

Meeting abstract

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## Bioinformatic analysis of gene regulation in *Geobacter sulfurreducens*

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### Background

*Geobacteraceae* are a family of microorganisms from the delta subdivision of *Proteobacteria*. They have potential for environmental bioremediation and electricity generation. In this presentation, we describe our recent bioinformatic analyses of gene regulation in *Geobacter sulfurreducens*, a model representative of this family.

### Results and conclusion

We have developed an online database, GSEL (*Geobacter* Sequence Elements), which compiles regulatory information for *G. sulfurreducens*. We have recently completed the development of a new, significantly expanded and updated, relational version 2 of the GSEL database and its accompanying online query system, which compiles manually curated information on operon organization and transcription regulatory elements in the genome of *G. sulfurreducens*. GSEL v. 2 incorporates a graphical browser and provides significantly expanded search capabilities. It also includes new information on predicted and/or experimentally validated genome regulatory sites and provides links to information from microarray experiments stored in public gene expression databases, and to original publications describing how particular regulatory interactions were identified.

Using sequence and gene expression analyses, we investigated target genes and promoters regulated by RpoN, an alternative RNA polymerase sigma factor, which regulates a variety of important cellular processes in *G. sulfurreducens*. Our current studies are focusing on an investigation of several transcription regulatory systems involved in RpoN-dependent regulatory pathways. We have investigated target regulatory sites for an enhancer binding protein, PilR, which participates in RpoN-dependent transcriptional regulation of the *pilA* gene encoding structural pilin. We predicted multiple PilR-regulated sites upstream of operons related to biosynthesis, assembly, and function of pili and flagella, type II secretory pathways, and cell wall biogenesis.

We also investigated sequence changes and molecular classification of the TetR family of transcriptional regulators. In *G. sulfurreducens*, we identified RpoN-regulated promoters upstream of several operons containing *tetR* family genes. The genome of *G. sulfurreducens* contains nine *tetR* family genes. Some of them are located upstream of operons encoding functionally important *c*-type cytochromes. In order to better understand the roles of TetR family members in the ability of *Geobacteraceae* to participate in electron transfer, we investigated phylogenetic relationships among TetR proteins in *Geobacteraceae*

and in other microbial species. We identified their conserved and variable domains, which may be important for the diversity of their functional roles, and classified them into subgroups based on sequence similarities.

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