Title

Comparative Transcriptomic and Ortholog Analysis of Purple Sulfur Bacteria Reveals Conserved and Novel Genes in Sulfur Oxidation Pathways

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Abstract

Purple sulfur bacteria (PSB) are central to anoxygenic photosynthesis and global sulfur cycling, yet many genes that mediate their sulfur oxidation and electron transfer remain poorly characterized. Building upon ongoing research on the metabolic versatility of *Allochromatium vinosum,* this project expands the investigation to include multiple PSB species to identify both conserved and previously unrecognized genes involved in sulfur metabolism. Using a comparative genomics and differential transcriptomics framework, we will analyze RNA-seq datasets from *A. vinosum* and related taxa such as *Chromatium oklahomense*, *Ectothiorhodospira shaposhnikovii*, *Halorhodospira halophila*, and others to identify genes related to the utilization of specific forms of sulfur.

Differentially expressed genes under various sulfur substrates will be quantified using standard RNA-seq pipelines that include programs such as Trimmomatic, Bowtie2, RSEM, and DESeq2. These expression profiles will be integrated with results from OrthoVenn3, which clusters orthologous proteins across species, to incorporate transcript abundance into the orthologous clusters. This combined analysis will allow the identification of core sulfur oxidation modules such as *FccAB*, *SoxYZ*, *Sqr*, and *Dsr/Apr*, alongside with co-expressed yet unannotated genes that may represent new redox or electron transfer components. Enrichment of the orthogroups with parallel expression trends across PSB will help distinguish universally conserved pathways from species specific adaptations.

By linking ortholog detection with transcriptomic co-expression, this work aims to uncover the genetic architecture that enables PSB to utilize solid phase and soluble sulfur compounds. The results are expected to reveal both the shared and unique regulatory frameworks that underpin sulfur oxidation, expanding our understanding of how these microorganisms sustain energy metabolism under diverse environmental conditions.