

Title: Systematic mapping of two component response regulators to gene targets in a model sulfate reducing bacterium

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Project Goals: The goal of this project is to elucidate the mechanisms by which bacteria connect core metabolic functions to environmental cues and stresses. Such signaling remains poorly understood even in the best-studied model organisms. As part of near-term goals, we developed methods to understand signal transduction pathways and the corresponding regulatory networks in the sulfate reducing bacterium, *Desulfovibrio vulgaris*. Specifically we focused on two component signal transduction systems. In ongoing research our goal is to understand the physiological relevance of the regulatory maps we have discovered. Long-term goals of this project are to extend our methods to evaluate multiple organisms that coexist in an ecological niche and deduce the connections between the environment and a microbial community that exists in it.

Abstract: *Desulfovibrio vulgaris* is an environmentally relevant bacterium that serves as a model system for dissimilatory sulfate reduction. It is an important member of anaerobic syntrophic communities and is of interest for its metal reduction ability. The strain Hildenborough encodes a large number of two component regulatory systems, none of which are characterized. We sought to map the transcriptionally acting response regulators of these signal transduction systems to their gene targets. In order to accomplish this goal, we developed an in

vitro DNA-affinity-purified-Chip method. We successfully determined 200 gene targets for 24 response regulators, which constitute the majority of this class of regulators in *D. vulgaris*. Our results enabled functional predictions and the identification of binding site motifs for several regulators (1). As expected, several simplex and complex regulatory modules were discovered. Of these an important regulatory network uncovered in our study is centered on the lactate utilization pathway, which appears to be under the control of multiple response regulators. The regulators include a lactate-responsive, a nitrite-responsive, a phosphate-responsive regulator and a potential oxidative stress responsive regulator. Here we present the comprehensive set of regulatory maps obtained using the DAP-chip method. Further, we describe the results from our experiments to evaluate the response of *D. vulgaris* carbon utilization pathway to various stresses such as nitrite and phosphate.

References

(1) Rajeev L, Luning EG, Dehal PS, Price MN, Arkin AP, Mukhopadhyay A* Systematic mapping of two component response regulators to gene targets in a model sulfate reducing bacterium. *Genome Biology* **2011**

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