



ARMILLARIA PHYLOGENY BASED ON *tef-1α* SEQUENCES SUGGESTS ONGOING DIVERGENT SPECIATION WITHIN THE BOREAL FLORISTIC KINGDOM

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INTRODUCTION

Armillaria plays diverse ecological roles in forests worldwide, which has inspired interest in understanding phylogenetic relationships within and among species of this genus. Previous rDNA sequence-based phylogenetic analyses of *Armillaria* have shown general relationships among widely divergent taxa, but rDNA sequences were not reliable for separating closely related North American species, such as *A. gallica*, *A. calvescens*, *A. cepistipes*, and *A. sinapina*, or other closely related Eurasian species (Kim et al. 2006). Recent studies have shown that *translation elongation factor 1-α* (*tef-1α*) sequences appear quite useful for phylogenetic analysis of *Armillaria* spp. from diverse global regions (Maphosa et al. 2006; Antonin et al. 2009; Hasegawa et al. 2010; Ota et al. 2011; Brazee et al. 2011; Mulholland et al. 2012; Ross-Davis et al. 2012; Tsykun et al. 2012). The objective of this study is to determine phylogenetic relationships among northern hemisphere *Armillaria* spp. based on available *tef-1α* sequences from well-characterized isolates.

MATERIALS AND METHODS

The *tef-1α* sequences used in this study were reported by Maphosa et al. (2006), Antonin et al. (2009), Hasegawa et al. (2010), Ota et al. (2011), Brazee et al. (2011), Mulholland et al. (2012), Ross-Davis et al. (2012), and Tsykun et al. (2012). In addition, *tef-1α*

sequences from GenBank and from *Armillaria* isolates from Mexico and Eurasia were included in the phylogenetic analyses. The *tef-1α* sequences of *Pleurotus pulmonarius* (D480: EU204111) and *Tricholoma myomyces* (KMS589: DQ367429) were obtained from GenBank to serve as outgroups. A phylogenetic network analysis was implemented using SplitsTree (Huson and Bryant 2006) (Figure 1). Additional phylogenetic analyses are being conducted using maximum likelihood and Bayesian methods (data not shown).

RESULTS AND DISCUSSION

According to the preliminary *tef-1α*-based phylogeny from this study (Figure 1), *Armillaria* spp. from the Boreal Floristic Kingdom are distributed among several major clades, including 1) *A. solidipes/ostoyae* clade (North American *A. solidipes/ostoyae*, *A. gemina*, and *A. sinapina*; and Eurasian *A. borealis* groups, *A. solidipes/ostoyae*, *A. cepistipes*, and *A. sinapina*); 2) *A. gallica* clade (North American *A. gallica* groups, *A. calvescens*, *A. cepistipes*, *A. nabsnana*, and *A. altimontana*; Japanese *A. nabsnana* and Nag E; Asian *A. gallica*; and European *A. gallica*); 3) *A. mellea* clade (North American *A. mellea* groups; European *A. mellea*; and Japanese *A. mellea*); and 4) exannulate *Armillaria* clade (Eurasian *A. ectypa* and *A. socialis/tabescens* groups; and North American *A. tabescens*). A separate, fifth, clade comprises an undescribed *Armillaria* species from Mexico, but further work is needed to characterize members of this clade.

These results provide preliminary evidence that 1) currently recognized *A. mellea* likely comprises multiple species; 2) currently recognized *A. gallica* likely comprises multiple species; 3) currently recognized *A. borealis* apparently comprises at least two distinct species; 4) Eurasian *A. cepistipes* and North American *A. cepistipes* reside in distinct major clades and likely represent very distinct species; 5) North

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American *A. solidipes/ostoyae* is genetically distinct from Eurasian *A. solidipes/ostoyae*; 6) North American *A. socialis/tabescens* appears phylogenetically distinct from Eurasian *A. socialis/tabescens*; 7) a well-separated clade comprises *Armillaria* isolates from Mexico that

represent an undescribed species (Elias-Roman et al. this proceedings); and 8) the genus *Armillaria* likely comprises multiple other cryptic species. Continued phylogenetic studies are needed to confirm genetic relationships within the *Armillaria* genus.

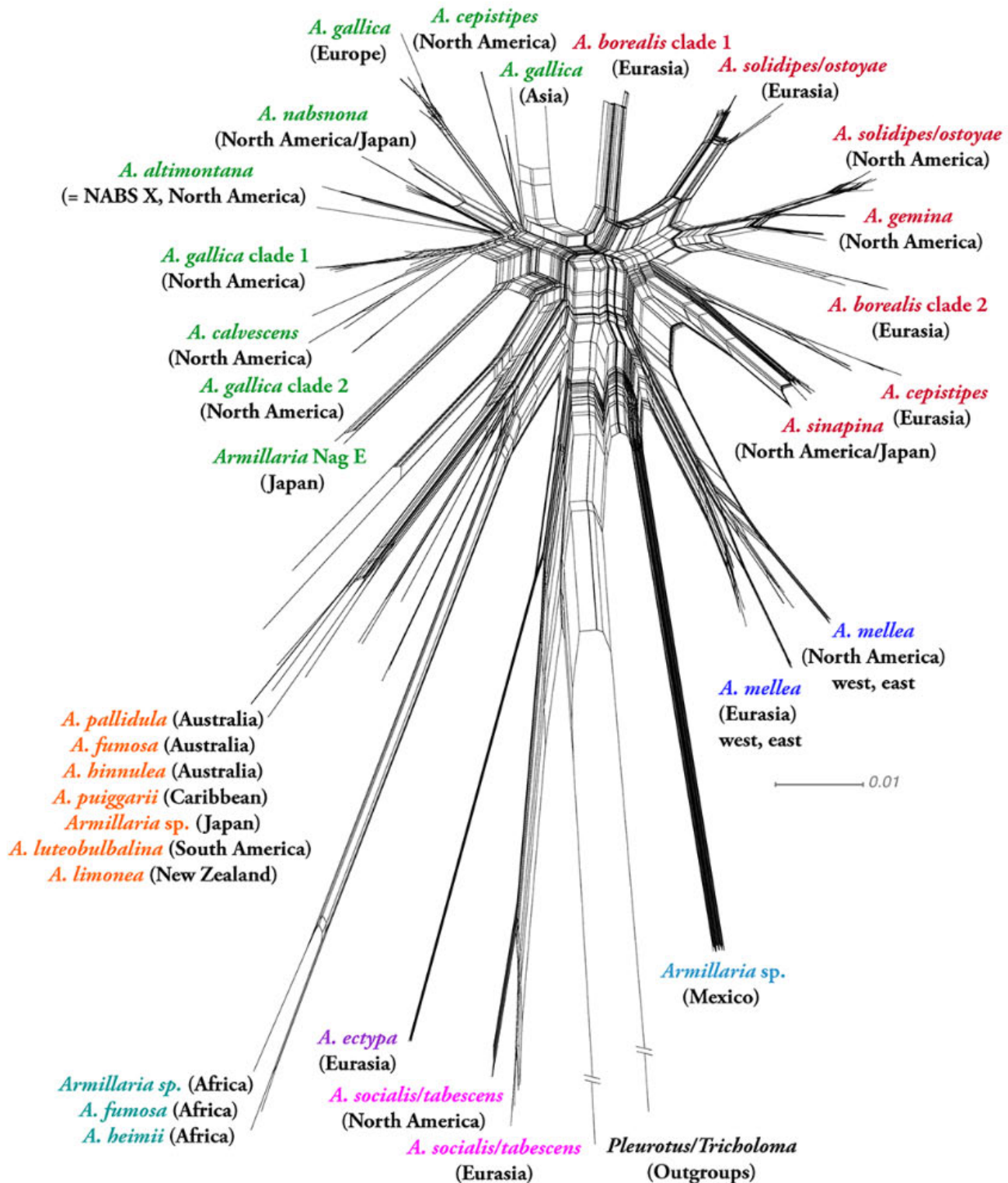


Figure 1. SplitsTree phylogenetic network of global *Armillaria* spp., based on translation elongation factor 1- α .

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