Investigating the Effects of Groundwater Plumes OU2 and OU3 on the Biodiversity and Soil Health of Bethpage, NY

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Abstract

In the mid-1900s, military industrial plants were established in Bethpage. Subsequent years of unsafe chemical handling led to toxins seeping into the ground. The contaminated soil and water in Bethpage created two major dangerous groundwater plumes. Clean-up efforts were undertaken, but the hazardous chemicals can still be detected today. In the present study, we examined the soil health and biodiversity of a contaminated area compared to an unaffected area. We assessed for biodiversity by collecting insect samples and using DNA analysis techniques. It was found that biodiversity in both areas were similar as shown by phylogenetic trees. This indicates that cleanup efforts have been largely effective at establishing a normal level of biodiversity, despite the area being devastated by industrial waste in the past.

Introduction

The soil is home to more than a quarter of all organisms on Earth and as humans and apex predators, we depend on the soil for all of our energy ("Soil Biodiversity"). However, chemical pollution is a major negative factor in soil biodiversity, where harmful substances such as lead and arsenic kill essential organisms.

In the 1930s, the Northrop Grumman Corporation Site, and in 1941, the Naval Weapons Industrial Reserve Plant, were established in Bethpage, NY. The facilities conducted research, testing, and manufacturing operations for the Navy and the National Aeronautics and Space Administration, situated on 605 acres ("Naval"). These facilities had open seepage basins, a type of drainage system where wastewater is disposed into the ground, and sometimes they even dumped into surrounding grounds. Over years of these unsafe practices, chemicals seeped into the ground, contaminating the soil and water in Bethpage. This created groundwater plumes, a shallow one called the OU2 plume was discovered in 1986, and a larger, deeper one called the OU3 plume was discovered in 2009 ("Northrop Grumman"). Hazardous industrial wastes have been detected in contaminated areas, such as trichloroethylene (TCE), chromium, cadmium, arsenic, and polychlorinated biphenyl (PCB) among various others. Clean-up efforts have been made, but the hazardous chemicals can still be detected today. Currently, the plumes are traveling south and have split into fingers ("Postscript").

This project aimed to examine the effects these groundwater plumes have had on the biodiversity of Bethpage. By surveying areas affected by the plumes to control areas that have not been affected, we used DNA barcoding techniques to examine differences in biodiversity. Furthermore, we surveyed soil contaminant levels; testing for levels of pH, phosphorus, potassium, nitrogen, and mercury. We predicted that in contaminated areas, the biodiversity will be less than those of non-contaminated areas.

Materials and Methods

Samples were taken from a contaminated area, Bethpage Community Park, and a control area, Washington Avenue Park. Currently, the Bethpage Park remains at the northern tip of both the OU2 and OU3 plumes. However, cleanup efforts have been taken to reverse the effects of the plumes in the park. Therefore, this makes the site a great location for sampling an area that has been affected by the plume and studying how effective cleanup efforts have been. On the other hand, Washington Avenue Park is about five and a half miles south of the Bethpage Park. It has not been affected by the plume, but due to the current southward movement of the plumes, it may be in the future. This allows us to test for biodiversity and soil contamination of the Washington Avenue Park now, and possibly again in the future if the plume moves southward to affect it. These sites are depicted in Figure 1.

Multiple samples were collected on May 8, 2017 in each park within a six inch radius at the base of a post. First, four soil samples were taken using a one foot soil core sampler from each site. Each sample was approximately ninety degrees from each other, circling the post. Then, ten insect samples were taken from each site. Insect samples PHC-001 to PHC-011 were collected from the contaminated site and insect samples PHC-012 to PHC-021 were collected from the control site.

In the lab, samples were documented frozen for preservation. A portion of soil samples were measured for soil health by testing for levels of pH, phosphorus, potassium, and nitrogen. Next, the DNA was isolated following procedures outlined on the DNA Barcoding website ("*DNA Barcoding*"). Then, the DNA was amplified through polymerase chain reaction and analyzed with gel electrophoresis. Finally, the DNA was sent to be sequenced in both the forward and backward directions.

Results

From the soil test, it was found that the contaminated area was slightly acidic with a pH of 6, had low amounts of nitrogen, high amounts of phosphorus, no mercury, and high amounts of potassium. The control area was neutral with a pH of 7, had trace amounts of nitrogen, no phosphorus, no mercury, and medium amounts of potassium. This is shown in Figure 2.

From our gel electrophoresis, depicted in Figure 3., we found that sample PHC-004's DNA was not properly amplified as shown by the very faint band, and therefore not sent in for sequencing. Samples PHC-013 and PHC-015 also showed faint bands, but this is suspected due to a defect in the gel as it did not affect DNA sequencing results. However, samples PHC-008 and PHC-021's faint bands proved to be a problem as they resulted in unreliable DNA sequencing results.

After receiving the DNA sequencing results back, the sequences were trimmed, the forward and backward sequences paired, and a consensus was met for each sample using the DNA Subway program. Samples PHC-008 and PHC-021 were found to be unreliable. Next, by using the Basic Local Alignment Search Tool (BLAST), each sample's DNA sequence was compared to that of those in the CyVerse database. This resulted in confident matches for most samples, however, samples PHC-007 and PHC-014 were additionally ran through the Barcode of Life Data (BOLD) System for more precise identification. The top BLAST result for all samples are shown in Figure 4. Then, a phylogenetic tree was constructed with all samples alongside reference data set Common insects. Sample PHC-016 was selected as the outgroup. The tree is depicted in Figure 5.

Discussion

From our BLAST sequence results, there were no samples with much significance. All species identified were native to the east coast and did not indicate any potential hazards. In addition, the phylogenetic tree did not show any notable patterns, where samples collected from the contaminated and control sites were evenly spread throughout the tree. These results are promising as they do not show any significant difference from the contaminated and control sites, indicating that cleanup efforts at the contaminated site, Bethpage Community Park, have been successful.

In 2013, the Town of Oyster Bay excavated approximately 175,000 cubic yards of soil contaminated with the chlorinated solvents, PCBs, metals and Freon compounds dichlorodifloromethane (R-12) and chlorodifloromethane (R-21), replacing the materials with clean soil. In addition to the excavation, a groundwater extraction, treatment, and containment system has been set up along with a soil vapor extraction and treatment system ("Northrop"). Four years after the cleanup process, we can now establish that the topsoil biodiversity is normal compared to that of a control area. Knowing this, it gives us reassurance that the health effects on humans have also been lowered. However, without reference data of biodiversity before and during the contamination period, we cannot see how biodiversity has changed.

In addition, we found that the contaminated area contained higher levels of nitrogen, phosphorus, and potassium. High levels of nutrients can indicate the use of fertilizer, which may be attributed to the soil excavation and replacement efforts. This can be beneficial to the biodiversity as it helps plants grow and should not pose a problem as long as no harmful chemicals were used in the fertilizer that could seep into the soil and runoff. We unfortunately were unable to test for such chemicals, but could do so in the future.

Furthermore, in further studies we hope to test for the biodiversity of the soil deeper down. Due to the soil excavation and replacement efforts, it is expected that the topsoil to be clean, however, soil deeper down may still be contaminated.

In addition, we hope to monitor the plumes' movements. While containment systems have been put in place, the plumes have been moving south. If the plumes come to affect our control area, Washington Avenue Park, we hope to collect samples from the site again, allowing for us to compare the biodiversity of the area before and after the contamination.

Overall, while this study has shown that cleanup efforts at Bethpage Community Park have worked to maintain a normal level of biodiversity in the topsoil, we must be wary about the other effects the plumes may have had and the future of the plumes.

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Figure 1. Collection Sites

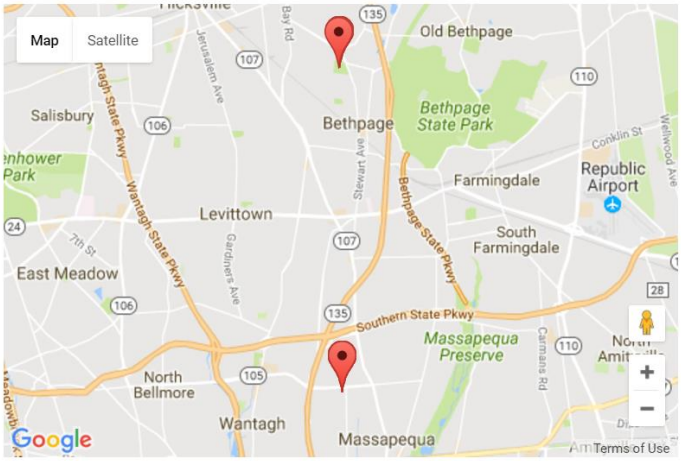

Figure 2. Soil Health

	Contaminated Area	**Control Area**
pH	6	7
Nitrogen	low	trace
Phosphorus	high	none
Mercury	none	none
Potassium	high	medium

Figure 3. Gel Electrophoresis

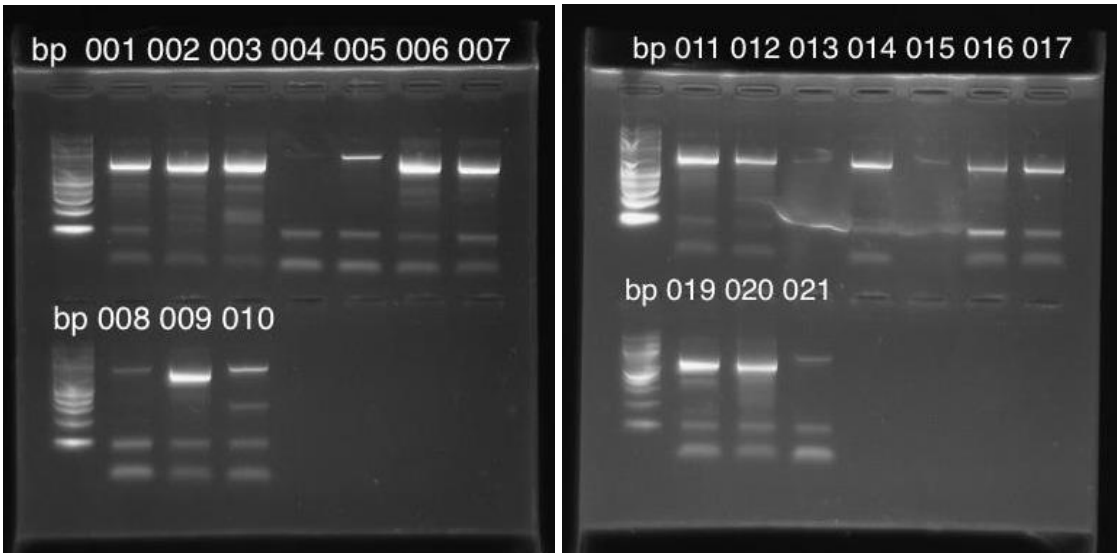

Figure 4. DNA Sequence BLAST Results

Sample #	Details	Alignment Length	Bit score	Mis-matches
PHC-001	Orfelia nemoralis	651	1175	0
PHC-002	Deroceras reticulatum	646	1166	0
PHC-003	Nephelodes minians	585	1034	3
PHC-005	Chortophaga viridifasciata	534	931	7
PHC-006	Lasius neoniger	650	1168	1
PHC-007**	Philoscia muscorum	100% similarity	--	--
PHC-008*	Aporrectodea trapezoides	438	468	79
PHC-009	Solenopsis molesta	654	1171	2
PHC-010	Dysdera crocata	465	839	0
PHC-011	Tasgius melanarius	654	1180	0
PHC-012	Pagaronia minor	657	1126	13
PHC-013	Tetramorium caespitum	654	1180	0
PHC-014**	Allocosa funerea	99.4% similarity	--	--
PHC-015	Oxyopes scalaris	520	827	23
PHC-016	Lumbricus castaneus	552	996	0
PHC-017	Reticulitermes flavipes	652	1141	6
PHC-019	Udea rubigalis	654	1180	0
PHC-020	Leptopterna dolabrata	653	1178	0
PHC-021*	Pelegrina galathea	287	434	19

* signifies unreliable results
** signifies identified using Barcode of Life Data (BOLD) System

Figure 5. Phylogenetic Tree