

THE ROLE OF REX IN REGULATION OF SULFATE REDUCTION IN
DESULFOVIBRIO VULGARIS HILDENBOROUGH

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ABSTRACT

Although the enzymes for dissimilatory sulfate reduction by microbes have been studied, the mechanism for transcriptional regulation of the encoding genes remain unknown. In the work presented here, the model sulfate-reducing microbe *Desulfovibrio vulgaris* Hildenborough (DvH) was used to determine the role of Rex in sulfate reduction regulation. A deletion of the putative *rex* gene was made in DvH. the Rex mutant was assayed for growth with different combinations of electron donors and acceptors. Growth of the Rex mutant was less efficient on thiosulfate-containing medium. Here we propose a new model for thiosulfate reduction in SRB and examine a putative thiosulfate reductase. Additionally, transcript expression studies focused on *sat*, encoding sulfate adenylyl transferase, showed increased levels in the Rex mutant relative to the parental strain confirming Rex to be a repressor of *sat*. The putative Rex-binding site upstream of *sat* was also confirmed. We established *in vitro* that the presence of elevated NADH disrupted the interaction between Rex and DNA. these data support the role of Rex as a transcription repressor for *sat* that senses the redox status of the cell through NADH/NAD⁺.