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**Title** Revisiting Modes of energy generation in sulfate reducing bacteria

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**Author** Joachimiak, Marcin

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M.P. Joachimiak<sup>1</sup>, R. Chakraborty<sup>1</sup>, A. Zhou<sup>2</sup>, J. L. Fortney<sup>1</sup>, J.T. Geller<sup>1</sup>, Z. He<sup>2</sup>, J. Wall<sup>3</sup>, J. Zhou<sup>2</sup>, A.P. Arkin<sup>1</sup>, T.C. Hazen<sup>1</sup>, J.D. Keasling<sup>1</sup> and S.R. Chhabra<sup>1</sup> 1. Lawrence Berkeley National Lab, Berkeley, CA 2. University of Oklahoma, Norman, OK 3. University of Missouri, Columbia, MO.

UCSF

Ecosystems and Networks Integrated with Genes and Molecular Assemblies

# WIMSS Virtual Institute for Microbial Stress and Survival

Abstract

Sulfate reducing bacteria (SRB) play an important role in global sulfur and carbon cycling through their ability to completely mineralize organic matter while respiring sulfate to hydrogen sulfide. They are ubiquitous in anaerobic environments and have the ability to reduce toxic metals like Cr(VI) and U(VI). While SRB have been studied for over three decades, bioenergetic modes of this group of microbes are poorly understood, Desulfovibrio vulgaris strain Hildenborough (DvH) has served as a model SRB over the last decade with the accumulation of transcriptomic, proteomic and metabolic data under a wide variety of stressors. To further investigate the three hypothesized modes of energy generation in this anaerobe we conducted a systematic study involving multiple electron donor and acceptor combinations for growth. DvH was grown at 37°C in a defined medium with (a) lactate + thiosulfate, (b) lactate + sulfite (c) lactate + sulfate, (d) pyruvate + sulfate, (e) H2 + acetate + sulfate, (f) formate + acetate + sulfate, q) formate + sulfate and (h) pyruvate fermentation. Cells were harvested at mid-log phase of growth for all conditions for transcriptomics. when the optical density at 600nm was in the range 0.42-0.5. Initial results indicate that cells grown on lactate do not appear to significantly differentiate their gene expression profiles when presented with different electron acceptors. These profiles however differ significantly from those observed during growth with other electron donors such as H2 and formate, as well as during fermentative growth. Together the gene expression changes in the presence of different electron donors provide insights into the ability of DvH to differentially reduce metals such as Cr(VI). Here we present revised modes of energy generation in DvH in light of this new transcriptomic evidence.

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Schematic representation of the experimental plan: 3 cultures grown to mid-log phase for each media variation Samples harvested for 3 categories of investigation - Membrane response, metal reduction and genomic response





Transcriptomic Responses



equation:

Z= (log<sub>2</sub>(treatment/control))/

(0.25+∑variance)1/2



Desulfovibrio spp. derive energy for growth from redox reactions in which electron donors such as organic acids, alcohols, or hydrogen are oxidized by electron acceptors such as sulfate, thiosulfate, or sulfite. ATP synthesis may proceed by multiple mechanisms as shown in the figure above for growth on lactate, pyruvate, formate, or hydrogen and sulfate. ATP formed by substrate level phosphorylation equals that required for activation of sulfate. Hence growth on lactate- and sulfate-containing medium would be expected to require proton motive force-driven ATP synthesis. The hydrogen cycling hypothesis proposed by Odom and Peck suggested that protons and electrons generated during lactate and pyruvate oxidation are converted to hydrogen by a cytoplasmic hydrogenase and that this H<sub>2</sub> diffuses to the periplasm, where it is reoxidized. However, the pathway components involved in this cycling hypothesis still need to be elucidated.

Energy metabolism

0.80

	Indeed ATP production during grow pyrruvate and sulfate is likely to be than indicated in the figure above. indicates that hundreds of gene pr several membrane-associated red could be involved. A combinatorial study involving sy: acceptor changes such as the one this poster can be used to identify of genes acting in concert to enable in the SRB.	vth on lactate or much more complex The genome sequence oducts, including px protein complexes, stematic donor- described in the combinations e ATP synthesis	60 mM lact mid 1 VS. LS4D mid 1 120mM pwru mid 1 VS. LS4D mid 1	60mM lacta nid 1 VS. LS4D nid 1	60mM lacta mid 1 VS. LS4D mid 1	no lactate mid 1 VS. 30 mM sulf mid 1 formate 10 mid 1 VS. 1540 mid 1	1200M pyru - MM - Late- VS. LS4D - MM - Mid-1	100mM form - mM - Late- VS. LS4D - mM - Mid-1			
9	Energy metabolism Energy metabolism Energy metabolism 1 actate mi formate 10 120mH pyru - wH 100mH form - mH	- mid 1 VS. LS40 mid 1 - mid 1 VS. LS40 - mid 1 - mid 1 VS. LS40 - mid 1 - mid 1 VS. LS40 - mid 1 d 1 VS. JS40 - mid 1 d 1 VS. JS40 - mid 1 - mid 1 VS. LS40 - mid - mid 1 - Later VS. LS40 - mid - mid-1 Later VS. LS40 - mid - mid-1							Pearson correla	No Data tion coefficit 1.00 0.90 0.60 0.50 0.40 0.20 0.20 0.10 -0.20 -0.20 -0.30	ent
sion	A cluster diagram derived from eight out of the ten conditions from this study is shown above and								n above and	-0.40	

his cluster diagram clearly suggests distinct modes of energy ge the electron donor as compared to formate during sulfate reduction. We are currently in the process of mapping the corresponding gene expression profiles to the biochemical routes of energy generation in D. vulgaris as depicted in the figure above

### Reference

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Odom, J. M., and H. D. Peck, Jr. 1981. "Hydrogen cycling as a general mechanism for energy coupling in the sulfate-reducing bacteria Desulfovibrio sp." FEMS Microbiol. Lett. 12:47-50.

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