Metapopulation dynamics and metacommunity assembly in the freshwater snails of Guadeloupe

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Abstract

Metapopulation models are often used to understand whether a single species can persist in a landscape with multiple patches of potentially connected habitat. However, these models do not take into account the coexistence of multiple species inhabiting the same landscape. It is currently unclear whether the assembly of metacommunities can be understood by modeling the metapopulation dynamics of multiple species independently of one another or whether a community context, where species influence one another's extinction and colonization, is needed.

We analyzed metapopulation dynamics for 27 species of freshwater snails inhabiting 278 sites on the island of Guadeloupe, sampled annually from 2001 to 2015. For each species, we used occurrence data to estimate colonization and extinction rates as well as the effects of environmental covariates, such as habitat connectivity and rainfall, using a multistate occupancy model. The Bayesian model, implemented in JAGS, estimates the probability of transitioning between occupied and unoccupied states and considers the influence of imperfect species detection and persistence of aestivating snails in dry sites.

For most species in the system, extinction rates exceeded colonization rates, but these were influenced by environmental covariates in differing ways for each species. However, the models do not take into account species interactions, and do not consider that the extinction and colonization rates of some species may differ after the extinction of other species. An important next step for metapopulation models is to determine the influence not only of environmental heterogeneity among sites, but also biodiversity in the system.

Keywords: metapopulation, metacommunity, landscape ecology

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