Introduction:
• Rhizoremediation, the use of plant associated microbes to biodegrade a pollutant, may be an inexpensive clean-up strategy
• A hypothesized mechanism for rhizoremediation: via the release of plant secondary metabolites into the root zone
• Alaskan tree species release a high quantity and diversity of secondary compounds which may encourage the growth and activity of indigenous pollutant degrading bacteria

Objectives:
• Screen microbial functional potential of native Alaskan tree species for rhizoremediation
• Investigate microbial community composition and structure in non-contaminated Alaskan soils

Methods:
• Soils were collected from the organic horizon at 8 sites located in the Bonanza Creek Long term Ecological Research area (BNZ LTER). Tree stands selected include:
  - White Spruce (Picea glauca): 3 stands
  - Black Spruce (Picea mariana): 3 stands
  - Aspen (Populus tremuloides): 1 stand
  - Paper Birch (Betula neoalaskana): 1 stand
• Total microbial community DNA was extracted and hybridized with the GeoChip version 3.0 as previously described per He et al 2010
• 454-pyrosequencing analysis of 16S rRNA extracted from the same soils
• Primers 8f, 357r with MID labels were designed according to to Engelbrektson et al 2010

Results:
Figure 1: DCA of all functional genes. Black circles indicate samples of same dominant tree species. The first two axes account for 67.8% of total variance (eigen values: 0.4196 and 0.2662)

![DCA of all functional genes](image)

Table 1: Shannon H diversity indices of soil from each of the tree stands.

<table>
<thead>
<tr>
<th>Compound</th>
<th>WtSp1</th>
<th>WtSp2</th>
<th>WtSp3</th>
<th>BlkSp1</th>
<th>BlkSp2</th>
<th>BlkSp3</th>
<th>Birch</th>
<th>Aspen</th>
</tr>
</thead>
<tbody>
<tr>
<td>Biphenyl</td>
<td>2.67</td>
<td>-</td>
<td>1.82</td>
<td>2.13</td>
<td>1.99</td>
<td>1.30</td>
<td>1.26</td>
<td>1.82</td>
</tr>
<tr>
<td>Benzoate</td>
<td>4.58</td>
<td>0.96</td>
<td>3.68</td>
<td>4.27</td>
<td>3.79</td>
<td>2.80</td>
<td>2.69</td>
<td>3.58</td>
</tr>
<tr>
<td>Chlorinated</td>
<td>3.73</td>
<td>0.00</td>
<td>2.69</td>
<td>3.17</td>
<td>2.98</td>
<td>1.21</td>
<td>1.30</td>
<td>2.37</td>
</tr>
<tr>
<td>Aromatic</td>
<td>3.89</td>
<td>0.71</td>
<td>2.54</td>
<td>2.75</td>
<td>2.83</td>
<td>1.96</td>
<td>1.28</td>
<td>2.62</td>
</tr>
<tr>
<td>BTEX</td>
<td>3.61</td>
<td>0.71</td>
<td>2.54</td>
<td>2.75</td>
<td>2.83</td>
<td>1.96</td>
<td>1.28</td>
<td>2.62</td>
</tr>
<tr>
<td>Pesticides</td>
<td>3.21</td>
<td>-</td>
<td>1.95</td>
<td>2.56</td>
<td>2.20</td>
<td>1.75</td>
<td>1.08</td>
<td>1.28</td>
</tr>
</tbody>
</table>

Conclusions:
• Functional genes vary by dominant tree species within a forest ecosystem
• Microbes with the genetic potential to degrade chlorinated solvents, hydrocarbons, herbicides, pesticides, and other aromatic compounds are present in varying amounts in the rhizosphere of each tree species
• Functional genetic diversity is highly variable according to tree type

Future Work:
• Phylogenetic identification of community GeoChip experiments
• Pot study to determine PCB disappearance and changes in soil toxicity

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