

DNA Barcode Identification of Macrofungi by Community Scientists

E. Cantonwine¹, T. Osmundson², S. Russell³ & B. Sheehan⁴



¹Valdosta State University, Valdosta, GA; ²University of Wisconsin-La Crosse, La Crosse, WI; ³The Hoosier Mushroom Society, IN; ⁴Fungal Diversity Survey, Athens, GA

INTRODUCTION

Nearly two thousand sequences from thirty-five projects associated with the Fungal Diversity Survey, formerly known as the North American Mycoflora Project Inc., were assessed to estimate scientific outcomes of the program.

METHODS

Seventeen projects included a professional or amateur with high-level of expertise and were classified as advanced. The remaining (18) were classified as standard projects.

- ITS sequences were generated using Sanger Sequencing
- Sequences were BLASTED to GenBank.
 - The numbers of reference matches at species-level (97% identity, >1000 Bit-score) were counted.
 - Sequences were classified as very common (>10 matches), common (4-10 matches), uncommon (1-3 matches) or novel based in number of species-level matches.
 - T-tests compared advanced and standard projects.
 - Barcode identifications were assessed to species, genus, or higher based on taxa of matched references.
 - Novel sequences were reassessed for eDNA matches.
- Taxa of novel and uncommon sequences were compared to curated collections of Mycoportal to estimate new State reports.

RESULTS

For sequences with at least one match, most were barcoded to species- or genus-levels (Figure 1).

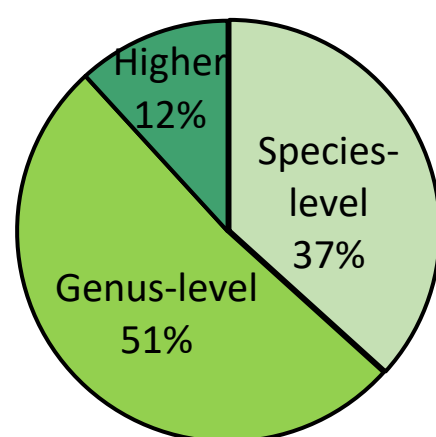


Figure 1. Taxonomic clarity of Barcode Identifications.

RESULTS CONTINUED

Advanced projects generated more novel sequences than standard projects (Figure 2).

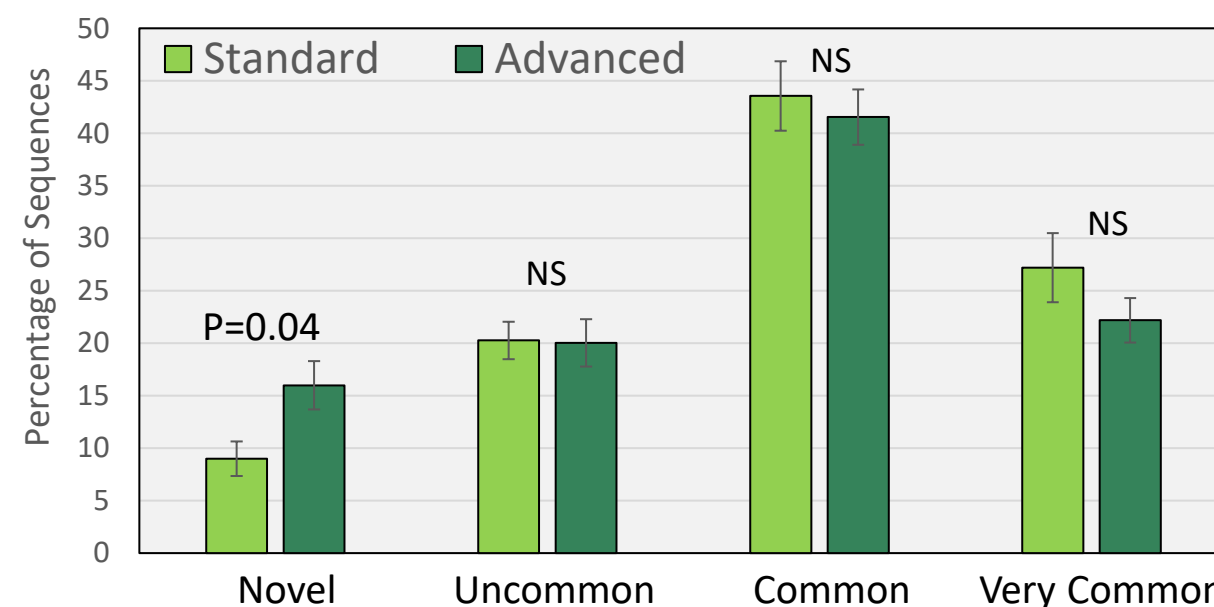


Figure 2. Sequences by category and expertise.

Thirty-one sequences matched to eDNA (Table 1). Of the collections screened on Mycoportal, 15% were first State records (Figure 3).

Table 1. Numbers of FunDiS sequences and eDNA matches by Family.

FAMILY	#	eDNA #
Amanitaceae	1	8
Boletaceae	4	4
Cantherellaceae	1	3
Cortinariaceae	1	12
Entolomataceae	2	32
Gomphaceae	2	2
Hygrophoraceae	2	3
Inocybaceae	5	105
Mycenaceae	2	93
Nidulariaceae	1	2
Russulaceae	6	77
Tricholmataceae	2	83
Unclassified	3	59

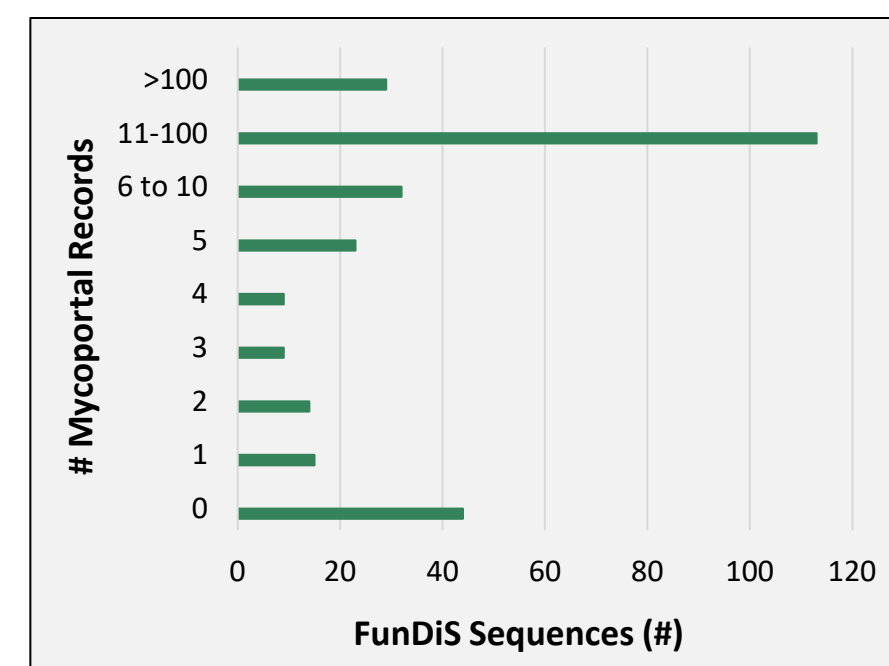


Figure 3. Curacted collections of novel and uncommon sequenced taxa within the collection State.

CONCLUSIONS

Barcoding to species occurred for 1/3 of the collections sequenced by community scientists. Scientific outcomes include populating reference databases, and when accompanied by high quality vouchers, extending species ranges. Expert involvement can improve scientific outcomes, but may not be necessary.

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