

The phylogenetic relationships of three genera of lizards with the use of DNA barcoding

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Funded by the
Pinkerton Foundation
and Science Sandbox



Abstract

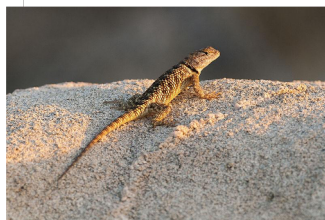
- The goal of this research is to analyze the DNA barcodes of over fifty different lizard samples of five different predetermined lizard species, to expand and reaffirm current knowledge about these lizards and its family, the Phrynosomatidae.
- The tree's results shows multiple samples had clades within the tree separate from the rest showing that there are nine different species within the samples.

Introduction

- The family Phrynosomatidae is a diverse group of lizards composed of approximately 148 species (Wiens et al. 2009)
- Phrynosomatids are confined to North and Central America, making the group an important model for research in evolution and ecology in the area (Wiens et al. 2009)
- Introgression has been found with *U. ornatus* mitochondrial DNA in lizards with *U. graciosus* nuclear DNA however not vice versa. (Haenel 2016)
- Previous studies have suggested the possibility of undiscovered species within the *S. graciosus* group, as indicated by multiple lineages with large genetic differences between them (Chan et al. 2013)
- Mitochondrial DNA of *U. ornatus* and *U. graciosus* have strongly supported diverged clades that does not correlate to other morphological species designation. (Haenel 2016)
- The five species that are investigated in this study are *Sceloporus magister*, *Cophosaurus texanus*, *Sceloporus graciosus*, *Urosaurus graciosus*, and *Urosaurus ornatus*
- Studying using DNA barcoding to identify the lizard species helps as a tool for species delineation and assessment.

Materials & Methods

- Tissue samples were obtained from several natural history museums and preserved at below freezing temperatures.
- DNA was extracted from the tissue samples using a standard DNA extraction kit. The mitochondrial COI gene of the samples was amplified and the PCR products were examined using gel electrophoresis.
- All successful reactions were sent to Genewiz for DNA sequencing in both forward and reverse directions. Raw DNA sequences were edited to remove low-quality bases.
- Once edited, the sequence identity was determined with BLAST to ascertain if the correct gene from the correct species was sequenced. After BLASTing the sequences multiple sequence alignment of all new sequences was performed using MUSCLE and Aliview.
- The alignment was used to infer a maximum likelihood phylogeny in the program IQ-TREE.
- The program, mPTP was used to determine if any new species are likely.



Results

- Phylogenetic analyses show that multiple species contain deep genetic differences.
- Results suggest a total of 10 different species found in this tree
- Sceloporus magister*,
 - S. magister_ROM14488* is most likely a different species than the other *S. magister* samples.
- Cophosaurus texanus*,
 - Sample *C. texanus_ROM15372* has many nucleotide differences from *C. texanus_ROM15105* and *15157* based on the branches.
 - All *C. texanus* are found in a highly supported clade
- Sceloporus graciosus*,
 - One of the three clades of *S. graciosus* has a *S. arenicolus* with a high support value, showing a close relationship between the two species. mPTP suggests that all of these individuals are within the same species.
- Urosaurus ornatus*,
 - U. ornatus* branches off in two different places showing that all of the *U. ornatus* samples are not descended from a common evolutionary ancestor or monophyletic.

Tables & Figures

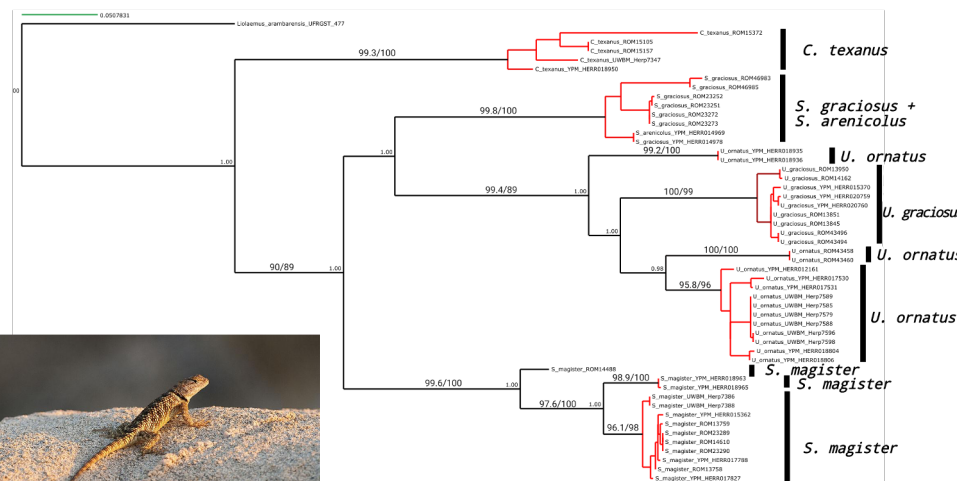


Fig. 1. Maximum likelihood tree and species delimitation results. Red branches represent coalescent events within species. The thick bars on the side represent different clades and the species identified using BLAST. Branch labels are support values for relationships and values greater than 80/95 are strongly supported. Other values at nodes represent support for speciation.

Discussion

- Results show putative new species found within the tree due to the fact that there were originally only five different species which the samples belong to before DNA barcoding.
- One of the most probable samples from the tree would be *S. magister_ROM14488* which would most likely be an entirely different species from the rest of the tree since its branches break off earlier than from the rest of *S. magister*.

References

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Acknowledgements

I would like to thank my science research teacher Dragic for offering this opportunity to do this type of research to me. I would like to thank CUNY City Tech to allow me to use their facility, and UBPR for sending me to an amazing mentor, Professor Blair, who helped me learn what it's like to do research professional and showed me the ropes around DNA barcoding.