

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*
- Previous studies suggested paraphyly within *Gekko* with the inclusion of species from the derived genera, *Luperosaurus* and *Ptychozoon*
- Using 5060 ultraconserved elements (UCEs), Wood et al. built concatenated maximum likelihood tree to answer research questions:
 - Are *Luperosaurus* and *Ptychozoon* monophyletic and are any taxa from these genera included within *Gekko*?
 - Is there a sister relationship between *L. iskandari* and *G. vittatus* as previous estimates have identified?
 - Is *L. gulat* correctly placed in *Gekko*?
 - How does *P. Rhacophorus* and *L. browni* fit in the phylogeny?

- Min. Evolution model searches for smallest sum of branch length estimates

OBJECTIVE

Compare phylogenetic relationships resulting from Wood et al.’s maximum likelihood model to relationships suggested by a minimum evolution model.

METHODS

- Aligned dataset from dryad [4] analyzed in MEGA program
- 42 species of lizards are included in and ingroup sampling (two species of *Lepidodactylus*, two species of *Pseudogekko*, five *Ptychozoon* species, seven *Luperosaurus* species, and 25 species of *Gekko*)
- Using bootstrapping method, we were able to perform Min. Evolution analysis on same dataset that Max. Likelihood was performed

RESULTS

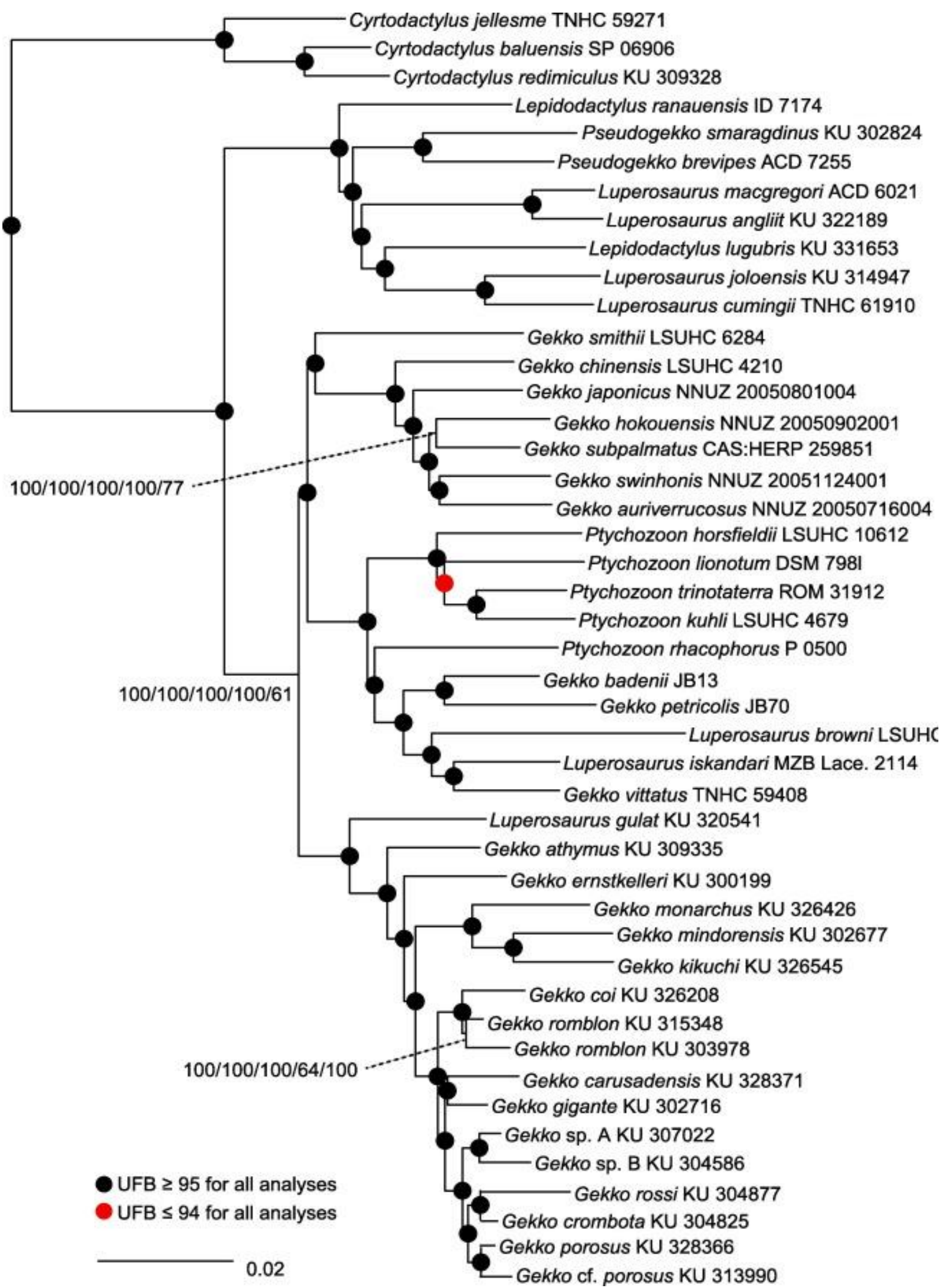


Figure 1. Maximum Likelihood phylogeny based on 10p dataset. (From Wood et al. 2020)

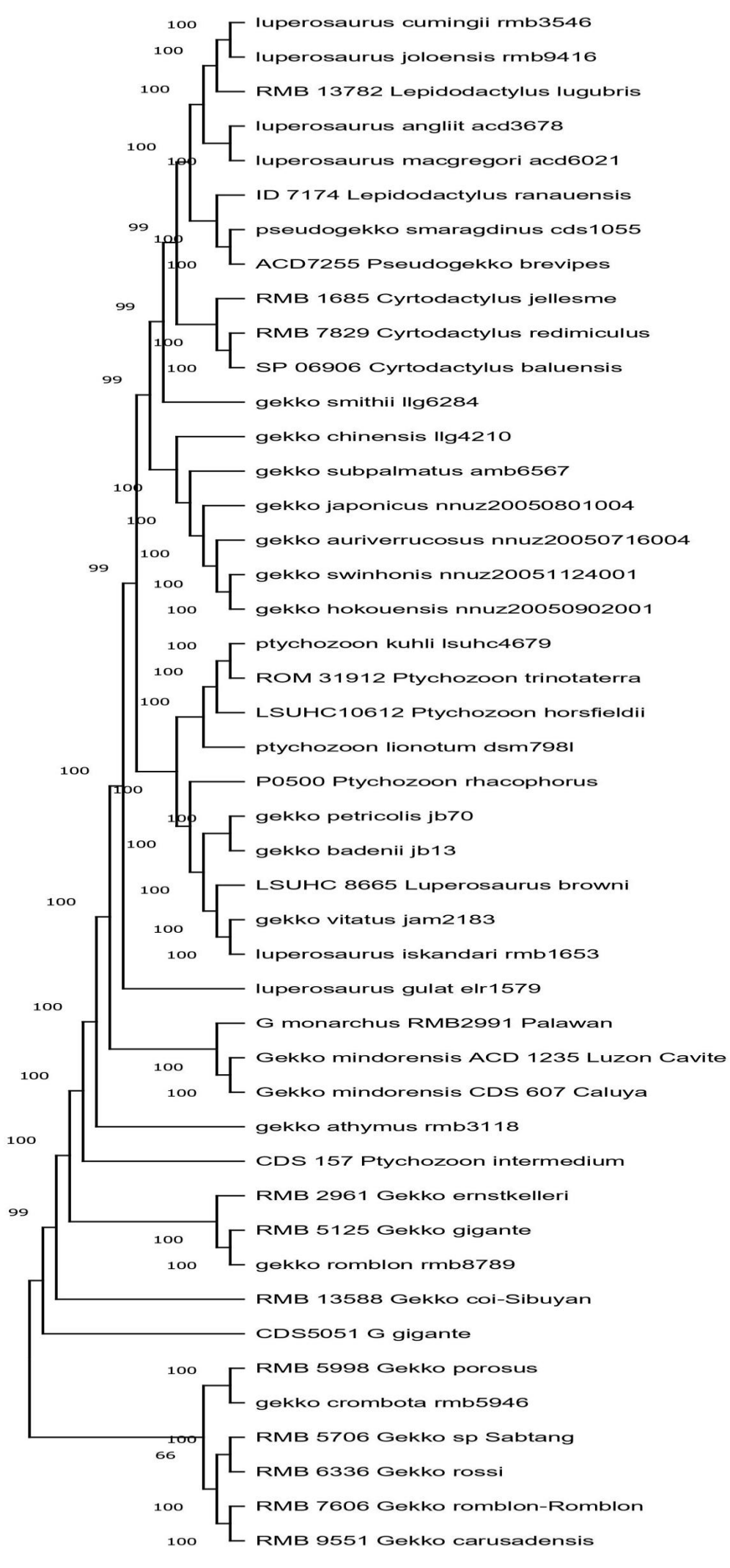


Figure 2. Minimum Evolution phylogeny based on 10p dataset.

DISCUSSION

- (1)Both models have *Luperosaurus* and *Ptychozoon* as non-monophyletic with taxa mixed in with *gekko*; (2)show *L. iskandari* and *G. vittatus* sister relationship; (4)show *P. rhacophorus* to be basal to *L. browni*
- (3)Min. Evolution places *L. gulat* outside of *gekko*, Max. Likelihood within *gekko*
- More robust bootstrapping methods used in Max. Likelihood leading to differentiation
- Min. Evolution modeling provided much different representation of *gekko* genus relationships
- Clades related to relative geographic location not seen in new model
- Problems with modeling program led to trouble obtaining correct outgroup
- After only completing Min. Evolution model on 10p dataset, how would tree compare at a higher degree of loci completeness?

Literature Cited

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[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>

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