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Identification of Small RNAs in *Desulfovibrio vulgaris* Hildenborough

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**Abstract**

*Desulfovibrio vulgaris* is an anaerobic sulfate-reducing bacterium capable of facilitating the removal of toxic metals such as uranium from contaminated sites via reduction. As such, it is essential to understand the intricate regulatory cascades involved in how *D. vulgaris* and its relatives respond to stresses in such sites. One approach is the identification and analysis of small non-coding RNAs (sRNAs); molecules ranging in size from 20-200 nucleotides that predominantly affect gene regulation by binding to complementary mRNA in an anti-sense fashion and therefore provide an immediate regulatory response. To identify sRNAs in *D. vulgaris*, a bacterium that does not possess an annotated Hg gene, RNA was pooled from stationary and exponential phases, nitrate exposure, and biofilm conditions. The subsequent RNA was size fractionated, modified, and converted to cDNA for high throughput transcriptomic deep sequencing. A computational approach to identify sRNAs via the alignment of seven separate *Desulfovibrio vulgaris* genomes was also performed. From the deep sequencing analysis, 2,256 reads between 20 and 250 nt were identified with expression above genome background. Analysis of those reads limited the number of candidates to ~87 intergenic, while ~140 appeared to be antisense to annotated open reading frames (ORFs). Further BLAST analysis of the intergenic candidates and other *Desulfovibrio vulgaris* genomes indicated that eight candidates were likely portions of ORFs not previously annotated in the *D. vulgaris* genome. Comparison of the intergenic and antisense data sets to the bioinformatical predicted candidates, resulted in ~54 common candidates. Current approaches using Northern analysis and qRT-PCR are being used to verify expression of the candidates and to further develop the role these sRNAs play in *D. vulgaris* regulation.

**Materials and Methods**

- **mVISTA**, a genome browser, was used to align and compare seven *Desulfovibrio vulgaris* genomes (1,3).
- The program XRater was used to re-estimate branch length and conserved secondary structure was determined by windowcutter, a scanning algorithm, resulting in a list of putative sRNA candidates (2).
- High throughput transcriptomic deep sequencing was also used to identify novel sRNAs (Fig. 1).
- Sequenced cDNA was scored based on abundance and mapped to the genome of *Desulfovibrio vulgaris* Hildenborough.
- mRNAS, fragments, possible mRNA tail or leader sequences, and candidates smaller than 40 nt were disregarded.
- Remaining candidates were separated into intergenic putative sRNAs and those antisense to existing open reading frames (ORFs) and ordered by abundance and presence in previous computational approaches (Fig. 2).
- Northern analysis was performed on 10 µg of *D. vulgaris* Hildenborough exponential and stationary RNA separated on a 8% polyacrylamide/7M Urea gel and transferred to a nylon membrane by electroblotting.
- Expression of candidates was verified with hybridization of membrane with (\(5'\)-P)-ATP radiolabeled oligo probes (Fig. 3).

**Results**

Figure 2. Venn diagram comparing high throughput deep sequencing candidates with classic genome comparison computational techniques.

Non-Solexa based Computational Candidates

Corresponding to annotated ORFs in other *Desulfovibrio vulgaris* genomes

Intergenic Candidates

<table>
<thead>
<tr>
<th>sRNA</th>
<th>Expt</th>
<th>Stat.</th>
</tr>
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<tbody>
<tr>
<td>Dv SIC3</td>
<td>Exp.</td>
<td>Stat.</td>
</tr>
<tr>
<td>Dv SIC6</td>
<td>Exp.</td>
<td>Stat.</td>
</tr>
<tr>
<td>Dv SIC7</td>
<td>Exp.</td>
<td>Stat.</td>
</tr>
<tr>
<td>Dv SAC4</td>
<td>Exp.</td>
<td>Stat.</td>
</tr>
<tr>
<td>Dv SAC5</td>
<td>Exp.</td>
<td>Stat.</td>
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</table>

**Conclusions**

- High throughput transcriptomic deep sequencing as well as classic genome conservation computational approaches yields a plethora of novel putative sRNAs throughout the genome of *Desulfovibrio vulgaris* Hildenborough.
- Roughly 50% of the candidates tested for expression in exponential or stationary phase RNA yielded bands.
- Northern blot analysis and qRT-PCR experiments are underway to determine how expression of the sRNAs change from exponential to stationary phase.
- Northern analysis and qRT-PCR under various stresses will be utilized to determine expression levels in the genome.

**References**


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