

# Phylogenetic Analyses of the genus *Gekko* using Maximum Likelihood and Minimum Evolution Models

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## INTRODUCTION

- Wood et al. (2020) sought to resolve phylogenetic relationships within the genus *Gekko* [5]
- Previous studies suggested paraphyly within *Gekko* with the inclusion of species from the derived genera, *Luperosaurus* and *Ptychozoon* [1,2]
- Using 5060 ultraconserved elements (UCEs), Wood et al. constructed five different datasets (10p, 50p, 75p, 95p, and 100p) with varying percent loci completeness of sampled individuals
- A Maximum Likelihood phylogenetic tree for all levels of loci completeness was developed with all having similar results (Fig. 1)
- Minimum Evolution, a distance-based analysis, may offer a faster method to obtain statistically consistent results to that of Maximum Likelihood [4]
- Minimum Evolution assigns the smallest sum of total branch length estimates as the truest topology

## OBJECTIVE

Compare phylogenetic relationships resulting from Wood et al.’s Maximum Likelihood model to relationships suggested by a Minimum Evolution model

## METHODS

- 10p dataset from Wood et al. was downloaded from Dryad [4] and analyzed through MEGA to construct a Minimum Evolution phylogenetic tree
- 42 species of lizards were included as ingroup taxa: (2) *Lepidodactylus*, (2) *Pseudogekko*, (5) *Ptychozoon*, (7) *Luperosaurus*, and (25) *Gekko*
- A distantly related outgroup taxon, *Cyrtodactylus*, was chosen to root the trees
- Bootstrapping was performed on the produced Minimum Evolution tree to find proposed relationship probabilities

## RESULTS

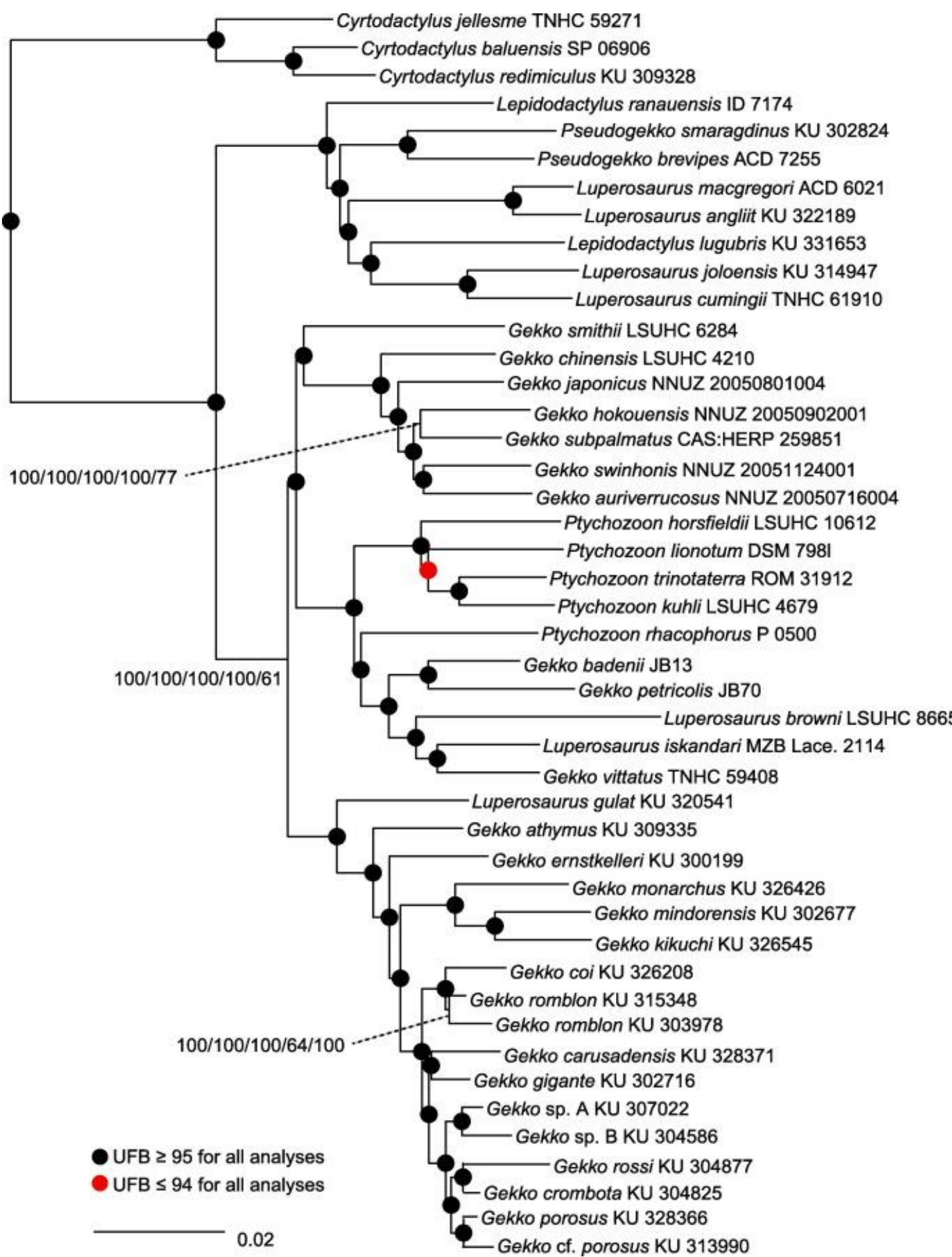


Figure 1. Maximum Likelihood phylogeny based on 10p dataset. (From Wood et al. 2020)

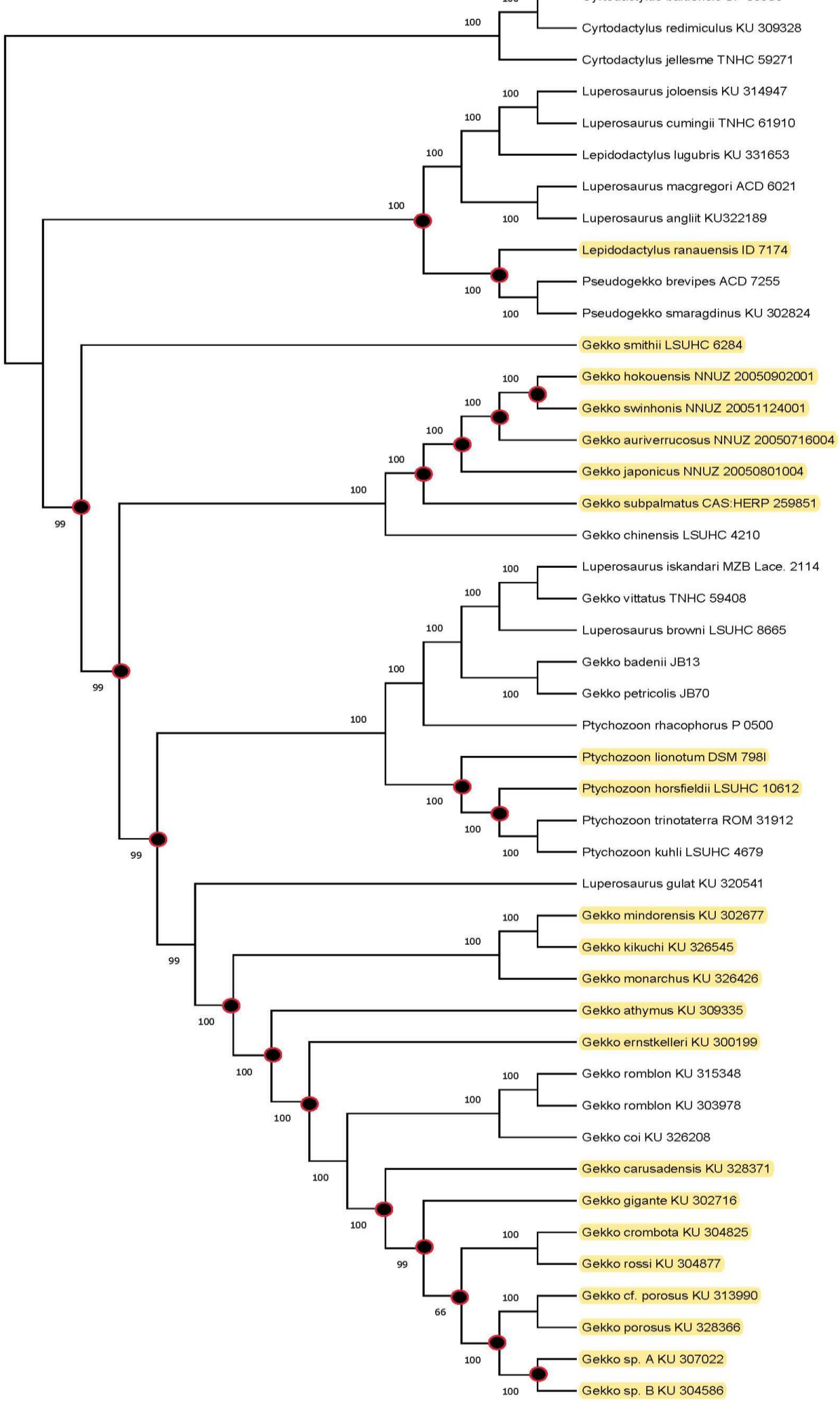


Figure 2. Minimum Evolution phylogeny based on 10p dataset. Highlighted taxa represent differences in placement compared to the Wood et al. Maximum Likelihood tree. Circles represent differences in sister and ancestral relationships compared to the Maximum Likelihood tree.

- ***Gekko smithii* is basal from rest of *Gekko* taxa in the Minimum Evolution phylogeny**
- ***Gekko smithii* is monophyletic in the Maximum Likelihood phylogeny, producing a clade with Chinese *Gekko* taxa (*G. chinensis*, *G. japonicus*, *G. hokouensis*, *G. subpalmatus*, *G. swinhonis*, *G. auriverrucosus*)**
- **Minimum Evolution phylogeny produced different sister relationships and ancestral history estimates within the most derived *Gekko* taxa**

## DISCUSSION

- Phylogenetic relationships within *Gekko* taxa differed between the Maximum Likelihood and Minimum Evolution models
  - Minimum Evolution’s search for the simplest explanation of genetic change does not take into account the variance of inputted data [3]
    - Lack of variance may result in incorrect relationships
  - Distance-based analyses, including Minimum Evolution, have trouble developing accurate phylogenies due to inability to emulate a proper evolutionary process mechanism
  - Our Minimum Evolution model does not appear to provide consistent results with Wood et al.’s Maximum Likelihood model
- How would a Minimum Evolution tree created with a higher degree of loci completeness compare?

## FURTHER QUESTIONS

### Literature Cited

[1] Brown, R. M., Meneses, C. G., Wood, P. L., Fernandez, J. B., Cuesta, M. A., Clores, M. A., Tracy, C., Buehler, M. D., & Siler, C. D. (2020). Unexpected discovery of another new species of Philippine false gecko (Gekkonidae; pseudogekko) from the Bicol Peninsula of Luzon Island. *Herpetologica*, 76(3), 315.

[2] Brown, R. M., Oliveros, C., Siler, C. D., & Diesmos, A. C. (2009). Phylogeny of gekko from the northern Philippines, and description of a new species from Calayan Island. *Journal of Herpetology*, 43(4), 620–635. <https://doi.org/10.1670/08-207.1>

[3] Gascuel, O., Bryant, D., & Denis, F. (2001). Strengths and limitations of the minimum evolution principle. *Systematic Biology*, 50(5), 621–627. <https://doi.org/10.1080/106351501753328767>

[4] Huelsenbeck, J. P. (1995). Performance of phylogenetic methods in simulation. *Systematic Biology*, 44(1), 17. <https://doi.org/10.2307/2413481>

[5] Wood, P. L., Guo, X., Travers, S. L., Su, Y.-C., Olson, K. V., Bauer, A. M., Grismer, L. L., Siler, C. D., Moyle, R. G., Andersen, M. J., & Brown, R. M. (2020). Parachute geckos free fall into synonymy: Gekko phylogeny, and a new subgeneric classification, inferred from thousands of ultraconserved elements. *Molecular Phylogenetics and Evolution*, 146, 106731. <https://doi.org/10.1016/j.ympev.2020.106731>