

Molecular phylogenetics uncovers remarkable and unexpected diversity in ammotrechid camel spiders of Baja California Sur, Mexico

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INTRODUCTION

The Baja California peninsula harbors a rich desert biota with extraordinary levels of endemism. Scorpions, for instance, are more diverse there than anywhere else in the world (Williams, 1980; Graham et al., 2014). Such diversity is thought to be the product of vicariance events caused by the region's complex and somewhat enigmatic geologic history. Prior to ~12.3 Ma, Baja was part of the Mexican mainland. Rifting along the San Andreas fault caused a progressive formation of the Sea of Cortez, beginning in the south near Los Cabos at ~7.5 Ma and extending north to the Salton Trough of California by 6.3 Ma. Genetic discontinuities from a variety of terrestrial taxa suggest that the peninsula may have then occurred as an archipelago at times as trans-peninsular seaways isolated northern and southern populations (reviewed in Dolby et al., 2015). Interestingly, geological evidence of such seaways is largely lacking.

Here, we explore trans-peninsular seaway hypotheses with genetic data generated from ammotrechid camel spiders collected throughout Baja California Sur (BCS; Fig. 4A). Family Ammotrechidae is particularly understudied, and although DNA sequences have been generated for a few species, no phylogenetic analysis has been conducted with this group. Additionally, ammotrechid diversity and species limits in BCS have never been assessed. Thus, in addition to testing for the potential impact of vicariance by seaways, this study also provides baseline phylogenetic data for further investigations on this widespread group of arachnids, which are distributed throughout North and South America.

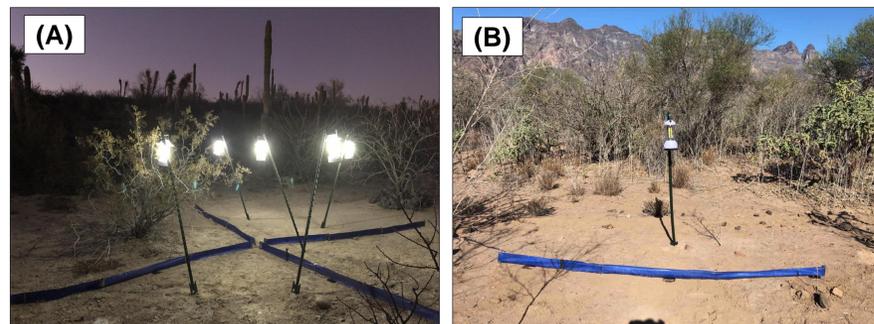


Figure 1. Examples of pitfall light traps used to collect ammotrechids in BCS; (A) 9-cup array near San Ignacio, and (B) 3-cup array at Puerto Escondido.

METHODS

Taxon Sampling

- Pitfall light traps were set at 10 locations in BCS (Figs 1A, 1B & 4B) following Cushing & González-Santillán (2018) and Graham et al. (2019)

Molecular Techniques

- Extracted genomic DNA from leg tissue using Qiagen DNeasy kit
- Vacuum concentrated DNA extractions
- Amplified mitochondrial *COI* following Cushing et al. (2015), verified amplicons using gel electrophoresis, and cleaned PCR products using ExoSAP-IT
- Bidirectional sequencing conducted by Eton Bioscience Inc.

Phylogeny, Divergence Dating & Species Delimitation

- Sequences were assembled and aligned in Geneious 7.0.2
- We simultaneously assessed phylogenetic patterns and estimated divergence by implementing a rate calibration from Santibáñez-López et al. (2021) in BEAST 1.8.0
- ASAP species delimitation was used to estimate species limits from genetic distances using the K2P model

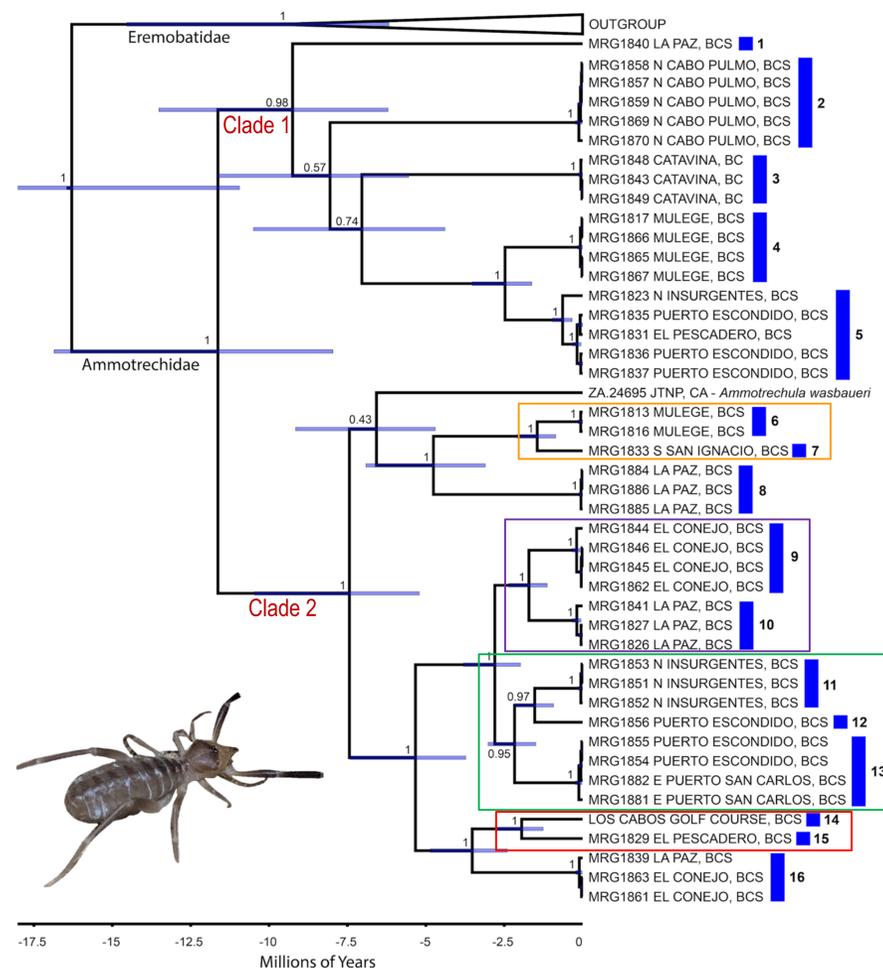


Figure 2. Time-calibrated, mitochondrial *COI* phylogeny of ammotrechid camel spiders from BCS. Numbers at nodes represent posterior probability values. The 16 species identified by ASAP analysis are represented by blue bars. Colored outlines correspond to clades mapped in Figure 3.

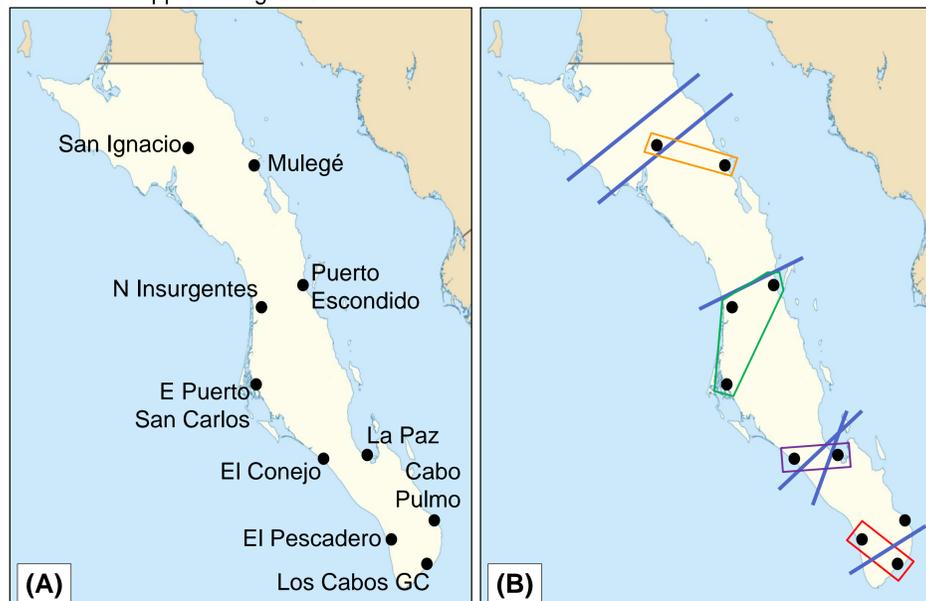


Figure 3. (A) Map depicting ammotrechid collection localities in BCS. (B) Distributions of clades with origins in the Pleistocene in relation to locations of genetic discontinuities attributed to hypothesized Plio-Pleistocene trans-peninsular seaways (blue lines).

RESULTS

- Ammotrechidae is monophyletic with respect to outgroup (Fig. 2)
- Baja California ammotrechids are paraphyletic with respect to *Ammotrechula wasbaueri* from JTNP in California, USA (Fig. 2)
- Two main clades with Miocene origins, both broadly distributed along peninsula (Fig. 2)
- ASAP estimates that we sampled 15 spp. in BCS; 1 sp. in BC (Fig. 2)
- High endemism with 10 species found at a single site (Fig. 2)
- Four clades with Plio-Pleistocene origins and distributional patterns suggesting strong north-south genetic discontinuities (Figs 2 & 3B)

CONCLUSIONS

The remarkable level of genetic diversity in ammotrechids from BCS was unexpected. Given that the two major clades have origins in the Miocene, we hypothesize that the proto-peninsula was inhabited by a least two ammotrechid lineages before it rifted away from mainland Mexico. Each lineage appears to have diversified along the peninsula through the Late Miocene, Pliocene, and Pleistocene, resulting in a diverse ammotrechid fauna. Additional surveys would undoubtedly recover many more ammotrechid species, but given our sampling we do see evidence of numerous north-south genetic discontinuities, corroborating previous genetic studies on terrestrial taxa of the region and pointing again at the potential for trans-peninsular seaways. Ultimately, this study highlights (1) the potential of ammotrechid camel spiders for elucidating biogeographic insights in geologically complex areas, and (2) the dire need for thorough molecular systematic revisionary work on this poorly understood group of arachnids.

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