Microbial Pathways for the Reduction of Mercury in Saturated Subsurface Sediments

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ABSTRACT

Mercury in contaminated subsurface soils may be leached to the saturated zone where its reduction to the elemental form, Hg(0), may enhance its environmental mobilization. Therefore, microbial transformations that reduce the mercury species Hg(II) to Hg(0) are of key importance to the remediation of mercury-contaminated subsurface sediments. Microbes may reduce Hg(II) by the activity of the inducible mercuric reductase (MR), the gene product of merA, or by the activity of the constitutive mercuric reductase (mmer), the gene product of mmer.

High diversity and novel clusters in a merA clone library from mercury-contaminated sediments

A PCR approach to encompass the known diversity of MerA in gram-negative bacteria

Enrichment cultures belonging to novel merA clones were isolated

Hg(II) resistant bacteria were isolated from Meadowlands sediment enrichments under fermentative or denitrification conditions. Genus-specific primers were designed to oligoprobes designed for unique clones II - V

• mer operon from strains belonging to mer clades II, III, and V are currently analyzed

Figure 4: DNA hybridization signals with biotin-labeled probes for unique mark clones (A) Specificity of the probes to clade V. (B) Identification of enrichment culture 1A2 as belonging to clade V. (C) Identification of enrichment cultures 2B1 and 283 as belonging to clade V

Cultures currently under study are:

<table>
<thead>
<tr>
<th>Taxon of closest relative</th>
<th>Clade</th>
<th>% Similarity</th>
</tr>
</thead>
<tbody>
<tr>
<td>Pseudomonas sp. 1A2</td>
<td>II</td>
<td>97%</td>
</tr>
<tr>
<td>Bacillus sp 2B1</td>
<td>V</td>
<td>97%</td>
</tr>
<tr>
<td>Staphylococcus sp. 2B3</td>
<td>V</td>
<td>97%</td>
</tr>
<tr>
<td>Paenibacillus sp. N10</td>
<td>III</td>
<td>97%</td>
</tr>
</tbody>
</table>

CONCLUSIONS

• An experimental approach and methods for the study of the diversity of genes encoding for mercuric reductase enzymes in environmental microbial biomasses are available

• A high, and hitherto unrecognized, diversity of merA was found in the microbial community of a contaminated anoxic sediment

• This study will be expanded to the microbial biomass of subsurface sediments