Microbial Community Mapping of Long Island Pine Barren Forest Soil, NY.

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Abstract

Management of any ecosystem requires the information on the flora and fauna present in the environment. The current management plans for terrestrial ecosystem are mainly based on the macrofauna. While microorganisms are very critical for maintaining the balance in an ecosystem, no information is available on the types and behavior of microorganisms in the soil of Pine Barren Forest. Thus the existing management plan for an ecosystem does not consider the influence of the actions on the microbial diversity. In the first study of its kind, we mapped the Long Island Pine Barren Forest Soils (LIPBF) based on its microbial community level physiological profile (CLPP). Soil samples were collected from different parts of the forest and upon preparation of the inoculum, BIOLOG® EcoPlates were inoculated. The clustering analysis based on color intensities illustrate that the entire LIBPF can be divided into four different clusters at every horizon. However, the physiological response of microbial community at each horizon and cluster is different. No correlation between sampling sites and the physiological profile was obtained based on vegetation or geographical location. Also, comparing the physiological profile of the microbial community from each horizon, one can make a list of substrates that are utilized more throughout the LIPBF.

Introduction

The vegetation known as the Pine Barrens is scattered throughout northeastern United States and beyond. Compared to other vegetation, the Pine Barrens is a unique region owing to the sandy, acidic, nutrient-poor soil made up largely of coarse sands and gravels deposited by ancient glaciers. A few characteristics of Pine Barrens soil are:

- The soil of the Pine Barrens is acidic because of microbial activity on the plant litter (pH ranging from 4.0 to 4.5).
- Because of the acidic nature, the soil in the Pine Barrens contains high concentration of iron and aluminum.
- Fires are common in Pine Barrens and are necessary to maintain these regions as it replenishes the soil with nutrition; helps control insect infestation and dispersal of pine seeds.
- Water drains rapidly through layers of these porous soils to leave the surface droughty in spite of heavy rainfall in the region.

LIPBF is the second largest Pine Barrens in the country, next to the Pine Barrens in New Jersey. It contains regionally rare wetland communities and rare upland communities including pitch pine-oak-heath woodland and the dwarf pine plains. The goal of the current study is to identify the areas of LIPBF that displays same CLPP to further classify the forest areas into clusters displaying similar CLPP. Also, the study was aimed at obtaining information on the microbial community present in the soil of LIPBF.

Materials and Methods

- Soil samples were collected from 66 sampling locations across the LIPBF (Figure 1).

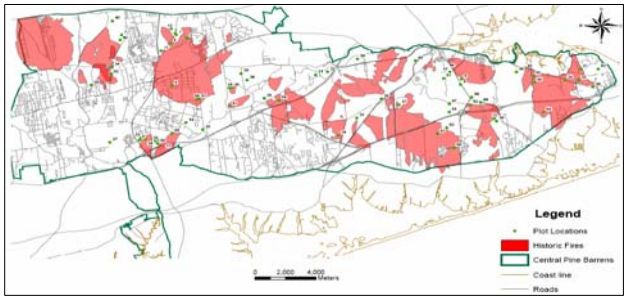

Figure 1. Sampling locations across the Long Island Pine Barren Forest used to map the soil microbial community

- Microbial inoculum was prepared by suspending the soil sample in sterile distilled water and vortexing the sample for five minutes.
- Upon dilution, Biolog® Ecoplates were inoculated and the plates incubated at 30°C for 48 h under 16/8 light/dark cycle. The incubation period was selected upon carrying out optimization studies to find out the least incubation time required for obtaining reliable data. Upon incubation of plates for more than 48 h, no change in substrate utilization pattern was observed. Only the intensity of the wells increased (Figure 2)

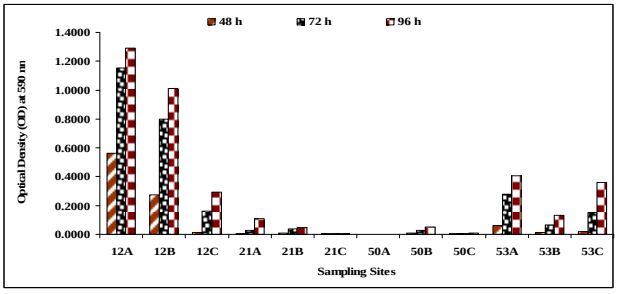

Figure 2. The average well color development observed in Ecoplates as a function of time.

- The plates were read at 590 nm using TECAN plate reader.
- Statistical analysis were carried out using STATISTICA v 8.0.
- Substrate richness (S), was calculated by tabulating the number of substrates having normalized absorbance of more than 0.25.
- The Shannon–Weaver index, *H*, was calculated using the formula

$$H = -\sum_{i=1}^{S} p_i \ln p_i$$

where *pi is* the proportion of microbial activity on substrate *i* in total microbial activity (S).

- The substrate evenness for the microbial composition is given by $E = H/\log S$.

Results and Discussion

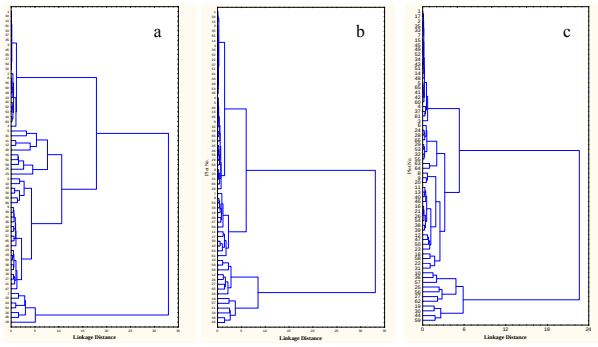

Figure 3. Distribution of microbial community structure by cluster analysis of intensity reactions. (a) Horizon O, (b) Horizon A, (c) Horizon B

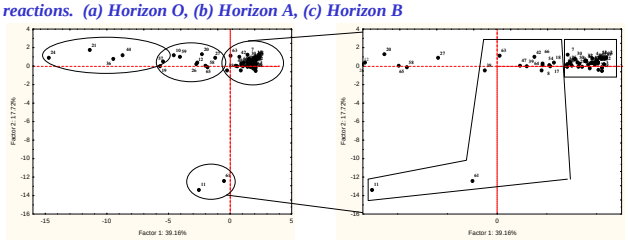

Figure 4. Multivariate analysis (PCA) of CLPP of different soil samples from Horizon A of LIPBF.

	H value			S value			E value				H value			S value			E value		
Site #	O	A	B	O	A	B	O	A	B	Site #	O	A	B	O	A	B	O	A	B
1	26	67	38	0	0	0	0	0	0	34	70	76	66	0	0	0	0	0	0
2	73	62	60	1	0	0	0	0	0	35	67	53	63	0	0	0	0	0	0
3	69	74	87	0	0	1	0	0	0	36	29	24	59	5	14	2	41	21	196
4	32	34	25	1	0	0	0	0	0	37	54	14	38	0	0	0	0	0	0
5	54	25	18	3	0	0	114	0	0	38	28	27	59	3	5	1	59	38	0
6	85	25	30	1	0	3	0	0	62	39	34	30	63	6	3	1	44	63	0
7	22	60	32	14	3	0	19	127	0	40	29	21	44	0	0	0	0	0	0
8	64	41	88	0	2	1	0	136	0	41	29	15	23	6	0	0	37	0	0
9	29	38	43	5	1	4	41	0	72	42	34	42	43	6	4	0	44	69	0
10	49	22	45	5	13	6	70	20	57	43	21	13	26	0	0	0	0	0	0
11	14	14	39	10	4	1	14	23	0	44	24	24	52	0	13	3	0	22	109
12	24	28	36	10	8	3	24	31	75	45	54	23	19	0	0	0	0	0	0
13	25	62	56	3	0	0	52	0	0	46	23	41	45	14	0	1	20	0	0
14	21	55	38	0	0	0	0	0	0	47	42	37	41	3	2	3	89	122	86
15	35	26	25	9	0	0	37	0	0	48	29	46	50	3	0	0	61	0	0
16	37	22	51	3	0	1	78	0	0	49	28	27	26	0	0	0	0	0	0
17	17	54	20	0	1	0	0	0	0	50	29	39	33	2	1	1	97	0	0
18	21	52	49	15	2	5	18	172	70	51	38	20	26	9	0	0	40	0	0
19	26	24	36	7	12	9	30	22	37	52	32	82	18	0	0	0	0	0	0
20	20	42	37	14	7	3	17	49	78	53	42	16	49	0	0	0	0	0	0
21	36	19	57	3	16	1	75	16	0	54	19	36	47	16	2	1	16	121	0
22	31	20	57	4	0	1	51	0	0	55	32	23	53	0	0	1	0	0	0
23	31	27	56	9	0	3	32	0	116	56	41	42	31	0	1	12	0	0	29
24	20	22	56	16	15	1	17	19	0	57	38	33	63	5	8	3	54	37	132
25	29	48	41	11	0	8	28	0	45	58	35	37	45	5	6	4	50	48	75
26	21	36	67	17	8	1	17	40	0	59	27	25	38	11	11	6	26	24	48
27	41	33	23	4	6	14	68	43	20	60	17	27	47	0	0	0	0	0	0
28	19	68	48	18	1	1	15	0	0	61	81	27	65	0	5	0	0	39	0
29	34	33	37	2	0	1	113	0	0	62	42	39	31	3	0	11	88	0	30
30	30	61	27	9	1	12	31	0	25	63	35	41	34	0	4	4	0	67	56
31	34	30	40	10	0	4	34	0	66	64	38	55	46	0	2	6	0	182	59
32	18	50	34	0	0	1	0	0	0	65	31	-3	17	5	8	0	44	0	0
33	75	80	0	0	0	0	0	0	0	66	24	0	48	7	2	1	29	0	0

Table 1: H, S, and E values of the microbial communities across the LIPBF.

Data shows that the following substrates are utilized largely by the soil microbial community of LIPBF: D-Galacturonic Acid, D-Glucosaminic Acid, D-Mannitol, Itaconic Acid, L-Asparagine, L-Phenylalanine, N-Acetyl-D-Glucosamine, Pyruvic Acid Methyl Ester, Tween 40, Tween 80, and γ-Hydroxybutyric Acid.

The clustering analysis indicate that based on CLPP, the entire LIPBF can be subdivided into four different clusters. In each cluster, the number of sites vary by horizon from 3 to 53.

As there is no correlation between the geographical locations of sampling sites, the history of fire or type of vegetation it could be inferred that the CLPP is influenced by soil chemistry. However, further studies need to be carried out to test this hypothesis.

References

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