

Islands within islands: Diversification of tailless whip spiders (Amblypygi, Phrynus) in Caribbean caves ^[1]

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El guabá es un organismo nocturno, familia de las arañas y los escorpiones. (Suministrada) [Molecular Phylogenetics and Evolution](#) [4] (Impact Factor: 3.92). 07/2015; 93.
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ABSTRACT

Islands have played a key role in understanding species formation ever since Darwin's work on the Galapagos and Wallace's work in the Malay Archipelago. Like oceanic islands, habitat 'islands', such as mountaintops and caves similarly may drive diversification. Here we examine patterns of diversification in the tailless whip spider genus *Phrynosoma* Lamarck, 1809 (Amblypygida: Phrynidae) a system that shows evidence of diversification under the influence of 'islands within islands'. We estimate phylogeographic history and measure genetic diversity among representatives of three nominal *Phrynosoma* species from epigeal and cave systems of Puerto Rico and nearby islands. Data from five loci (mitochondrial 12S, 16S, Cox1; nuclear H3, 28S) were used to generate phylogenetic hypotheses and to assess species monophyly and phylogeographic relationships. Genetic divergences and population limits were estimated and assessed using the Geneious barcoding plugin and the genealogical sorting index. We find that mtDNA sequence divergences within each of the three *Phrynosoma* species range between 15% and 20%. Genetic divergence is structured at three spatial scales: among islands in a manner consistent with the GAARlandia hypothesis, among bedrock formations within Puerto Rico, and among caves within these formations. Every isolated cave system contains a unique mtDNA genetic lineage of *Phrynosoma*, with divergence among cave systems far exceeding that within. In some localities epigeal specimens nest among cave taxa, in others caves are monophyletic. Remarkably, clades that show up to 20% mtDNA sequence divergence show little or no variation in the nuclear markers. We interpret this pattern as resulting from extreme conservation of our nuclear markers rather than male sex-biased dispersal, based on high conservation of 28S and H3 between our individuals and other amblypygid genera that are restricted to Africa. While this study includes but a tiny fraction of Caribbean caves, our findings suggest *Phrynosoma* may be much

more diverse than hitherto thought, at least in terms of mtDNA diversity, and that the arthropod fauna of caves may represent a dimension of biodiversity that is yet to be discovered in the Caribbean biodiversity hotspot.

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http://www.researchgate.net/publication/280587601_Islands_within_islands_Diversification_of_tailless_whip_spiders_amblypygi-phrynus

[6] [accessed Oct 21, 2015].

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- [Graduates](#) [12]
- [Postdocs](#) [13]
- [Faculty](#) [14]
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