GENETIC DIVERSITY WITHIN ALASKAN MORELS

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ABSTRACT

We isolated DNA from 12 “true morels” (Morchella) and one “false morel” (Gyromitra) collected in interior Alaska. We PCR amplified the internally transcribed spacer region of the mitochondrial DNA genes. After allele sequencing our amplified genes, we used the sequenced program to maximize the raw sequences. Cluster analysis of the aligned sequences across samples, and the GEMIT program to create a phylogenetic tree of evolutionary history, led us to identify 5 groups of similar evolutionary history. The number of branches in the tree is the product of 100 “bootstrap” replicates and represent the number of replicates that agree on the placement of that branch. Only fully supported branches are labeled.

INTRODUCTION

DESCRIPTION AND DIVERSITY

Morels are cup-shaped Ascomycete mushrooms often found growing prolifically in burned soil in the summer after a wildfire, and occasionally in other disturbed habitats. All members are edible and can be easily identified as a genus. However, morels exhibit a wide variety of forms and colors, and individual species are difficult to identify. Various species can be split into “Yellow” and “Black” groups, with all of our samples from Alaska falling into this “Yellow” group (Pisces et al., although we provided evidence that an entire species group aligns to the “Black” group).

BIOLGY

Morels are the sporocarps (fruiting bodies) of underground mycelia, the microscopic fungal threads that spread from the soil and collect water and nutrients. It is poorly understood whether morels are symbionts (organisms that live in a mutually beneficial relationship with other organisms), saprophytes (organisms that decompose decaying matter), or parasites (organisms that feed directly off of living organisms). It is known that across the various species of morels morel fungi are adapted as a result of fire and other disturbances. Others imply that the morels remain underground for long periods and then suddenly appear after a fire period that has burned the forest where the fungi were previously living (Koake and Keane 2012).

METHODS

The flush of organic matter from the roots of dead plants may provide the resources necessary for sporocarp production. However, it has also been suggested that the mycelia produce sporocarps for outgroup. We found that the “fuzzy foot” group has a low degree of certainty. It is distinct as a group, but it places in the tree is not certain (see Discussion).

RESULTS

Figure 1 Maximum Likelihood phylogeny. Our Alaskan samples are highlighted in yellow. Each branch in the tree represents a divergence in evolutionary history. Left to right signifies time, and longer branches signify rapid evolutionary change. The numbers at the branches are the product of 100 “bootstrap” replicates and represent the number of replicates that agree on the placement of that branch. Only fully supported branches are labeled.

Picture 1: Maximum Likelihood phylogeny. Our Alaskan samples are highlighted in yellow. Each branch in the tree represents a divergence in evolutionary history. Left to right signifies time, and longer branches signify rapid evolutionary change. The numbers at the branches are the product of 100 “bootstrap” replicates and represent the number of replicates that agree on the placement of that branch. Only fully supported branches are labeled.

DISCUSSION

WHERE ARE THE ESCUCENT AND OTHER YELLOW MORELS?

The diversity of morels in our study is rare that ours. If it is, there is a 90% chance that it may be a genetic construct. We do not have any members of the species “Yellow” group. However, our tree shows there is no genetic distinction, and we did not have any members of the species “Black” group. We did not have any members of the species “Gray” group. Interestingly, none of our samples are...