



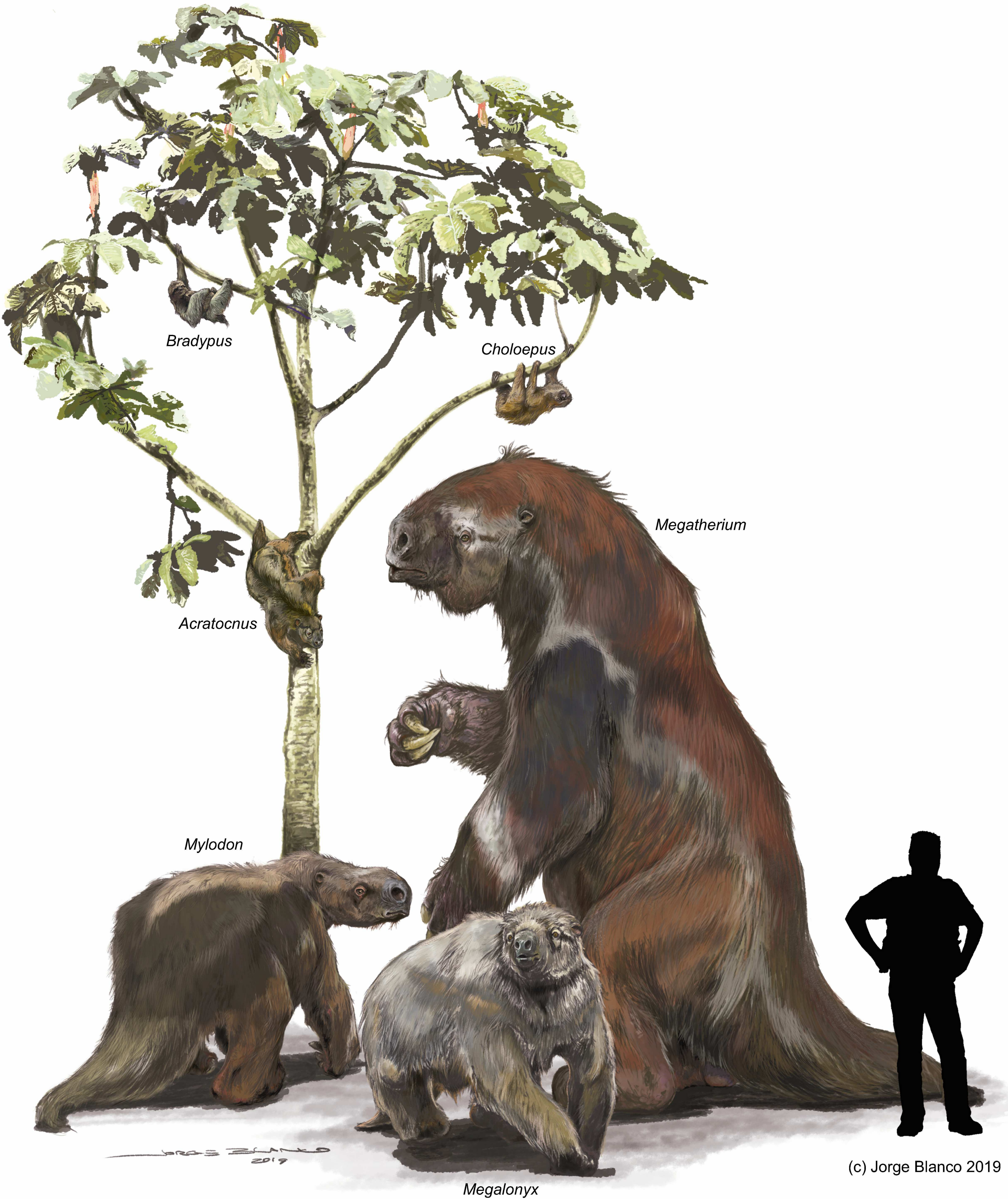
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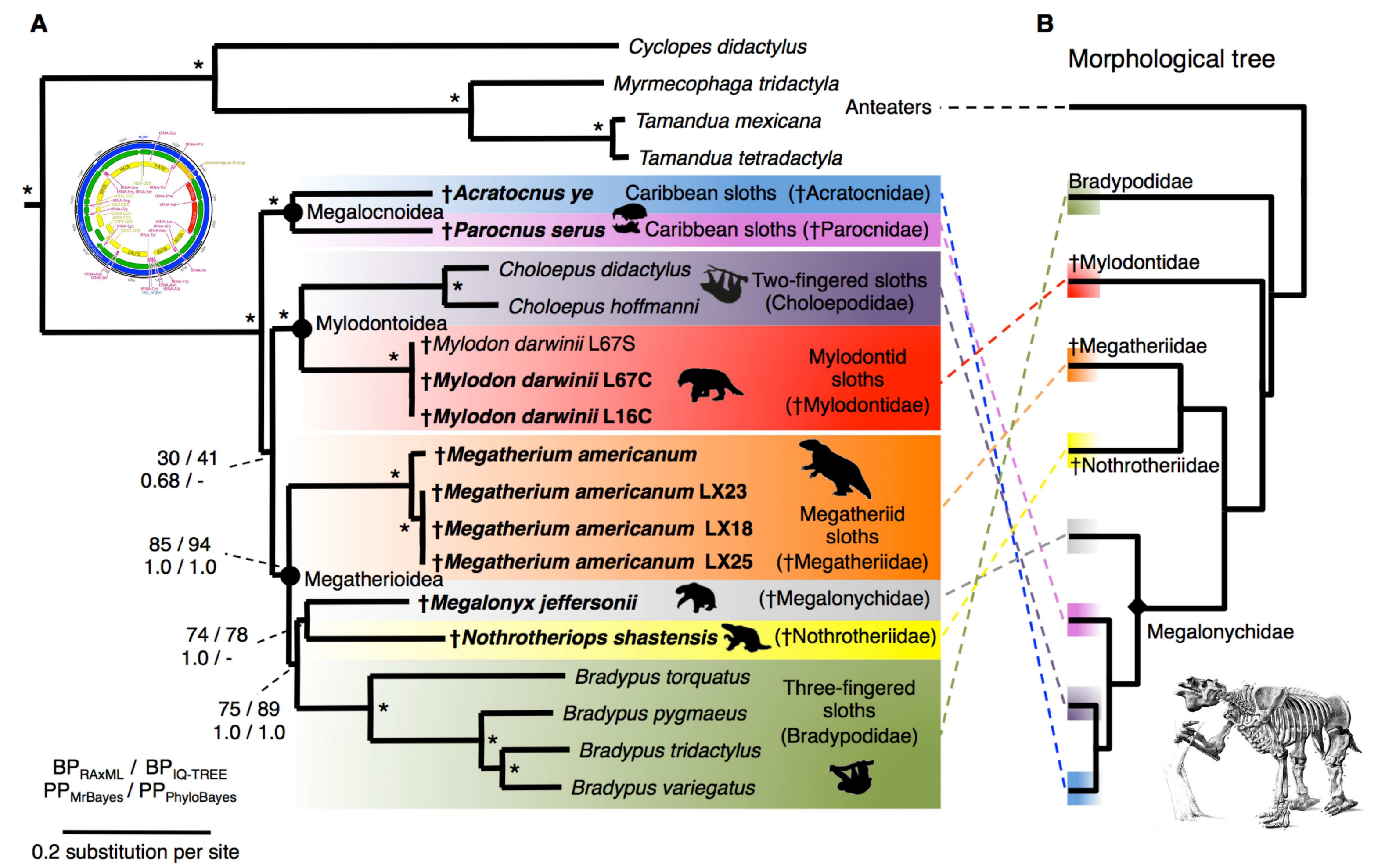
TEN NEW ANCIENT SLOTH MITOGENOMES

Ancient DNA sequence capture was used to assemble 10 new extinct sloth mitogenomes encompassing all major sloth lineages including the iconic continental ground sloths *Megatherium*, *Megalonyx*, *Mylonodon*, and *Nothrotheriops*, and the smaller endemic Caribbean sloths *Parocnus* and *Acratocnus*.



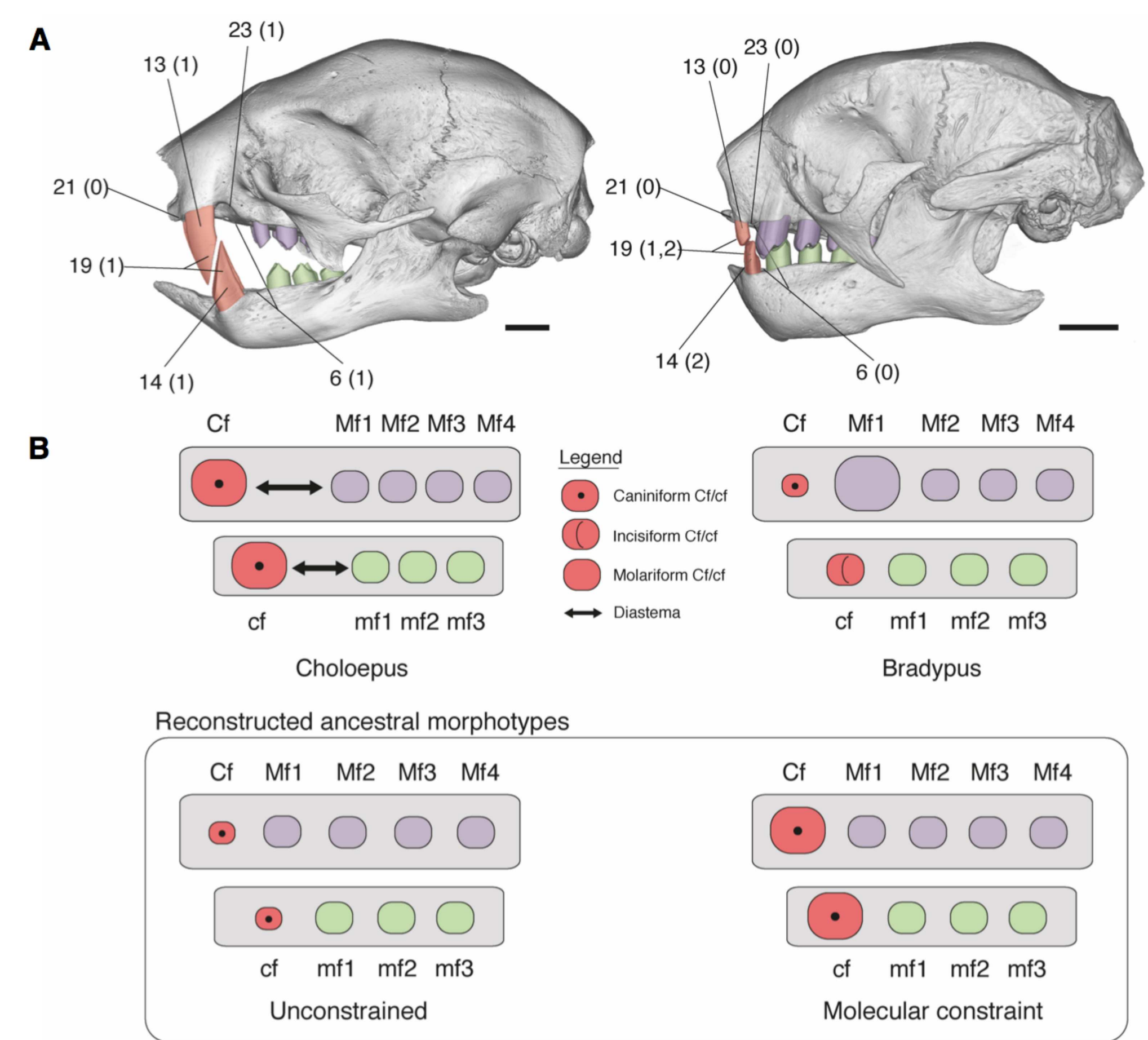
CONFLICT BETWEEN MORPHOLOGY AND MOLECULES

Phylogenetic analyses identified eight distinct lineages grouped in three well-supported clades and whose interrelationships were markedly incongruent with the currently accepted morphological topology.



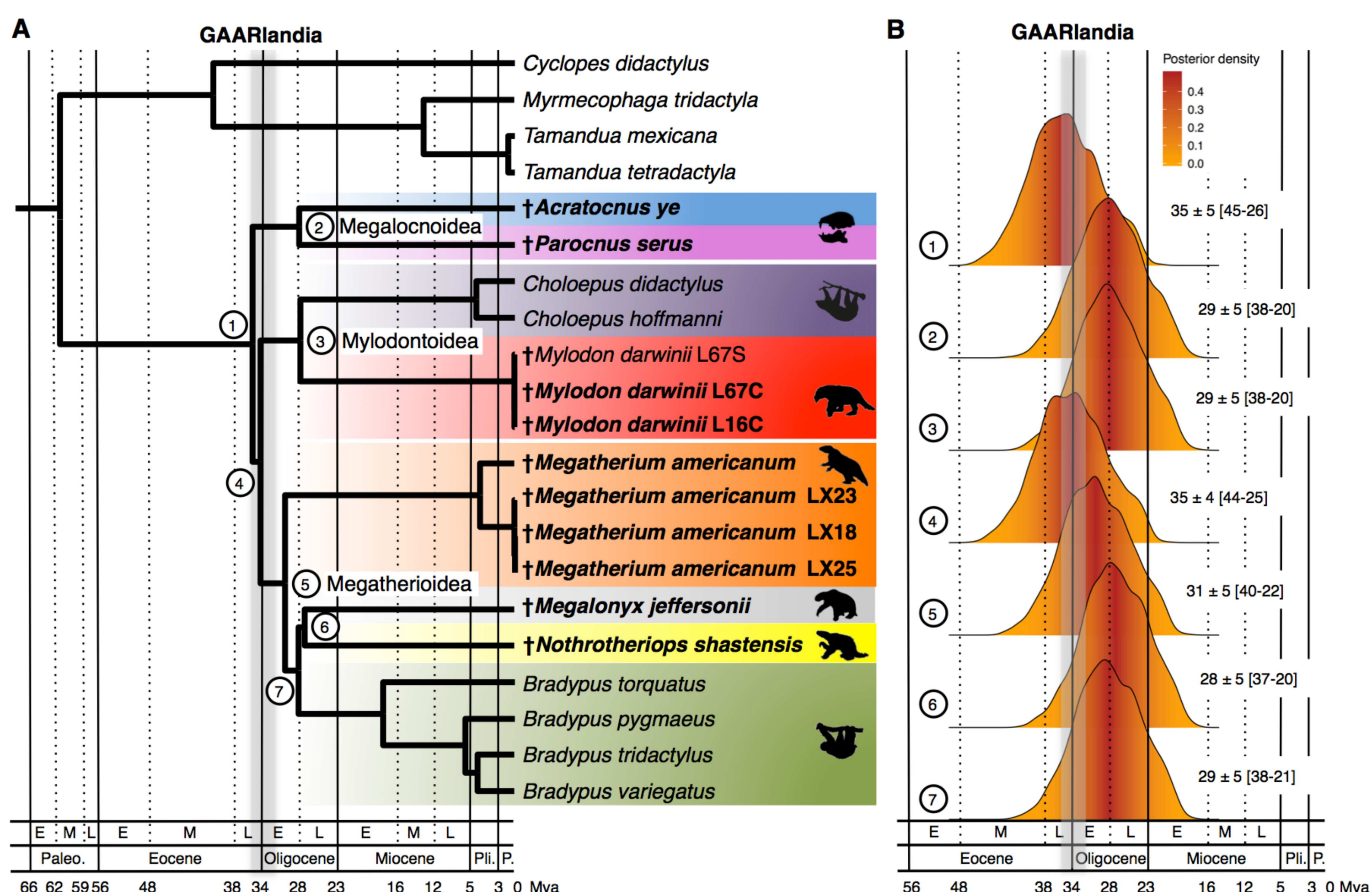
REINTERPRETING MORPHOLOGICAL CHARACTERS

Using the new molecular backbone allowed us to reinterpret the ancestral sloth dental formula showing that large caniniforms were the most likely ancestral state as suggested by developmental data and in agreement with the fossil record.



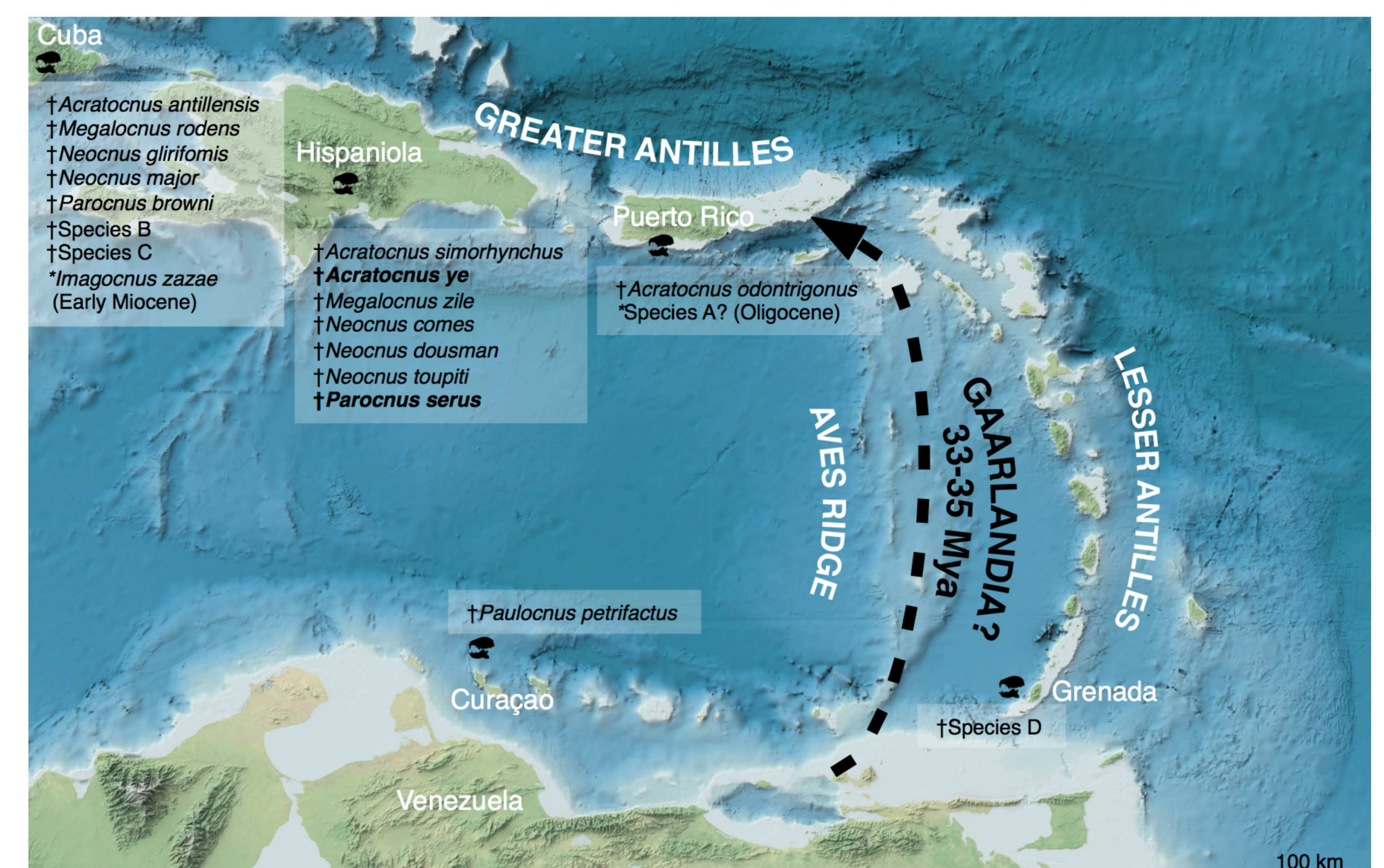
MOLECULAR DATING OF THE SLOTH RADIATION

Bayesian molecular dating showed that the eight newly recognized sloth families all originated 36-28 Mya, a period corresponding to a global glacial maximum marking the transition from humid tropical forests to drier open habitats in South America.



BIOGEOGRAPHIC IMPLICATIONS

The early divergence of extinct Caribbean sloths around 35 Mya would be consistent with the debated GAARlandia hypothesis postulating the existence of a biogeographic connection between northern South America and the Greater Antilles through the now submerged Aves Ridge.



REFERENCES

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Presslee S., Slater G.J., Pujos F., Forasiepi A.M., Fischer R., ... & MacPhee R.D.M. (2019). Palaeoproteomics resolves sloth relationships. *Nature Ecology and Evolution* 3:1121-1130. doi:10.1038/s41559-019-0909-z

FUNDING

