



Polypore Fungi and their Host Trees in Westchester County, NY

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Abstract

Polypores are essential to an ecosystem because of their ability to decompose and recycle nutrients back into the soil. The goal of the study was to evaluate the biodiversity of polypore fungi and their host trees in Westchester County, NY. The use of field guides, as well as iNaturalist, and DNA barcoding assisted us in identifying the fungi species. From the 39 samples that were collected we found 8 different fungal species.

Introduction

Background

- Grow on living/dead trees, fallen trunks, rotten wood, stumps, roots of trees, and soil
- Play a large role in nutrient cycling by forest ecosystems, in particular, the carbon cycle
- Diversity of polypores in an area may indicate high levels of dead trees and low forest health.

Research Goal

- To evaluate the biodiversity of polypore fungi in Westchester County and their relationship with host trees.

Hypothesis

- We hypothesized that with greater polypore biodiversity, forests have a high level of dead trees with a need for more nutrient cycling which can be performed by polypores who work as decomposers.

Materials & Methods

- Collected (December 2023 and January 2024) and identified a total of 39 various polypore samples
- Locations: Saxon Woods Park and the SUNY Purchase campus (White Plains and Purchase, NY)
- **Rapid DNA extraction** was performed as described in the UBP resource materials.
- The isolated DNA samples were **amplified** using the ITS1F and ITS4 primers
- Analyzed the PCR Products by **gel electrophoresis**
- Sent our DNA samples to be **sequenced** by biotechnological company, Genewitz.
- Upon receiving our DNA sequence results we used the **DNA subway** procedure which used **BLAST analysis** to identify our samples.

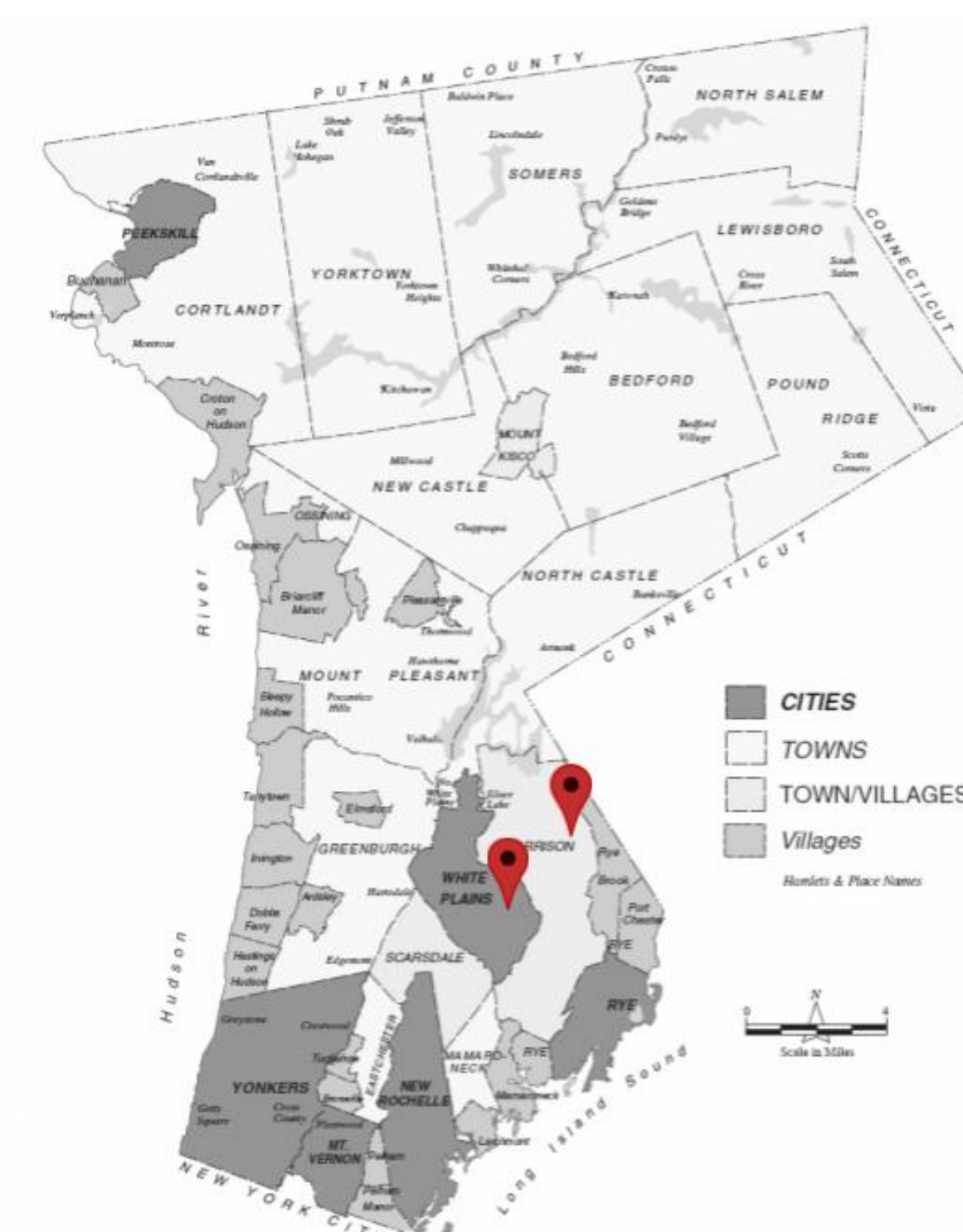


Figure 1: Map of Westchester County with sample areas pinpointed.

Results

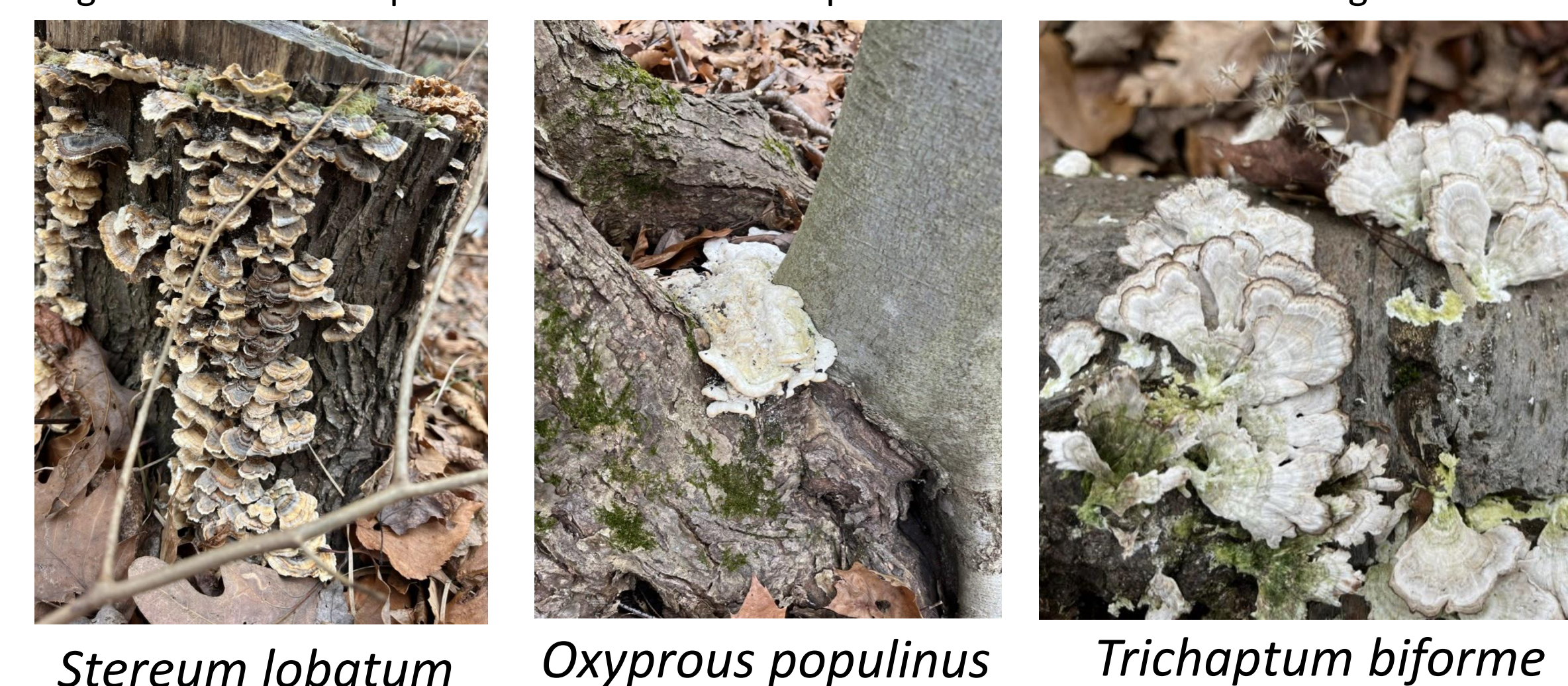
- 11 of the specimens yielded a DNA sequence which could be DNA barcoded
- 6/11 of the samples were barcoded with a high quality (error rate of less than 1%)
- All 39 samples were identified using iNaturalist and field guides
- iNaturalist identified 19 different species, 19 different species with field guides, and 8 different species with DNA barcoding
- Identified 13 different tree species consisting mainly of species of oak and maple.

Tables & Figures

Table 1: List of species of polypores identified by DNA barcoding.

Species 1	<i>Stereum lobatum</i>
Species 2	<i>Stereum complicatum</i>
Species 3	<i>Panellus stipticus</i>
Species 4	<i>Oxyprous populinus</i>
Species 5	<i>Neofavolus alveolaris</i>
Species 6	<i>Irpex lacteus</i>
Species 7	<i>Stereum fasciatum</i>
Species 8	<i>Trichaptum biforme</i>

Figure 2: Select samples and their identified species based on DNA barcoding.



Stereum lobatum

Oxyprous populinus

Trichaptum biforme

Discussion

- We collected 39 specimens of polypore fungi, 32 of them were found on dead trees, 7 of them were found on living trees.
- We found polypores on the following dead trees: Black oak (*Quercus velutina*), Red maple (*Acer rubrum*), and Shagbark hickory (*Carya ovata*). We found polypores on the following living tree: Sweet birch (*Betula lenta*).
- We identified 8 species of polypore fungi in 11 samples by DNA barcoding. In 7 cases identification coincided with iNaturalist and paper field guide identification.

Future Study

- Examine biodiversity in warmer seasons

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