



Who am I

I am a student researcher at Canadore College, where I work with the Genomics Research Hub to investigate environmental microbiomes, agricultural innovation, and biodiversity. My research interests lie in molecular biology, environmental genomics, and the development of sustainable biotechnologies. I am passionate about using DNA-based tools to inform conservation, agriculture, and ecological restoration. Through my work, I strive to bridge academic science and community engagement by promoting accessibility in research and fostering student-driven innovation.

Student role

As a student researcher at Canadore College, I was actively involved in all stages of these projects – from experimental design to data interpretation. My responsibilities included conducting a literature review, support project rationale and guide methodological decisions. I participated in field sampling, plant cultivation, and RNA/DNA extraction, applying standard molecular biology techniques such as Qubit quantification and metagenomic sequencing. I was also involved in experimental planning, troubleshooting experimental challenges, and prepared data visualizations for preliminary analysis. This hands-on experience sharpened my skills in environmental genomics, plant biology, and research communication.

Projects

Ecolution

Research Goal: This study evaluated the effects of the phytochemical-based biostimulant GROWMAS on tomato plant gene expression. The experiment was conducted in a controlled-environment grow pod at Canadore College using soil-based cultivation. In order to assess growth, a larger scale operation would be required for a better quantitative control.

Methods: Tomato plants (*Solanum lycopersicum*) were divided into treated and control groups. Treated plants received a 0.25% foliar spray of GROWMAS twice weekly. Plants were sampled at three timepoints:

- Week 3: Pre-treatment
- Week 10: Mid-treatment
- Week 15: Harvest

Fungal Workshop

Event Summary: In September 2024, Canadore College hosted its Fungal Biodiversity Workshop, combining public science education, outdoor forays, and genomic analysis. The event featured guest speakers on mushroom cultivation, foraging ethics, identification, and fungal ecology.

Approach:

- Expert led outdoor forays to collect, photograph, and document fungi along Canadore campus trails.
- Used iNaturalist to upload field observations and build regional biodiversity datasets.
- In the lab, sequenced DNA from 56 mushroom samples using the ITS barcode region.
- Employed qPCR for amplification and the Illumina MiSeq for sequencing.
- Compared sequences with reference databases to identify and classify the fungi.

Mikro-Tek

Research Goal: This collaborative study aimed to assess how fungal soil amendments influence fungal community diversity in boreal forest soils near Timmins, Ontario. The focus was on comparing microbial profiles between treated and untreated field plots.

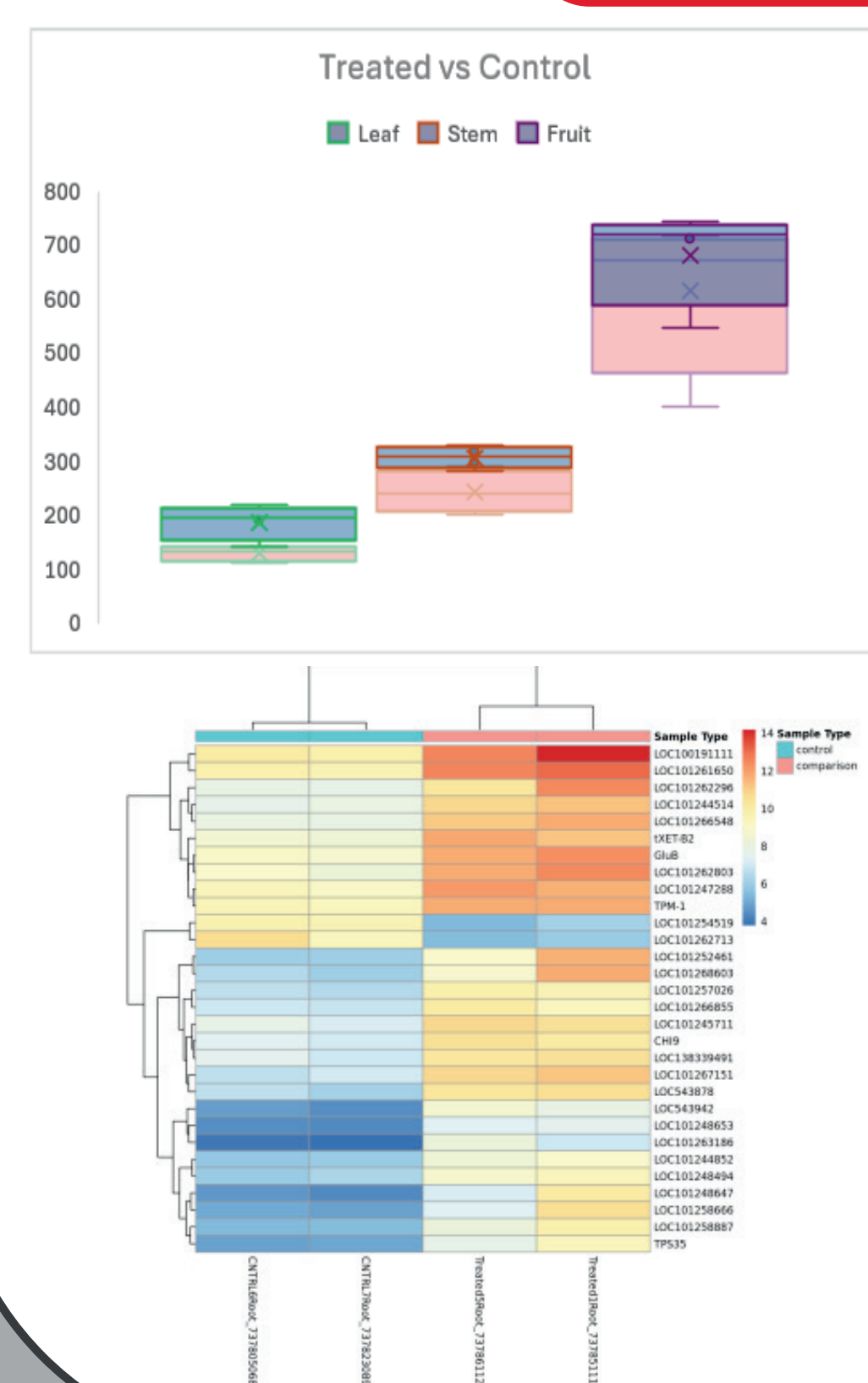
Treated plots had previously received applications of endo- and ectomycorrhizal fungi by Mikro-Tek, a biotechnology company specializing in mycorrhizal inoculants.

Methods:

- Environmental field-based sampling. Core samples extracted at 3 site locations (Site A (*Densely forested*), Site B (*Moderately forested*) and site C (*Sparsely forested*))
- DNA-based identification of microbial and fungal communities using amplicon sequencing and high-throughput pipelines.
- Multi-kingdom metagenomics, analyzing fungal (ITS)

Results

Ecolution

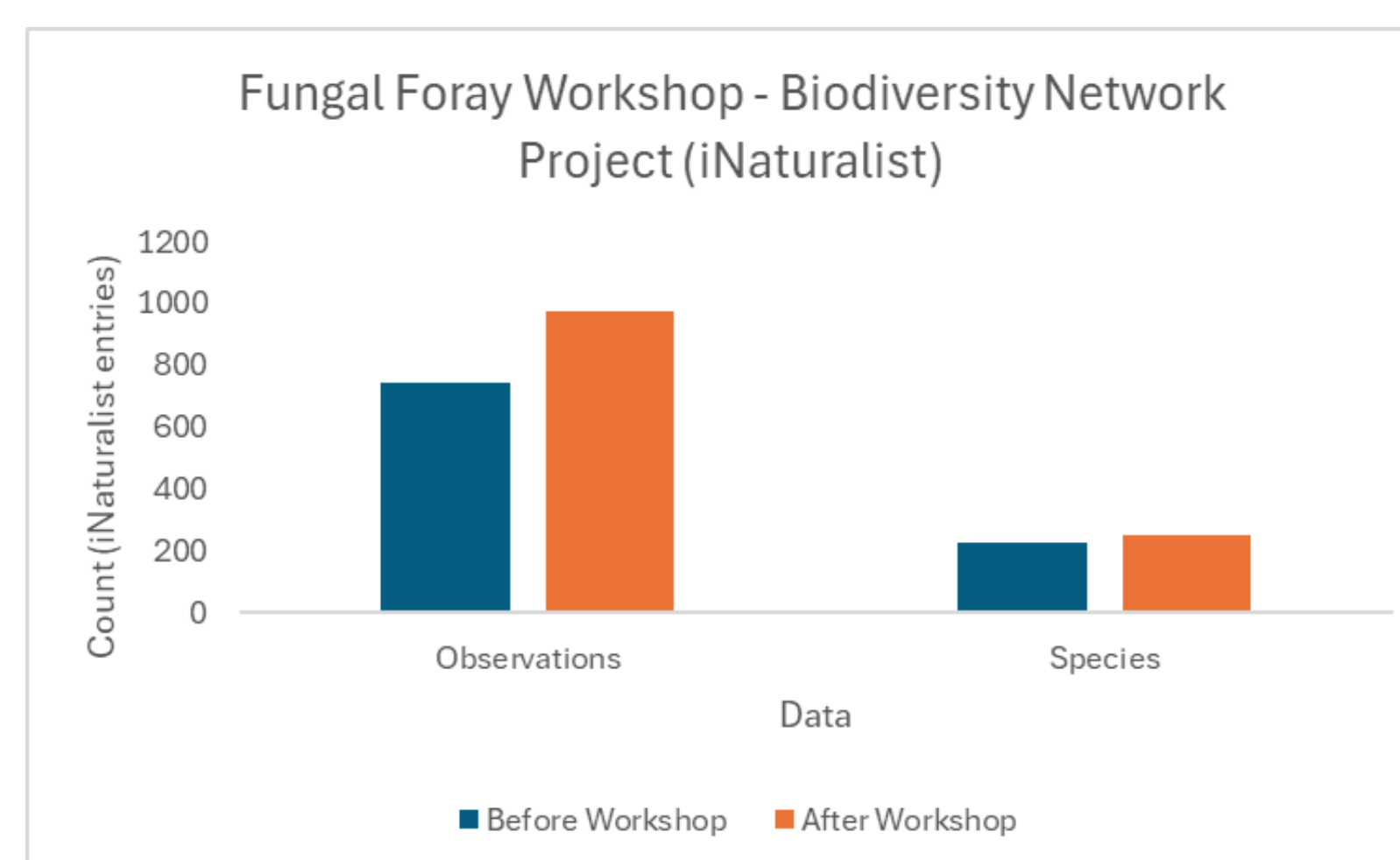


Growth Outcomes

- Leaf Mass: 47.6% ($p = 0.0078$)
- Stem Mass: 27.9% ($p = 0.0113$)
- Fruit Mass: 18% ($p = 0.0716$)

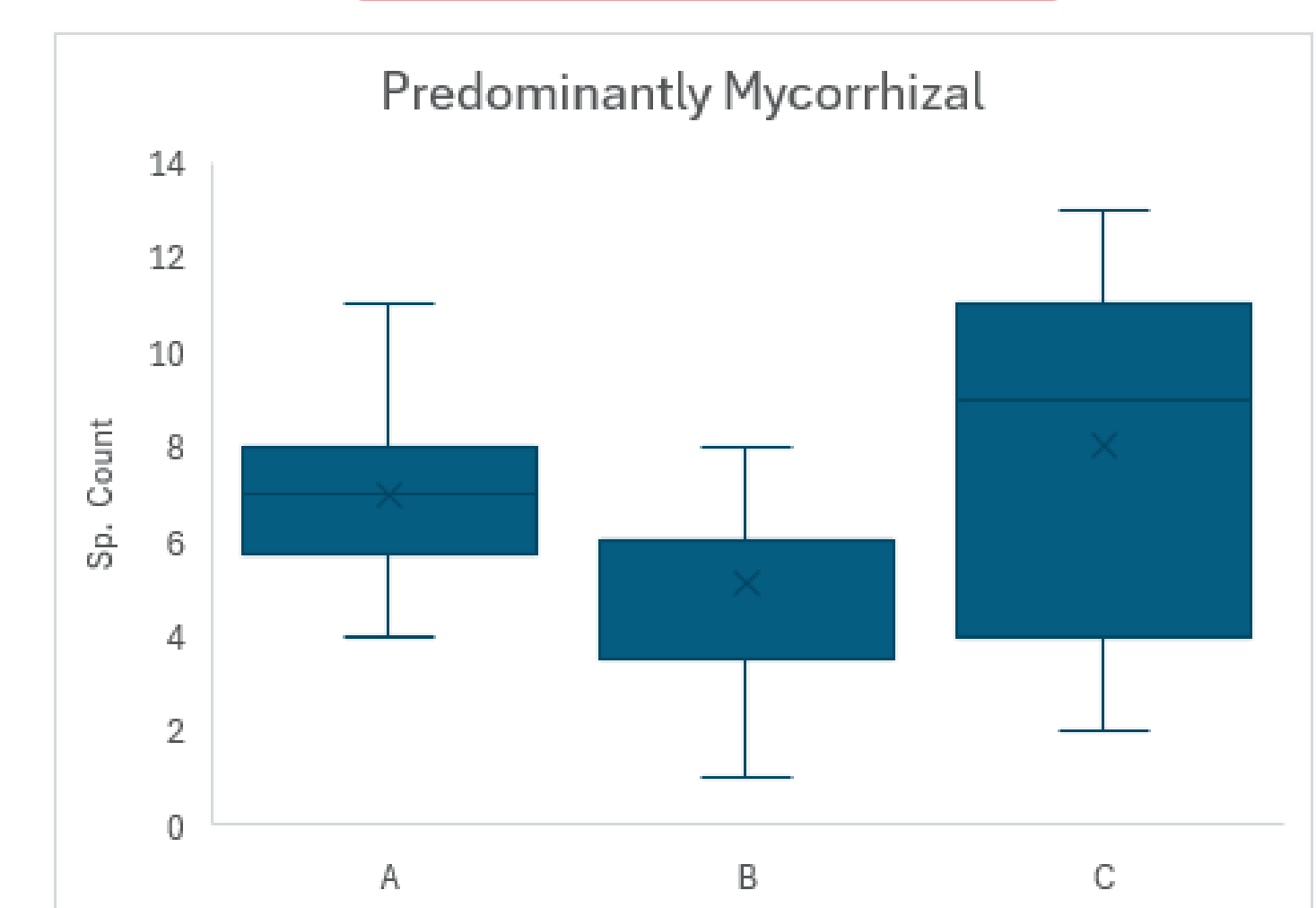
Heatmap displaying differential gene expression across treated and control tomato plants. Red indicates high expression levels, while blue indicates low expression.

Fungal Workshop



- High fungal species observed across multiple habitats, with distinct community compositions in forest, grassland, and wetland ecosystems.
- Potential relationships between fungal taxa and environmental factors (e.g., moisture, temperature).
- Identification of key fungal genera that may play significant roles in ecosystem functioning, such as decomposers and symbionts.

Mikro-Tek



- Notable differences in microbial community composition between treated and untreated areas.
- Higher microbial diversity observed in treated areas, especially in deeper soil layers.
- Specific fungal taxa associated with the mycorrhizal treatment were enriched in the treated soils.

Challenges

Ecolution

- **Complex transcriptomic data:** Interpreting RNA-seq results is complex, particularly when correlating gene expression changes to physiological traits.
- **Replication and scalability:** The experiment was conducted in a controlled environment, which may not reflect field conditions or larger-scale agricultural applications.

Fungal Workshop

- Morphological identification of fungi in the field is prone to error; DNA barcoding was likely needed for precise classification.
- Weather conditions (rainfall, humidity, temperature) during forays may influence fungal presence and abundance.
- Visibility and accessibility of fruiting bodies may skew results toward more conspicuous or surface-level fungi

Mikro-Tek

- **Lack of abiotic data:** No pH or moisture content data were collected, making it difficult to account for environmental factors influencing microbial community structure.
- **Primer bias:** Using different primers for sequencing may have introduced variation in taxonomic resolution and comparability between samples.
- **Temporal limitation:** Single-time-point sampling provides only a snapshot of microbial diversity without capturing seasonal or temporal shifts.

Skills I Gained

Molecular Biology & Lab Skills

- Conducted DNA and RNA extractions from soil and plant tissues using commercial kits (e.g., Qiagen PowerSoil, RNA extraction protocols).
- Prepared samples for high-throughput sequencing (MiSeq) and handled PCR amplification with primer optimization.

Bioinformatics & Data Analysis

- Analyzed metagenomic and transcriptomic sequencing data using platforms such as BaseSpace and DRAGEN pipelines.
- Interpreted microbial community diversity metrics (e.g., Shannon, Simpson indices) and differential gene expression outputs.

Experimental Design & Troubleshooting

- Designed and implemented multi-treatment experimental setups, including biological replicates and time-point sampling.
- Navigated challenges related to variable sequencing primers, limited metadata, and environmental heterogeneity.

Scientific Communication

- Synthesized complex results into clear bullet-point summaries, figures, and reports.
- Discussed limitations, proposed future directions, and translated findings for both academic and applied contexts.

Interdisciplinary Thinking

- Integrated knowledge from ecology, genomics, agriculture, and mycology to approach research questions from multiple angles.
- Linked microbial and fungal dynamics to plant health, ecosystem processes, and biostimulant performance.

Recommendations for Future Students

- Standardize sampling protocols early
- Create a clear, consistent protocol for sample collection and processing before starting fieldwork. Small inconsistencies can impact downstream analyses.
- Detailed lab notebook
- Document every step, even small troubleshooting decisions – it'll save you (and others) time later and make writing your methods section much easier.
- Start bioinformatics prep early
- Familiarize yourself with your data analysis platform (e.g., BaseSpace) early in the project. Don't wait until after sequencing to learn the tools.
- Ask questions & collaborate
- Don't be afraid to reach out to your supervisor, lab techs, or other students. Collaboration often leads to new insights and better solutions to unexpected problems.
- Be flexible in the field
- Conditions may not go as planned (e.g., rain, inaccessible sites, equipment issues). Adaptability and a backup plan are essential.
- Think beyond the project
- Try to understand how your work fits into broader scientific or applied goals (e.g., sustainable agriculture, conservation, climate resilience). It helps keep the work meaningful and can shape future research or career interests.

Acknowledgements

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