Biodiversity of Moss in Three Locations with Varying Degrees of Vehicular Traffic

Authors: Jessica Dai[1], Angela Youn[1], Rebeca Zapiach[1], Daphne Zhu[1]
Mentor:Dr. Christine Marizzi[2], Melissa Lee[2] Teachers: Mrs. Anat Firnberg[1]
[1]Tenafly High School; [2]Cold Spring Harbor Laboratory's DNA Learning Center

Abstract

Research has suggested that moss serve as bioindicators of air pollution generated from car exhaust, industrial emissions, and fuel combustion.[1] Based on this information, we have seen a clear contrast in biodiversity between areas of high vehicular pollution and those of low vehicular pollution. The moss samples were collected from three locations with differing degrees of traffic congestion and commercial activity, therefore having differing levels of vehicular pollution. Through DNA extraction, amplification, and analysis, we have identified a total of five species of moss with the highest BIT scores and genetic sequence compatibilities from the three locations. Four unique species of moss were found at the location with minimal pollution, suggesting a high level of biodiversity. On the other hand, only two species of moss were found in the areas of maximal vehicular pollution. This demonstrates that a higher level of exposure to pollution correlates to suppressed biodiversity.

Introduction

Research shows that emission from vehicles especially automobiles is responsible for an overwhelming amount of the air pollution in the typical urban area. The major pollutants emitted by motor vehicles including carbon monoxide, sulphur dioxide, nitrogen oxides, various hydrocarbons, lead, and suspended particulate matter have damaging effects on both human health and our ecology.[1]

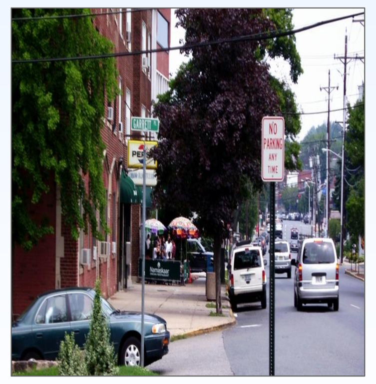
In addition, moss have been researched and proven to be bioindicators of vehicular pollution and air pollution.[2,3] The decline and absence of bryophyte populations, especially in species like moss that derive its moisture and nutrients from its surroundings, is a phenomenon primarily induced by air pollution.[4]

With this information, we sought to investigate and identify different species of moss in locations with differing degrees of vehicular pollution. The three locations were at the heart of the woods at Tenafly Nature Center, the moderately exposed area at Roosevelt Commons Park in Tenafly, and a busy commercial area on Palisades Ave. in Englewood. Our hypothesis was that there would be a direct correlation between high levels of biodiversity of moss in areas with less vehicular pollution, and likewise, low levels of biodiversity in areas with heightened vehicular pollution.

Fig. 1.1 Tenafly Nature Center

Fig. 1.2 Tenafly Roosevelt Commons Park

Fig. 1.3 Englewood Palisades Ave.



Materials and Methods

Five by five inches of moss samples were collected using a trowel from three distinct locations within a short range in Tenafly, NJ, and on Palisades Avenue in Englewood, NJ. In order to further ensure a consistency of nutrients in the soil and reduce any major variables, the selected moss were exposed to similar amounts of sunlight. The time, date and coordinates were labeled on disposable bags. The samples were then replanted in a terrarium and kept in indirect sunlight to imitate its natural environment. The standard process of DNA extraction was performed without any changes to the procedure.[5]

Figure 2.1 - Extracting the DNA

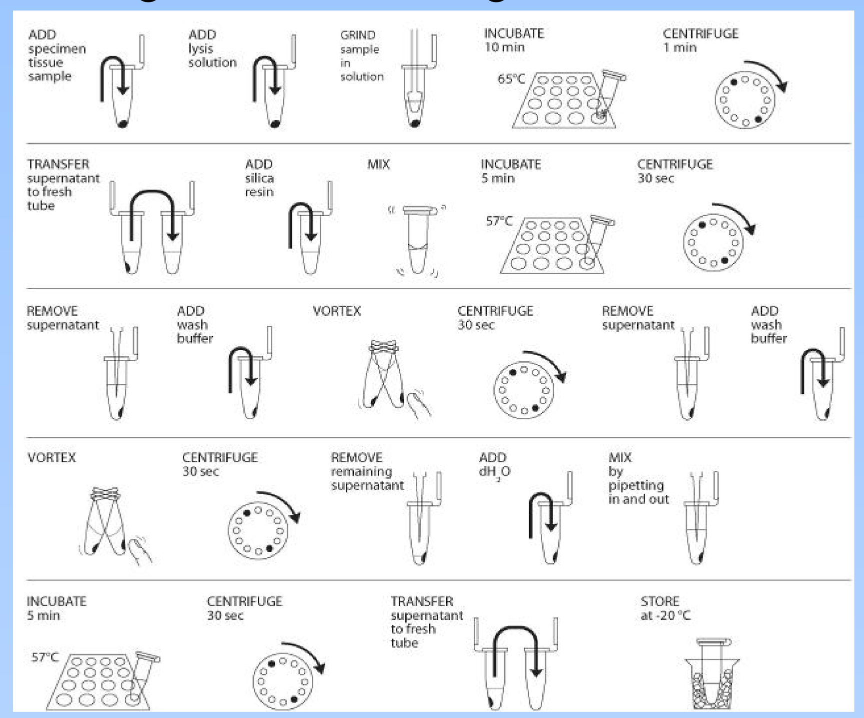
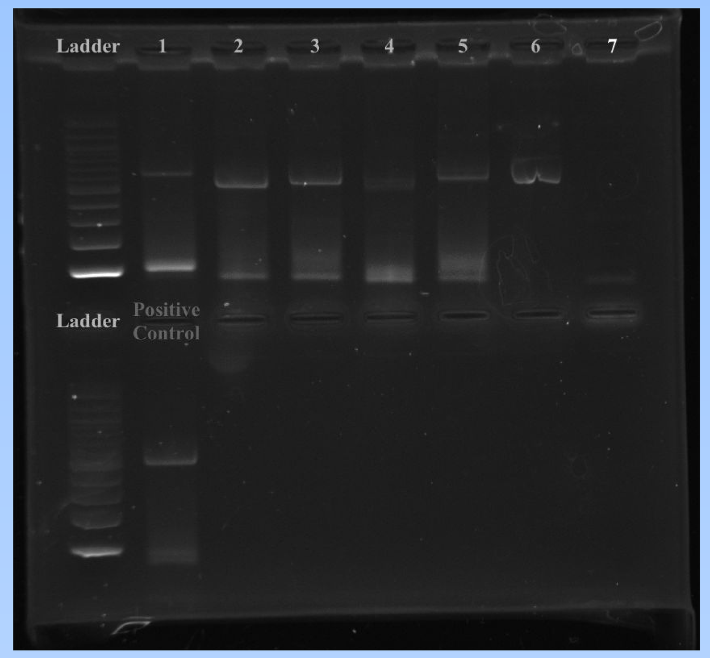


Figure 2.2 - Gel Electrophoresis Results



Results

Figure 3.1 - Genetic Sequence Similarities

	C	1	2	3	4	5	6	7	8	9	10	11
C	-	86.15	86.10	90.75	93.63	90.05	89.60	86.57	86.67	85.11	81.56	85.68
1	86.15	-	95.72	80.60	82.19	78.78	79.88	80.83	78.05	71.94	79.44	77.78
2	86.10	95.72	-	79.85	80.97	78.25	78.96	80.22	77.13	70.75	78.40	78.76
3	90.75	80.60	79.85	-	92.88	89.01	92.55	92.34	79.40	73.96	74.53	81.07
4	93.63	82.19	80.97	92.88	-	98.88	91.84	92.80	82.30	77.38	78.79	83.14
5	90.05	78.78	78.25	89.01	98.88	-	90.96	90.16	77.34	72.66	79.87	79.75
6	89.60	79.88	78.96	92.55	91.84	90.96	-	94.92	77.13	73.13	77.02	79.33
7	86.57	80.83	80.22	92.34	92.80	90.16	94.92	-	74.52	69.61	73.31	76.81
8	86.67	78.05	77.13	79.40	82.30	77.34	77.13	74.52	-	98.88	78.45	82.81
9	85.11	71.94	70.75	73.96	77.38	72.66	73.13	69.61	98.88	-	76.27	78.32
10	81.56	79.44	78.40	74.53	78.79	79.87	77.02	73.31	78.45	76.27	-	85.34
11	85.68	77.78	78.76	81.07	83.14	79.75	79.33	76.81	82.81	78.32	85.34	-

Figure 3.2 - BLAST Results

ATS-001

#	Accession #	Details	Aln. Length	Bit Score	e	Mis-matches
1(1).	KM502672.1	Dicranum flagellare - internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene and internal transcribed spacer 2, complete sequence; and 26S ribosomal RNA gene, partial sequence	360	614	1e-173	3

ATS-002

#	Accession #	Details	Aln. Length	Bit Score	e	Mis-matches
1(1).	KJ734137.1	Pseudotaxiphyllum obtusifolium - Zuo 595(HSNU) 5.8S ribosomal RNA gene, partial sequence; internal transcribed spacer 2, complete sequence; and 26S ribosomal RNA gene, partial sequence	420	241	1e-60	78

ATS-003

#	Accession #	Details	Aln. Length	Bit Score	e	Mis-matches
1(1).	KF871805.1	Scorpidium cossonii - 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed spacer 2, complete sequence; and 25S ribosomal RNA gene, partial sequence	395	538	1e-150	17

ATS-004

#	Accession #	Details	Aln. Length	Bit Score	e	Mis-matches
1(1).	KJ734130.1	Plagiothecium nemorale - Wang 123(HSNU) 5.8S ribosomal RNA gene, partial sequence; internal transcribed spacer 2, complete sequence; and 26S ribosomal RNA gene, partial sequence	284	352	2e-94	16

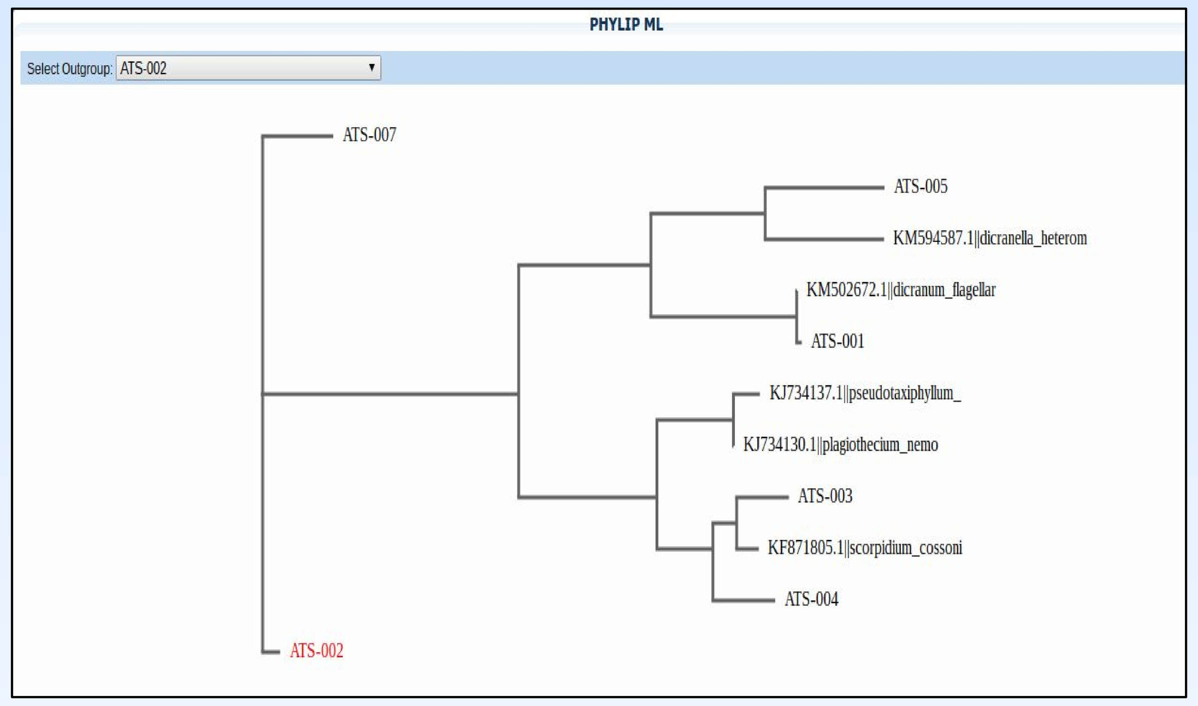
ATS-005

#	Accession #	Details	Aln. Length	Bit Score	e	Mis-matches
1(1).	KM594587.1	Dicranella heteromalla - 08-380 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed spacer 2, complete sequence; and 26S ribosomal RNA gene, partial sequence	408	295	7e-77	49

ATS-007

#	Accession #	Details	Aln. Length	Bit Score	e	Mis-matches
1(1).	KJ734137.1	Pseudotaxiphyllum obtusifolium - Zuo 595(HSNU) 5.8S ribosomal RNA gene, partial sequence; internal transcribed spacer 2, complete sequence; and 26S ribosomal RNA gene, partial sequence	456	298	5e-78	80

Figure 3.3 - Phylogenetic Tree (PHYLIP ML)



Tenafly Nature Center	*Dicranum flagellare*	*Pseudotaxiphyllum obtusifolium*	*Plagiothecium nemorale*	*Scorpidium cossonii*
Roosevelt Commons	*Dicranella heteromalla*			
Palisades Avenue	*Pseudotaxiphyllum obtusifolium*			

Fig. 3.4 - Chart of Final Moss Findings in Three Locations
Four species were found at Tenafly Nature Center and one species was found at Roosevelt Commons and at Palisades Avenue.

Discussion

The hypothesis that the areas with higher levels of vehicular pollution will have less biodiversity was proven to be true. By analyzing the biodiversity of moss, it was concluded that there is a more diverse range of species of moss at the Tenafly Nature Center than at Roosevelt Commons and Palisades Avenue. The higher level of vehicular pollution affects the diversity of the species of moss that is able to grow in that location.

This project has widespread implications in both our community in Tenafly and its neighboring towns, as well as in the larger picture in terms of the ecosystem and environmental status. We were motivated and inspired to choose this topic after learning about the "Northern Branch Corridor Project," which is a planned extension of the Hudson-Bergen Light Rail from its northern terminus into eastern Bergen County, New Jersey.[6] We hope that our findings will raise concern for the severe repercussions that vehicular pollution can have on our communities with the introduction of this rail line.

In the future we would like to test the pH of the soil to see if it affects the biodiversity of the moss in the three locations. Furthermore, we would like to examine other organisms in these locations to see if they follow the same biodiversity trend as the moss.

Acknowledgements

We would like to express our genuine gratitude towards Mrs. Anat Firnberg, our Science Research mentor and AP Chemistry teacher at Tenafly High School, for her continuous guidance and support during this project. We are very grateful for her valued insight and experience. We would also like to thank Dr. Christine Marizzi, the genetics researcher and educator at the DNA Learning Center under the Cold Spring Harbor Laboratory, for her assistance during our DNA barcoding process.

References

1. Bhandarkar, Shivaji. "Vehicular Pollution, Their Effect on Human Health and Mitigation Measures." *Science and Engineering Publishing Company* . N.p., June 2013. Web.
2. Palmieri, F., R. Neri, C. Benco, and L. Serracca. "Lichens and Moss as Bioindicators and Bioaccumulators in Air Pollution Monitoring." *Journal of Environmental Pathology, Toxicology and Oncology : Official Organ of the International Society for Environmental Toxicology and Cancer.* U.S. National Library of Medicine, 1997. Web. 29 Mar. 2017.
3. Winner, W. E., and J. D. Bewley. "Terrestrial Mosses as Bioindicators of SO2 Pollution Stress : Synecological Analysis and the Index of Atmospheric Purity." Oecologia. U.S. National Library of Medicine, Jan. 1978. Web. 27 Mar. 2017.
4. "Impacts of Air Pollution on Lychens and Biophytes (mosses and Liverworts)." *APIS.* N.p., 14 Oct. 2014. Web. 20 Mar. 2017.
5. "DNA Learning Center Barcoding 101." DNA Learning Center Barcoding 101. N.p., n.d. Web. 29 Mar. 2017.
6. "About the Project." *Northern Branch Corridor Project*. NJ Transit, n.d. Web. 8 May 2017.