

## Abstract

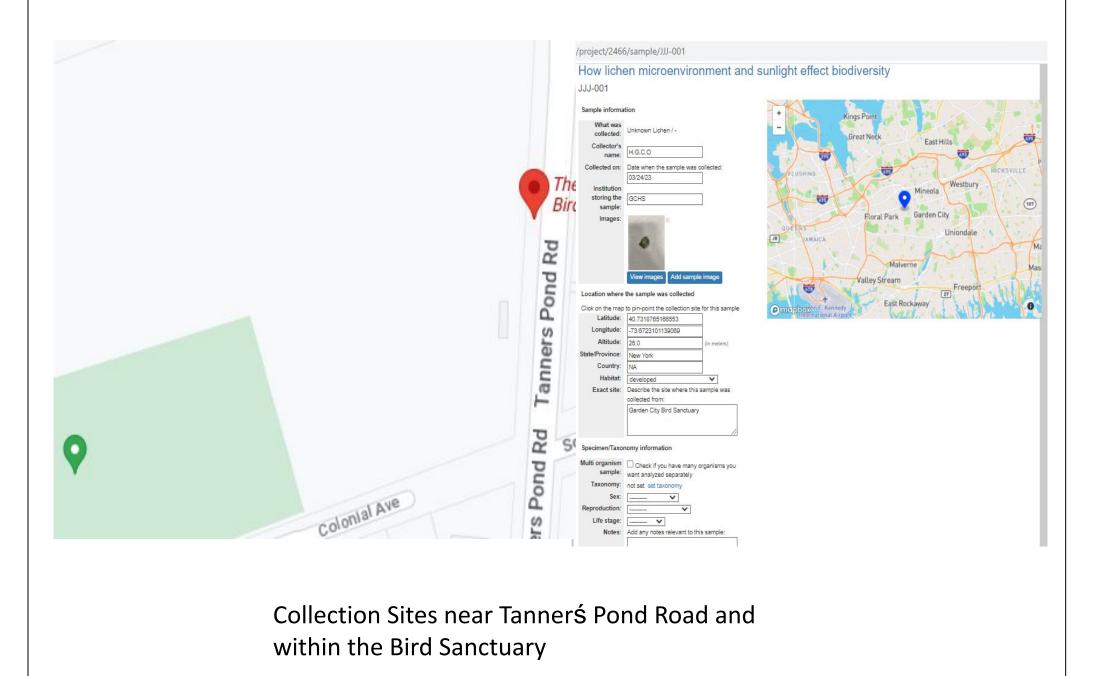
Lichen is a group of fungus and bacteria that form a culture together making a hybrid organism. Many lichen species are still unknown and undiscovered because of the little information available about lichen. The unknown factors makes it more interesting to see how different environmental factors affect the typing of these organisms we researched. The effects of micro environmental factors on the specific types of lichen native to Long Island and we hypothesized that a darker lichen is more likely to grow in areas with little sunlight in an environment compared to lichen exposed to light have a lighter color. We collected our samples of lichen exposed to different light levels in the Garden City Bird Sanctuary to keep the environment as a constant we then started the important process of barcoding our lichen samples with a PCR reaction specific to fungi (ITS-1) we used lysis buffer to to break down the samples and used silica to extract pure DNA. Then we proceeded to Barcode our DNA until we got our final sequences.

### Introduction

Our group tried to prove the effects of micro environmental factors on species in the environment, we mainly focused on light exposure in our experiment based on the peer reviewed article of lichens on road signs (see image below), which showed promise On the basis of the experiment where lichen was growing on two sides of a stop sign, one side had a larger exposure to light then the other which greatly affected the results. The published papers showed how there was a physical change in the lichen but didn't prove that these two organisms were the same or different species. Which is what my group is trying to prove.



https://www.newscientist.com/lastword/mg25433841-300-why-are-the-lichens-distributed-in-thi s-way-on-this-sign-pictured/





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# **Results:**

Our results were inconclusive as our barcoded DNA only had 80 % identity to other organisms and were low quality sequences. Some of our sequences clearly matched incorrect species such as stalked mushrooms, showing how ITS-1 sequences have been conserved evolutionarily across fungi species. When we proceeded to Barcode our DNA until we got our final sequences which were (below):

### Tables & Figures:

Sequence Name	Forward Sequence	Organism	Reverse Sequence		
JJJ-001	CCGCTTATTGGTANGCTTAAATTCAGCG GGTAGNCNGGCCTGATTTGAGGGTCCAG TTGGAANTGATGGTCTCTTGAGAGAGACA GTTGGAATCAGGTCCCTATAGGTTCACT AAGCCGAGGCGCAGAGAGAAATTATCACAC CAAGGCCGCCAAAGGGCTGCCCCAAATG TATGCNAGGAGAGCAGATCAGCCAGG GACCTGCNAGCTCCAAAATCCCGNCC AATGGCTTCCCAAAAAGATATCCGGNG GAGGAGTTCACGACGCTCGGACAGGC GTGCCCCNCGGAATGCCTAGGGGGCNC ANGGTGCGTTGAAGATTCGGTGATTCA CTGGATTNNGCANTTCACATTACTTATC GNATTTCNCTGCNTTCTTCGCCGATGC NAGAGCCAAGAGANCGGTTGNTGAAA CTTA	Poor quality	GGGAATCCTTGTTAGTTTCTTTCCTC CGCTTATTGATATGCTTAANTTCAGCGG GTAGTCCGTCCTGATTTGAGGTCAAGT TTGAANTGACTGTCTCTTGCNAGACG GTTGGAAGCAAGTCCCTATAGGTTCGC TAAGCCAAGGCNCAGATAATTATCACA CCAAGGCCGCAAAGGGCTTCCCTAAT GTATTCAAGGATAGCAGATCAACCAGG GACCTGCAAGCTCCCAAATCCCACCC CAATGCCTTCCNAAAAAGATATAGGGT GGAGGAGTTCACGACACTCAAACAGG CNTGCCCCTCGGAATGCCTAGGGGGCC CAAGGTGCGTTCAAAGATTCGGTGATT CACTGAATTCNGCAATTCACATTACTTA TCGCATTTNGCTGCNTTCTTCATCNAT CCNAGAGCCAAGAGATCCGTTGTTGA ACCTTATATTTGTGCGAGTTAACGCAG GGTACATTCTGATACTTTACNGGGGTAT GTATAAANGTTNGCATGC	Agaricomycet es sp. genotype (93%) obviously not because this is a stalked mushroom, showing how poor quality sequence can yield incorrect results	
JJJ-002	A N C N N N N T A T C T T G G N N GT N N TT T N N TT T N T N		TTCAGCGGGTAGTCNCGCCTGATTTGA GGTCAAGTTNGAACTGATTGCCTCTTG CAAGACGGTTGGAAGCAAGTCCCTATA GGTTCGCTAAGCCNAGGCGCAGATAAT TATCACACCAAGGCCGCAAAGGGCTN CCCTAATGTATTCAAGGANAGCACATC AGCCAGGGACCTGCAAGCTCCCAAAT CCCAGCCCATTGCCTTCCGAACAATAT ATATGGTGGAGGAGTTCACGACTCTCG AACAGGCGTGCCCCTCGGANTGCCAA GGGGCGCAAGGTGCGTTCAAAGATTC		

Although our sequence is low quality, one of our sequences showed the stalked mushroom, which is closely related to species of lichen. We only had two samples of DNA that showed up on the gel, because the third one wasn't a good DNA extraction or had few fungi species..

	С	1	2	3	4
С	-	49.34	83.40	86.74	86.96
1	49.34	-	<mark>40.4</mark> 9	37.73	39.53
2	83.40	<mark>40.4</mark> 9	-	75.62	74.84
3	86.74	37.73	75.62	-	77.70
4	86.96	39.53	74.84	77.70	-

NT							SEG	UENCE S	SIMILARITY %
100	200	300	400 👋					×	700
II				С	1	2	3	4	
			c	-	<mark>49.34</mark>	83.40	86.74	86 <mark>.96</mark>	
			1	49.34	-	40.49	37.73	39.53	
			2	83.40	40.49	-	75.62	74.84	
			3	86.74	37.73	75.62	-	77.70	
			4	86.96	<mark>39.5</mark> 3	74.84	77.70	-	

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Lichen by the national library of medicine Arnold DL, Krishnamurthy K. Lichen Planus. [Updated 2022 May 1]. In: StatPearls [Internet]. Treasure Island (FL): StatPearls Publishing; 2022 Jan-. Available from: https://www.ncbi.nlm.nih.gov/books/NBK526126/

Lichen by britannica Britannica, T. Editors of Encyclopaedia (2022, September 8). lichen. Encyclopedia Britannica. https://www.britannica.com/science/lichen

Lichen this sign (Ebsco) Why are the lichens distributed in this way on this road sign? The surfaces have the same texture. "Lichen This Sign." New Scientist, Reed Business Information, 29 Apr. 2022, https://www.sciencedirect.com/science/article/abs/pii/S0262407922007692.

CSH Cold Spring Harbor Laboratory DNA LEARNING CENTER

### Discussion

Our hypothesis was inconclusive about the effect of micro environmental factors on the species in the environment. Other articles and experiments in the scientific community along with some peer reviewed articles help the world have a broader understanding of a largely unknown species We wish we could have had a more purified DNA template in the future, If given the opportunity to continue with this research, we would like do this experiment over a larger area with many subtopics of research instead of focusing in on one.

The ITS-1 primer yielded only poor quality sequences. Although the sequences belonged to different species of fungi with about 86%-93% identity, they showed obvious errors. For example, Agaricomycetes was identified by BLAST (shown below), but since it is a stalked mushroom, it could not be our sample collected.

ricomycetes sp. genotype e50ss008 internal transcribed spacer ence ID: KM519352.1 Length: 1077 
 Query
 301
 CCTCGGAATGCCTAGGGGGCCCAAGGTGCGTTCAAAGATTCGGTGATTCACTGAATTCNGC
 360

 Sbjct
 334
 CCTCGGAATGCCAAGGGGGCGCAAGGTGCGTTCAAAGATTCGATGATTCACTGAATTCTGC
 275
Query 361 AATTCACATTACTTATCGCATTTNGCTGCNTTCTTCATCNATCCNAGAGCCAAGAGATCC Query 421 GTTGTTGAACCTTATATTTGTGCGAGTTAACGCAGGGTACATTCTGATACTTTACNGGGG 480 TATGTATAAANGTTNGCATGC 501 Sbjct 154 TATGT-TAAAGGTTTGCATGC 135



# References

Basidiomycete yeasts in the cortex of ascomycete macrolichens

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