

Phylogeography and population genetics of a widespread cold-adapted ant, *Prenolepis imparis*

Maria Tonione¹, Ke Bi², Rob Dunn³, Andrea Lucky⁴, and Neil Tsutsui⁵

¹UC Berkeley

²University of California Berkeley

³North Carolina State University

⁴University of Florida

⁵University of California, Berkeley

November 29, 2021

Abstract

Historical climate fluctuations have left genetic signatures on species and populations across North America. Here, we used phylogenetic and population genetic analyses from 1,402 orthologous sequences of 75 individuals obtained through sequencing of Ultraconserved Elements (UCEs) to identify population genetic structure and historical demographic patterns across the range of a widespread, cold-adapted ant, the winter ant, *Prenolepis imparis*. We relate the genomic patterns to those expected as a result of *in situ* diversification, maintained connectivity, or recent migration. We recovered five well-supported, genetically isolated clades across the distribution: 1) a basal lineage located in Florida, 2) populations across the southern United States, 3) populations that span the midwestern and northeastern United States, 4) populations from the western United States, and 5) populations in southwestern Arizona and Mexico. Using Bayesian clustering analysis in STRUCTURE and k-means clustering in ADEGENET, we investigated gene flow between these major genetic clades and did not find evidence of gene flow between clades. We did find evidence of localized structure with migration in the western United States clade. High support for five major geographic lineages and lack of evidence of contemporary gene flow indicate *in situ* diversification across the species' range, probably influenced by glacial cycles of the late Quaternary.

Hosted file

2021_1108_Prenolepis_Phylogeography.docx available at <https://authorea.com/users/448500/articles/547300-phylogeography-and-population-genetics-of-a-widespread-cold-adapted-ant-prenolepis-imparis>