Connecting mercury, the iron-cycle, and the legacy of California’s mining operations.

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Mercury can bind to fine silts, clays, and iron oxides. Once buried anaerobic microorganisms, including sulfate-reducing bacteria (SRB) and iron-reducing bacteria (FeRB), transform mercury into a potent neurotoxin (methyl-mercury) that bioaccumulates in the food chain causing developmental delays in wildlife and human populations (1). In iron-rich ecosystems, up to 50% of all biotic mercury methylation is thought to be performed by FeRB (2, 3, 4, 5). FeRB prefer biologically produced iron-oxides to abiotically produced oxides. Mercury bound to biotically produced iron-oxides may have increased bioavailability and thus increased mercury methylation. The biotic iron-cycle may play an important role in promoting biological mercury methylation and preventing permanent burial which could prolong the flux of mercury into the ecosystem. We hypothesize that mercury is concentrated and more bioavailable in iron-oxide-rich zones, concurrent with zones of elevated biological iron cycling.

We hypothesize that mercury is concentrated and more bioavailable in iron-oxide-rich zones.


<table>
<thead>
<tr>
<th>Sample Site</th>
<th>Iron-rich zone (mM)</th>
<th>Iron-poor zone (mM)</th>
<th>P-value @95% CI</th>
</tr>
</thead>
<tbody>
<tr>
<td>Stratified</td>
<td>41.6 ± 5.8</td>
<td>13.0 ± 1.3</td>
<td>0.02016</td>
</tr>
<tr>
<td>Root masses</td>
<td>29.0 ± 8.7</td>
<td>11.0 ± 1.1</td>
<td>0.01995</td>
</tr>
<tr>
<td>Burrow</td>
<td>19.4</td>
<td>3.2</td>
<td></td>
</tr>
</tbody>
</table>

Table 1. Within a very small spatial scale there was significant difference in the sediment iron concentration for all types of iron-cycling systems dissected. Iron-rich and iron-poor zones were separated by 4-5cm (stratified), 0.5 cm (root mass), and 0.5 cm (burrow).

Future directions
We will measure the mercury concentration in the iron-rich and iron-poor zones. Additionally we will determine the SSU rRNA gene sequences in the iron-rich and iron-poor samples from each iron-cycling system and look for known mercury methylating taxa within these data sets.

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