechanism of gene regulation without changing the DNA sequence, which is heritable in nature. Epigenetic regulation is poorly studied in prokaryotes and is associated with DNA methylation that regulates the DNA-protein interaction in bacteria which often plays a role in phenotypic variations. Our study focuses on biofilm-forming *Desulfovibrio alaskensis* G20 (DA G20), which are sulfate-reducing bacteria (SRB), thereby producing hydrogen sulfide as an end product. Hydrogen sulfide is responsible for metal corrosion which is directly proportional to the biofilms formation by the SRB on metal surfaces. Preliminary experiments were performed on the planktonic DA G20 cells grown under variable bioavailable copper conditions (0, 5, 15, and 30 μ M) in anaerobic serum bottles. DA G20 cell density decreased with an increase in copper ion concentration. The DNA from copper stress and non-stress cells of DA G20 were extracted, followed by epigenetics analyses. The samples were subjected to Whole-Genome Bisulfite Sequencing for epigenetic profiling. The sequencing data were processed using the Galaxy platform, wherein Bismark workflow was set up to map the m5C base modifications. Our results suggest that more than 20% methylation changes were present in the genes responsible for biofilm formation across CpG, CHG and CHH islands. The data is crucial to investigate the role of epigenetics in the biocorrosion of a metal surface by SRB biofilms.

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