Biodiversity of Lichen Found in Various Stages of Succession

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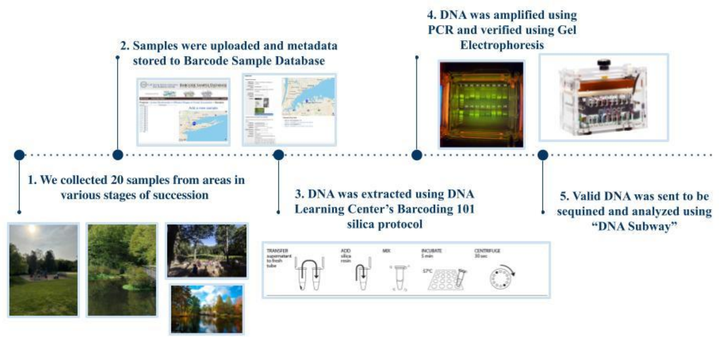
Abstract: We study the biodiversity of lichen in various stages of succession. Secondary succession occurs when a new ecosystem forms after a disturbance occurs.Our objective was to collect lichen from various stages of succession in order to determine the species and conclude the biodiversity. After performing our steps, we found that there was actually more biodiversity in earlier stages of succession opposed to later stages. We believe these results could be due to human error, as when we were in the forests (later stages of succession) the lichen was more abundant so we chose trees closer together causing similar species. When in the early stages of succession the trees were more spread out and with the human interference, they may have had to adapt.Our results of lichen could be due to human error or the fact that lichen of the same family are more abundant in later stages of succession

Introduction: With about 17,000 species, lichens are a diverse and common organism that cover 7% of the planet's surface. Lichens are an advanced form of life that are produced when a fungus and an alga work together in symbiotic relationship. By producing oxygen, retaining moisture, and providing other organisms with food and shelter, they play a crucial ecological role. In primary succession, living organisms first occupy newly exposed or newly created material. When a disturbance affects a culminating community or an intermediate community, secondary succession occurs as a regrowth of that ecosystem. As soil and nutrients are still present, the succession cycle is restarted but completely. We collected various samples of lichen, in various areas of developmental stages to determine the extent of biodiversity in different stages of succession. We collected from the FA playground and Forest School which are in early stages of succession and Shu Swamp and Bailey Arboretum as later stages of succession.

Acknowledgements: We are grateful to Mrs. Newitt and Vijay for supporting our research, as well as Dr. Pepenella and Dr. Margo for their assistance and teaching.

References

Methods and Materials



Results

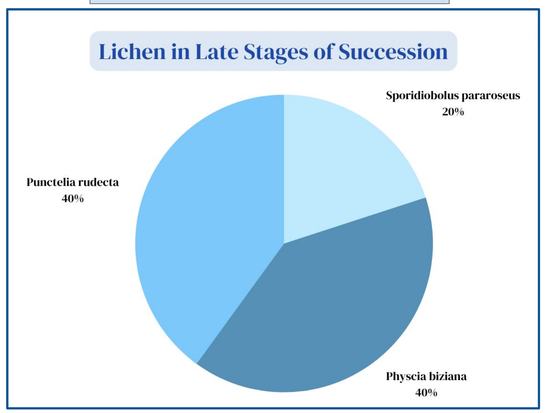


Figure 1: Lichen species abundance in an area with late states of succession

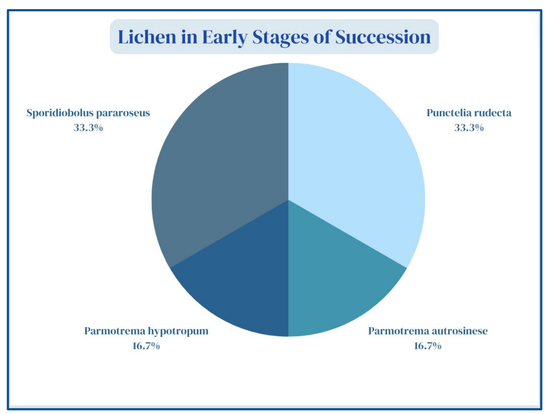


Figure 2: Lichen species abundance in an area of early stages of succession

Discussion: The data presented in this study indicates a lower level of biodiversity within later succession areas. The decreased variability observed in lichen species and genus in higher areas suggests that, in our experiment, there was greater biodiversity in the earlier stages of succession, specifically the playground and forest school sites. This observation also underscores the ability of lichens, such as *Punctelia*, to thrive and adapt to diverse ecological conditions as many of the *Punctelia* species were seen throughout the entire succession experiment. It is crucial to note, however, that there is a chance that human error could have affected these results. Tree selection in later succession areas led to a higher abundance of related tree and lichen species because of their close proximity, whereas early succession areas had trees that were more widely spaced out, producing more diverse results. Due to this intrinsic restriction, it is challenging to evaluate with certainty whether one stage exhibits greater biodiversity.

MUSCLE Alignment

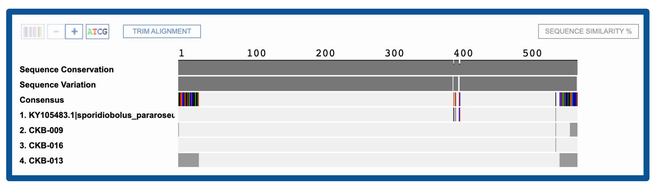


Figure 3: Three sample matches that indicate *Sporidiobolus pararoseus*

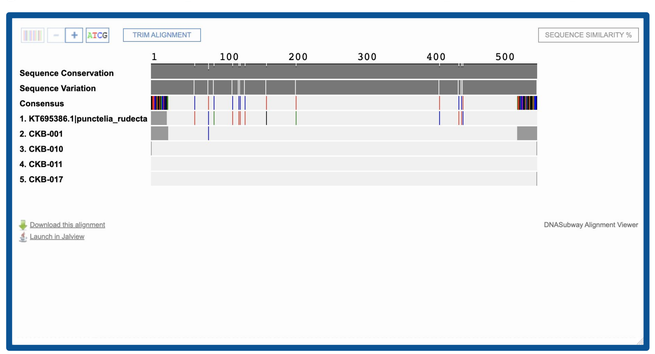
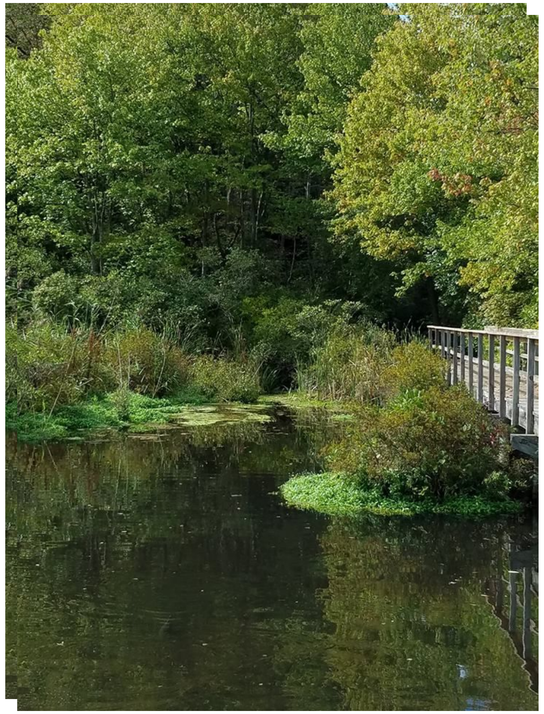


Figure 4: Three sample matches that indicate *Punctelia rudecta*

We collected 20 samples from areas in various stages of succession

Friends Academy Playground: a man made area in constant upkeep

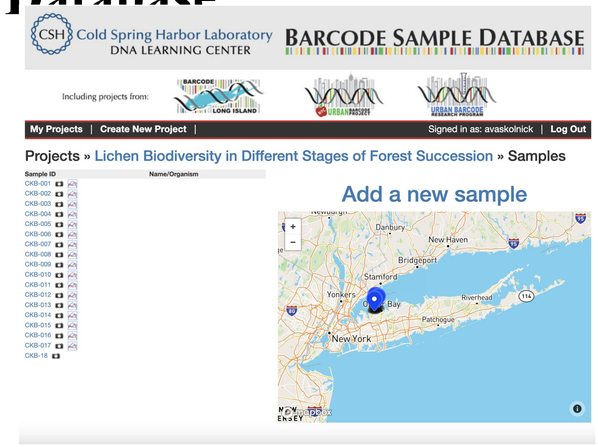


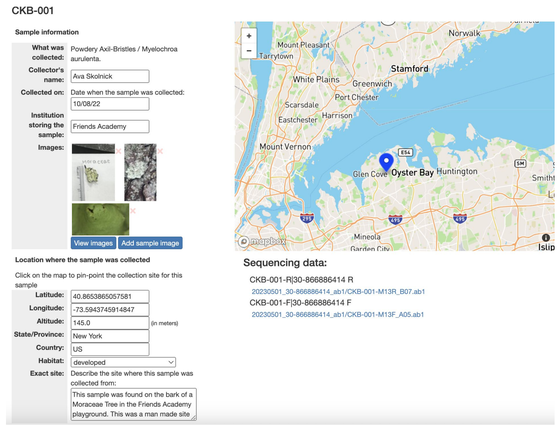
Shu swamp: an untouched nature preserve

Friends academy forest school: a newly cleared out area

Baileys Arboretum: a nature preserve that remains unaffected by humans

Samples were uploaded and metadata stored to Barcode Sample Database





Sequencing data:

CKB-001-R|30-866886414 R

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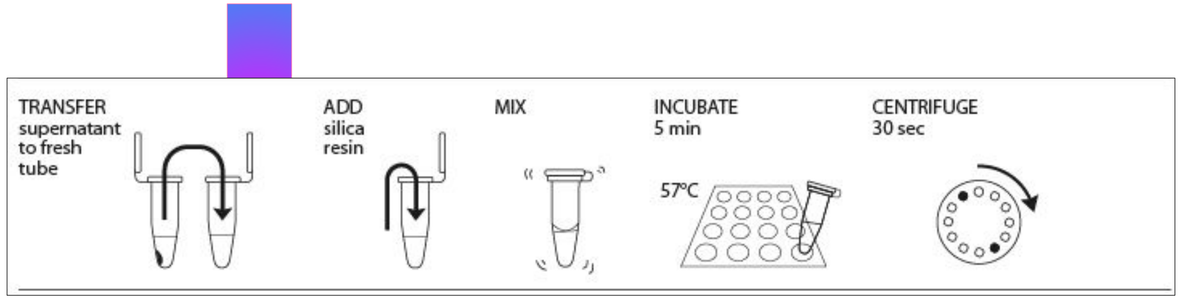
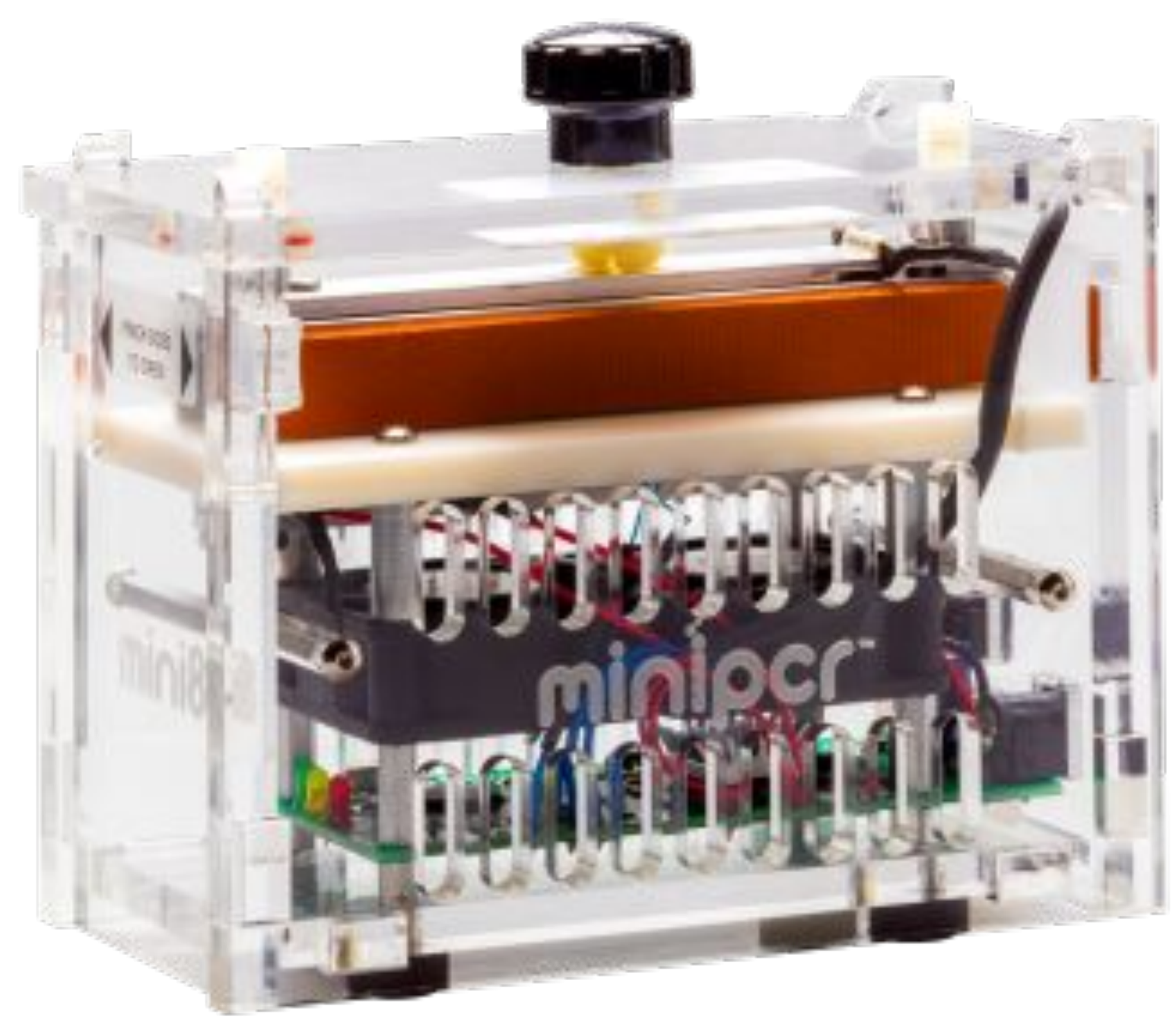
CKB-001-F|30-866886414 F

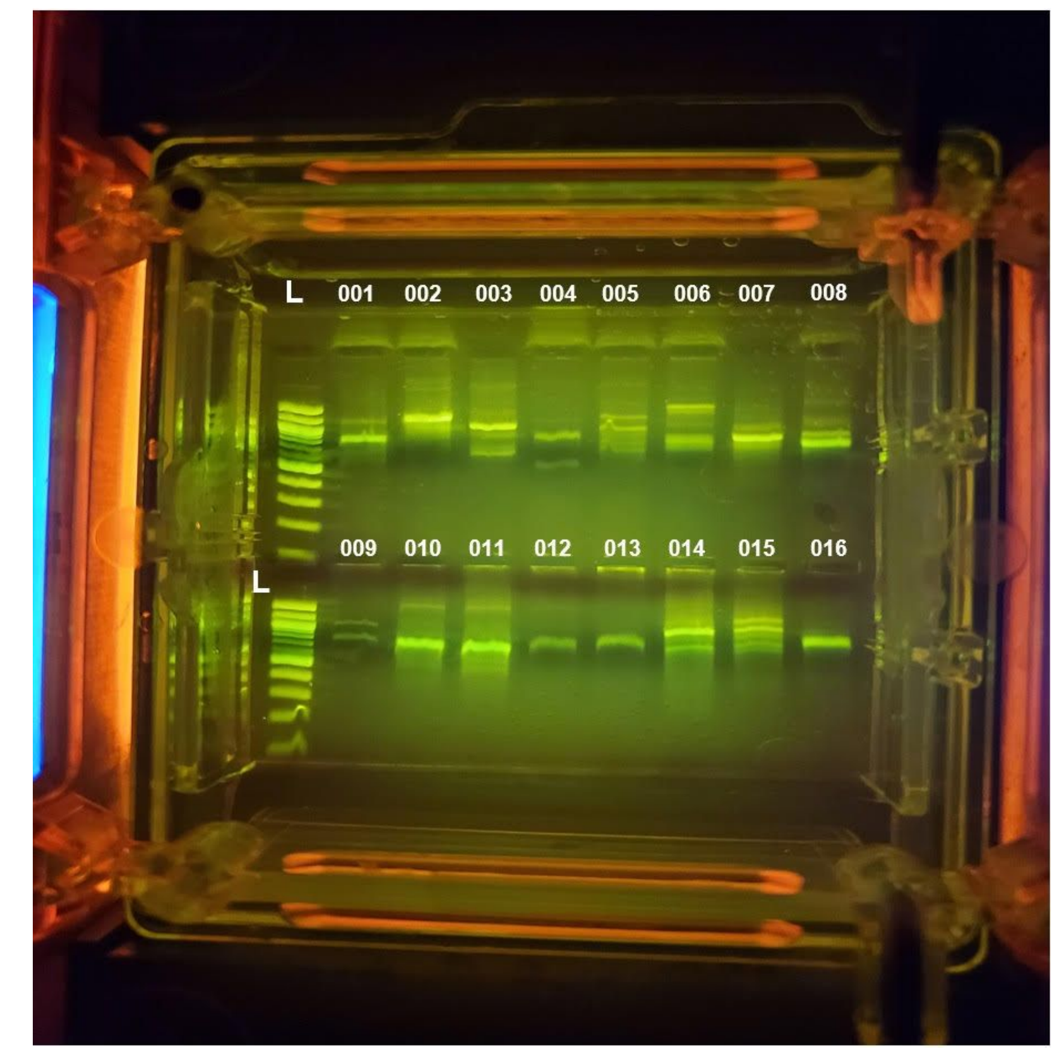
20230501_30-866886414_ab1/CKB-001-M13F_A05.ab1



DNA was extracted using DNA Learning Center's Barcoding 101 silica protocol

DNA was amplified using PCR and verified using Gel Electrophoresis





Valid DNA was sent to be sequined and analyzed using "DNA Subway"