

Disease hotspots or hot species? Infection dynamics in multi-host metacommunities controlled by species composition, not source location

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May 5, 2020

Abstract

Pathogen persistence in host communities is influenced by a hierarchy of heterogeneities from individual host to landscape-level attributes, but isolating the relative contributions of these heterogeneities is challenging. We developed theory to partition the influence of host species, habitat patches, and landscape connectivity on pathogen persistence within host-pathogen metacommunities. We used the framework to quantify the contributions of host species composition and habitat patch identity on the persistence of an amphibian pathogen across the landscape. By sampling over 11,000 hosts of six amphibian species, we found that a single host species could maintain the pathogen in 91% of the metacommunities we observed. Moreover, this dominant maintenance species contributed, on average, twice as much to landscape-level pathogen persistence compared to the most influential source patch in a metacommunity. Our analysis demonstrates substantial inequality in how species and patches contribute to pathogen persistence, with important implications for targeted disease management.

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