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Genomic data from alligator lizards help clarify their evolutionary history and support the recognition of a new genus

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Background

Genomic data continue to be used to help resolve difficult problems in phylogenetics and evolutionary biology¹. However, different analytical methods can lead to different conclusions, making it challenging for empirical researchers to decide on which methods to use. In this study, we expand upon recent studies² and use thousands of genomic markers called ultraconserved elements (UCEs) to reconstruct the evolutionary history of alligator lizards (genus *Gerrhonotus*) throughout the Mexican Transition Zone (MTZ). The MTZ constitutes a hyperdiverse region where Neotropical and Nearctic biotas overlap, and extends from the southwestern US to Nicaragua³. We specifically address the following questions:

1. What are the evolutionary relationships of alligator lizards throughout the MTZ?
2. Do different phylogenetic methods applied to the same data yield conflicting results?
3. How do divergence times correspond to major geological and climatic processes?
4. Do the data provide evidence for undocumented diversity?

Methods

- Tissue samples for all species were obtained from field sampling.
- Multiple individuals per species.
- Sequenced thousands of UCEs throughout genome.
- Inferred phylogenetic trees on the concatenated data using both maximum likelihood (ML; IQ-TREE) and Bayesian (ExaBayes) methods.
- Two different coalescent methods (SVDquartets, BPP) were used to assess congruence with concatenation.
- MCMCTree was used to estimate divergence times using the ExaBayes topology. Fossil information from the genus *Elgaria* used to time calibrate the root node.

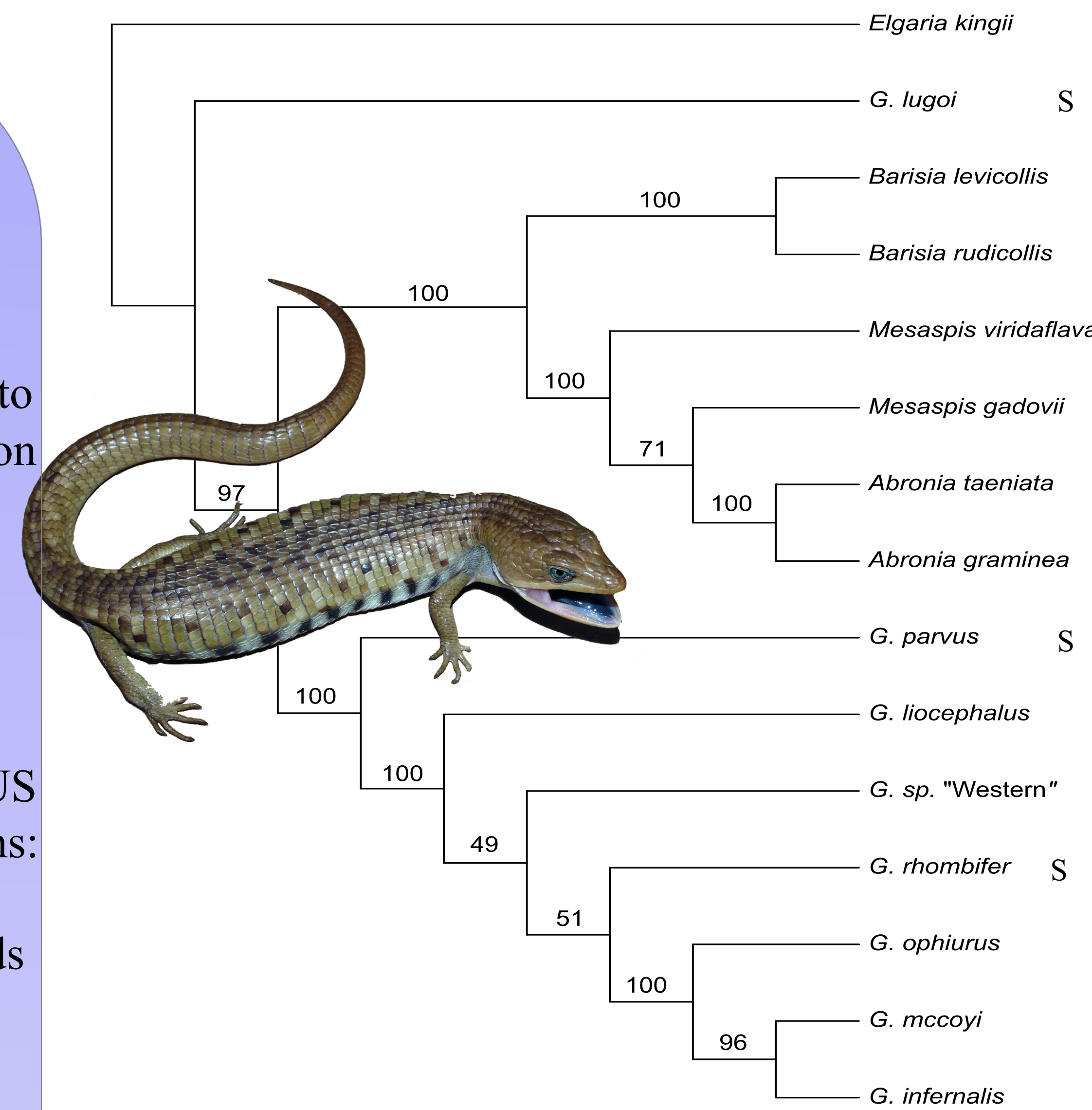


Fig. 1. SVDquartets species tree for *Gerrhonotus* and related anguid lizards. Values at nodes indicate support values from 100 bootstrap replicates. 'S' indicates species with smooth scales.

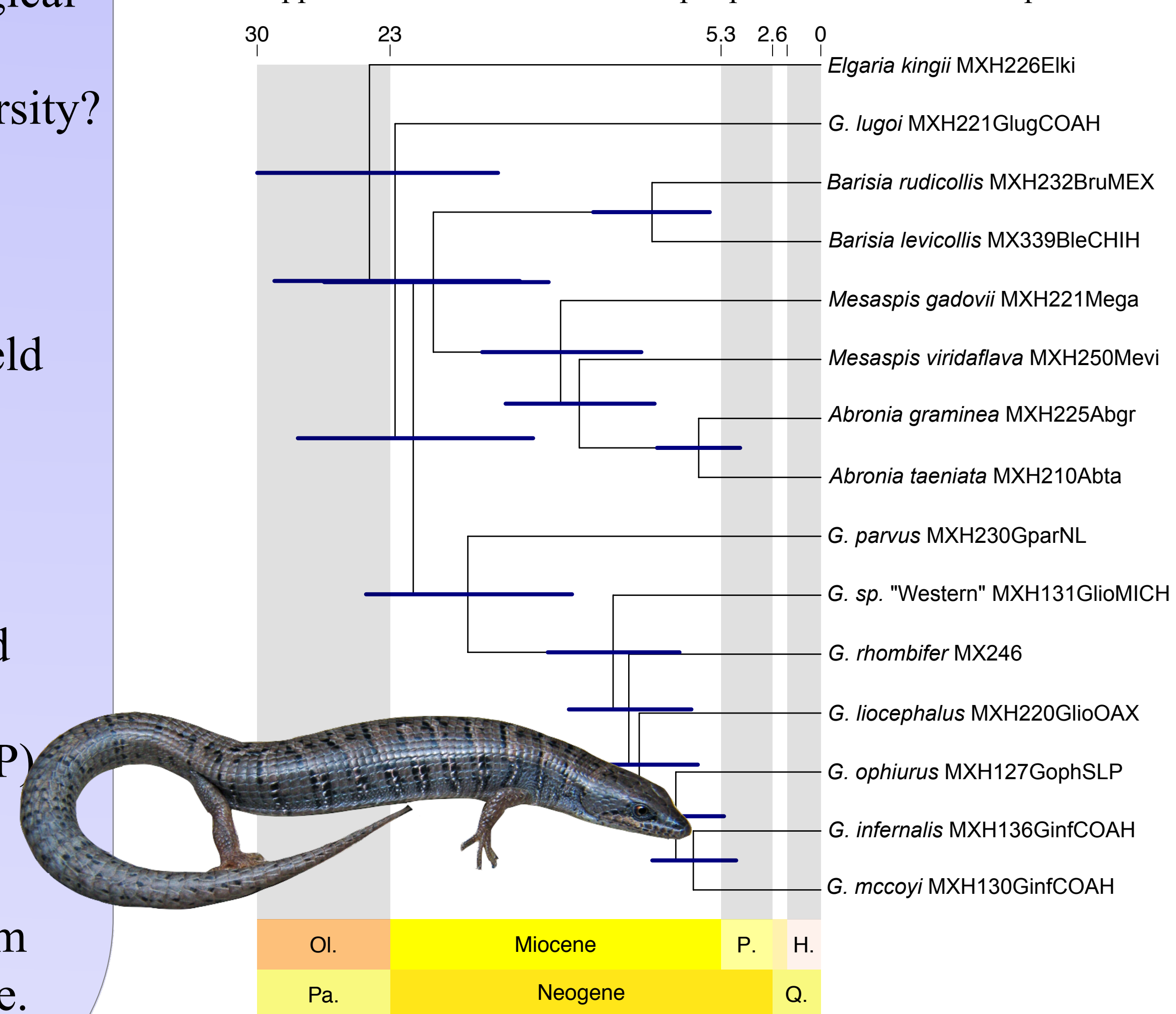


Fig. 2. Divergence times of all anguid lizards included in this study. Tree topology was inferred using ExaBayes. Horizontal bars represent 95% highest posterior density (HPD) values. Numbers on the top of the figure represent millions of years.

Results

- Concatenated ML and Bayesian trees yielded similar results.
- All current species monophyletic, except for *G. infernalis* + *G. mccoysi*.
- Two species, *G. lugoi* and *G. parvus*, very distantly related to other *Gerrhonotus*.
- Smooth-scaled species do not form a clade.
- Evidence for an undescribed species in western Mexico.
- Coalescent analyses similar to concatenation, and suggest that *G. lugoi* is distantly related (Fig. 1).
- Speciation of *Gerrhonotus* occurred in Neogene (Fig. 2).

Conclusions

- Well supported species tree with minor differences between phylogenetic methods.
- *Gerrhonotus lugoi* distantly related to congeners. Therefore, we combine molecular and morphological results to describe a new genus for this taxon (*Desertum gen. nov.*).
- Additional data needed to determine if *G. parvus* should be classified in a different genus.
- Speciation during the Miocene suggests a role of vicariance due to mountain formation or global climate change during the Miocene.
- Phylogeography studies needed to determine cryptic species.
- Study further highlights how genomic data can help resolve evolutionary radiations.

References

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