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ORIGINAL ARTICLE

Genetic population structure and distribution of a fungal polypore, *Datronia caperata* (Polyporaceae), in mangrove forests of Central America

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ABSTRACT

Aim We examine the genetic structure of a fungal polypore, *Datronia caperata* (Berk.) Ryvarden (Polyporaceae), colonizing white mangrove, *Laguncularia racemosa* (L.) Gaertn. f. (Combretaceae), of Central America.

Location Mangrove forests of Costa Rica and Panama.

Methods Sequences of elongation factor alpha (EFA), beta tubulin (BTUB) and nuclear ribosomal internal transcribed spacer (ITS) regions were obtained from 54 collections of *D. caperata* collected from Caribbean and Pacific *L. racemosa* forests in Central America. Measures of haplotype and nucleotide diversity, nested clade analyses and coalescent analyses were used to estimate the direction and extent of migration of the fungus, and the factors promoting population divergence. We also conducted phylogenetic analyses using Bayesian estimation to test whether putative *D. caperata* collected from *L. racemosa* was conspecific with *D. caperata* colonizing other hosts from diverse Neotropical forests.

Results Our results demonstrate that there is genetic isolation between *D. caperata* populations from Caribbean mangroves and those from Pacific mangroves. Our data suggest that the best explanation for the observed haplotype distribution is a recent range expansion from the Caribbean to the Pacific coasts, with subsequent isolation. This is supported by the infrequent overlap of haplotypes, unidirectional migration estimates from the Caribbean to the Pacific and the older estimated age of mutations in the Caribbean low-copy BTUB and EFA loci. In addition, our data suggest that *D. caperata* from mangroves are not conspecific with collections from other hosts found in diverse Neotropical forests.

Main conclusions The low frequency of shared haplotypes between coasts, coupled with the incomplete lineage sorting after cessation of gene flow, is consistent with isolation during the last Pleistocene glaciation. We hypothesize that the greater haplotype and nucleotide diversity in the Pacific occurs either because larger effective population sizes of *D. caperata* are maintained in Pacific mangroves or because *D. caperata* populations underwent a significant bottleneck as a result of local extinction followed by recolonization. In addition, we found that *D. caperata* found on *L. racemosa* was not conspecific with *D. caperata* from non-mangrove hosts and suggest that *D. caperata* found on *L. racemosa* may be a host specialist.

Keywords
Coalescent methods, Costa Rica, nuclear DNA, Panama, phylogeography, polypore fungus, white mangrove.

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