

## Latitude ranges and rates of diversification in a clade of symbiotic mushrooms

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Ectomycorrhizal (EM) fungi are essential components of temperate, boreal and tropical ecosystems. However, little is known on what are the processes and patterns affecting their extant diversity and distribution. Well-sampled species-level phylogenies allows us to test hypothesis about processes causing diversity. Recently, it has been proposed that EM fungi are more diverse in the temperate regions than in the tropics, an exception to what is found for other organisms such as plants and animals. Here we take a Bayesian approach to test this and other hypothesis related to global latitudinal gradients in a group of edible EM mushrooms (*Amanita* section *Caesareae*). Three nuclear genes (LSU, RPB2, TEF1) were sequenced for near 120 samples were sequenced, representing 60% of the species described for the section. Divergence times were estimated using a relaxed clock model and external fossil calibration points. We used 100 evenly sampled posterior trees from the 95% highest posterior density to estimate diversification rates. A continuous ancestral state reconstruction method was used to estimate ancestral latitudes and then segregating branching times based on a latitude threshold. Eight different diversification models including rate-constant and rate variable models were estimated and fitted using maximum likelihood methods and AIC. Our results support the "older area" and "cradle" hypotheses as most temperate lineages are comparatively recent and arose from tropical ancestors. Estimated rates of diversification (speciation, extinction, net diversification) are shown to be significantly higher in temperate regions as compared to the tropics, suggesting a higher species turnover. Finally, the protracted speciation model suggests that differences in speciation completion times in both regions might be responsible for current EM species richness observations.

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