The spatially explicit phylogenetic Janzen-Connell effect predicts realistic macroecological and macroevolutionary patterns

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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 to study the predictions of a phylogenetic J-C effect for common diversity 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 patterns, but hyperdiversity only results when the natural enemies are extremely species-specific.

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