

Incorporating eco-evolutionary interactions into a spatially explicit phylogenetic Janzen-Connell model predicts realistic macroecological and macroevolutionary patterns

Liang Xu¹, Hanno Hildenbrandt¹, and Rampal Etienne^{2,2}

¹Groningen Institute for Evolutionary Life Sciences

²University of Groningen

May 5, 2020

Abstract

The Janzen-Connell (J-C) hypothesis states that species-specific natural enemies (pathogens, predators) induce local-density dependence which explains high diversity observed in tropical tree communities. However, these natural enemies often attack phylogenetically related species as well. Here, we use a spatially explicit model in which the continuously changing phylogeny and abundances affect recruitment to study the predictions for common diversity and phylogenetic patterns. The species-area relationship is triphasic, while the species-abundance distribution has a rare species mode (neutral scenario), a two modes (large dispersal distance) or a single interior mode (small dispersal distance). Small dispersal distance forms clusters of species with large phylogenetic distance to the community while large dispersal distance makes species distribute uniformly. Phylogenetic trees show diversification slowdowns and imbalance, consistent with empirical patterns. However, the phylogenetic relatedness effect reduces diversity. We conclude that the spatially explicit phylogenetic J-C effect explains commonly observed diversity and phylogenetic patterns.

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