



Three new species in *Russula* subsection *Xerampelinae* supported by genealogical and phenotypic coherence

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ABSTRACT

Xerampelinae is a subsection composed of species of ectomycorrhizal fungi belonging to the hyperdiverse and cosmopolitan genus *Russula* (Russulales). Species of *Xerampelinae* are recognized by their fishy or shrimp odor, browning context, and a green reaction to iron sulfate. However, species delimitation has traditionally relied on morphology and analysis of limited molecular data. Prior taxonomic work in *Xerampelinae* has led to the description of as many as 59 taxa in Europe and 19 in North America. Here we provide the first multilocus phylogeny of European and North American members based on two nrDNA loci and two protein-coding genes. The resulting phylogeny supports the recognition of 17 species-rank *Xerampelinae* clades; however, higher species richness (~23) is suggested by a more inclusive nuclear rDNA internal transcribed spacer region ITS1-5.8S-ITS2 (ITS barcode) analysis. Phylogenetic and morphological analyses support three new species with restricted geographic distributions: *R. lapponica*, *R. neopascua*, and *R. olympiana*. We confirm that the European species *R. subrubens* is present in North America and the North American species *R. serissima* (previously known as *R. favrei*) is present in Europe. Most other *Xerampelinae* appear restricted to either North America or Eurasia, which indicates a high degree of regional endemism; this includes *R. xerampelina*, a name widely applied to North American taxa, but a species restricted to Eurasia.

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INTRODUCTION

The genus *Russula* Pers. (Russulales, Russulaceae) is among the most species-rich fungal genera, with an estimated global diversity above 2000 species (Adamčík et al. 2019). Species of *Russula* are specialized ectomycorrhizal (ECM) symbionts typically associated with trees (Looney et al. 2022b) but can also associate with shrubs, sedges, and herbs (Noffsinger and Cripps 2021). The genus is almost cosmopolitan and distributed from the tropics to arctic regions, with peak diversity in temperate and boreal areas (Looney et al. 2016; Taylor and Alexander 1989). *Russula* is one of the most diverse and abundant genera in ectotrophic ecosystems, especially in tropical areas of the Americas,

Africa, and Southeast Asia (Corrales et al. 2022). Despite significant efforts to build a global and complete *Russula* phylogeny (Buyck et al. 2018; Looney et al. 2016), a majority of subsections within *Russula* are under-sampled in multilocus phylogenies (Adamčík et al. 2019). Building of phylogenies at lower ranks with data across distant geographic areas is relatively rare in *Russula* but has been done for subsections *Roseinae* Singer ex Sarnari (Looney et al. 2022a; Manz et al. 2021) and *Amoeninae* Singer ex Buyck (Wisitrassameewong et al. 2020, 2022). *Russula* studies often rely on sequences of nuclear rDNA from the internal transcribed spacer region ITS1-5.8S-ITS2 (ITS barcode) or D1-D2 domains of 28S (28S) in support of