Screening Alaskan Trees for Rhizoremediation Potential using the GeoChip and 454-Pyrosequencing

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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 labeles were designed according to to Engelbrektson et al 2010

Results:

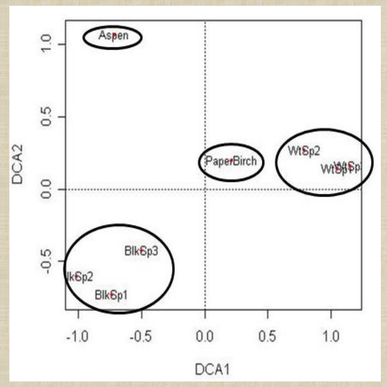

Figure 1: DCA of all functional genes. Black circles indicate samples of same dominant tree species. The first two axes account for 67.8% of total variance (eigen values: 0.4196 and 0.2662)

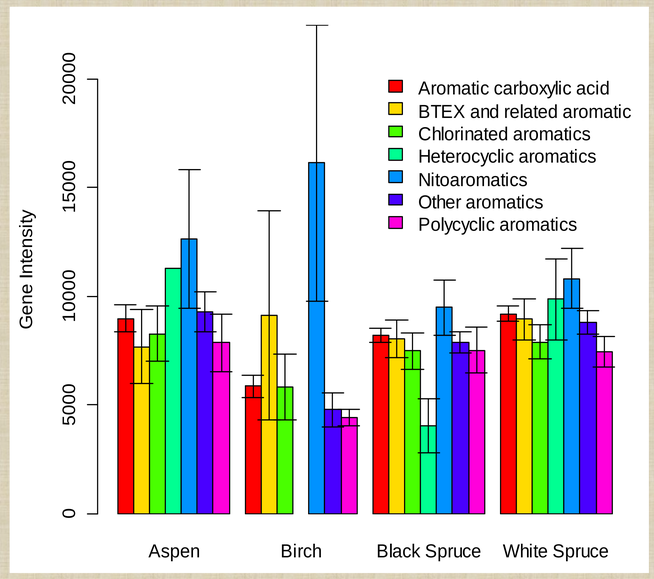

Figure 2: Total signal intensity from all genes present in each sub group of aromatic degradation genes

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

Compound	WtSp 1	WtSp 2	WtSp 3	BlkSp 1	BlkSp 2	BlkSp 3	Birch	Aspen
Biphenyl	2.67	-	1.82	2.13	1.99	1.30	1.26	1.82
Benzoate	4.58	0.96	3.68	4.27	3.79	2.80	2.69	3.58
Chlorinated Aromatic	3.73	0.00	2.69	3.17	2.98	1.21	1.30	2.37
BTEX	3.61	0.71	2.54	2.75	2.83	1.96	1.28	2.62
Pesticides	3.21	-	1.95	2.56	2.20	1.75	1.08	1.28

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

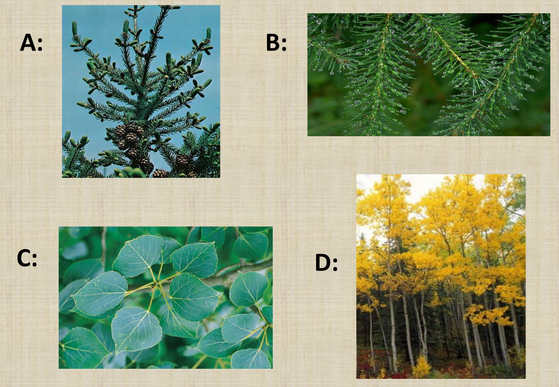

Figure 3. The four tree species investigated for rhizoremediation potential: (A) Black Spruce, (B) White Spruce, (C) Aspen, and (D) Birch.

Future Work:

- Phylogenetic identification of community GeoChip experiments
- Pot study to determine PCB disappearance and changes in soil toxicity

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