

Pleistocene persistence and expansion in tarantulas on the Colorado Plateau and the effects of missing data on phylogeographical inferences from RADseq

Matthew Graham¹, Carlos Santibáñez-López¹, Shahan Derkarabetian², and Brent Hendrixson³

¹Eastern Connecticut State University

²Harvard University

³Millsaps College

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Abstract

Few phylogeographical studies exist for taxa inhabiting the Colorado Plateau province. We combined mitochondrial and genomic data with species distribution modeling to test Pleistocene hypotheses for *Aphonopelma marxi*, a large tarantula endemic to the plateau region. Mitochondrial and genomic analyses revealed that the species comprises at least three main clades that diverged in the Pleistocene. A clade distributed along the Mogollon Rim appears to have persisted in place during the last glacial maximum, whereas the other two clades probably colonized the central and northeastern portion of the species' range from small refugial areas along river-carved canyons. Climate models support this hypothesis for the Mogollon Rim, but late glacial climate data appear too coarse to detect suitable areas in canyons. Locations of canyon refugia could not be inferred from genomic analyses due to missing data, encouraging us to explore the effect of missing loci in phylogeographical inferences using RADseq. In phylogenetic analyses, node support for major clades decreased with the addition of samples with significant amounts of missing data (more than 30%). Population genomic structure was greatly influenced by missing data, with the group membership of many taxa changing as samples with missing loci were added. Results from DAPC, a distance-based method, did not change as samples with significant amounts missing data were added. We conclude that the specific loci that are missing matters more than the number of missing loci, and that samples with missing data can still add information to RADseq-based analyses as long as results are interpreted cautiously.

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