

Tempo and mode of evolution of the genus *Conus* (Gastropoda: Neogastropoda) in the Cape Verde Islands

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OUTLINE

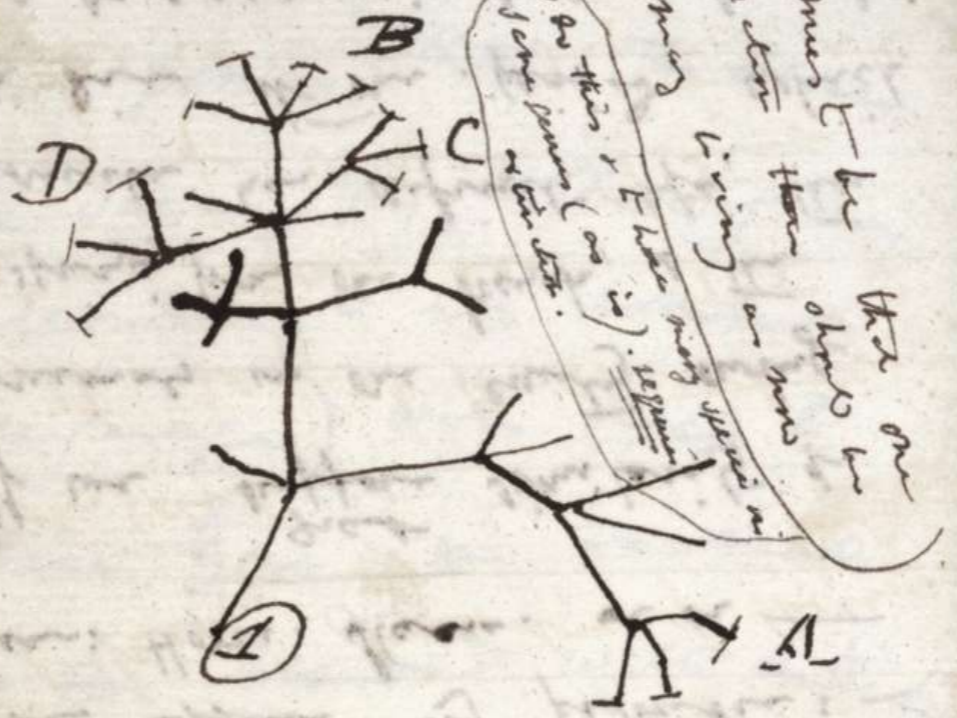
01

A brief introduction to molecular phylogenetics

02

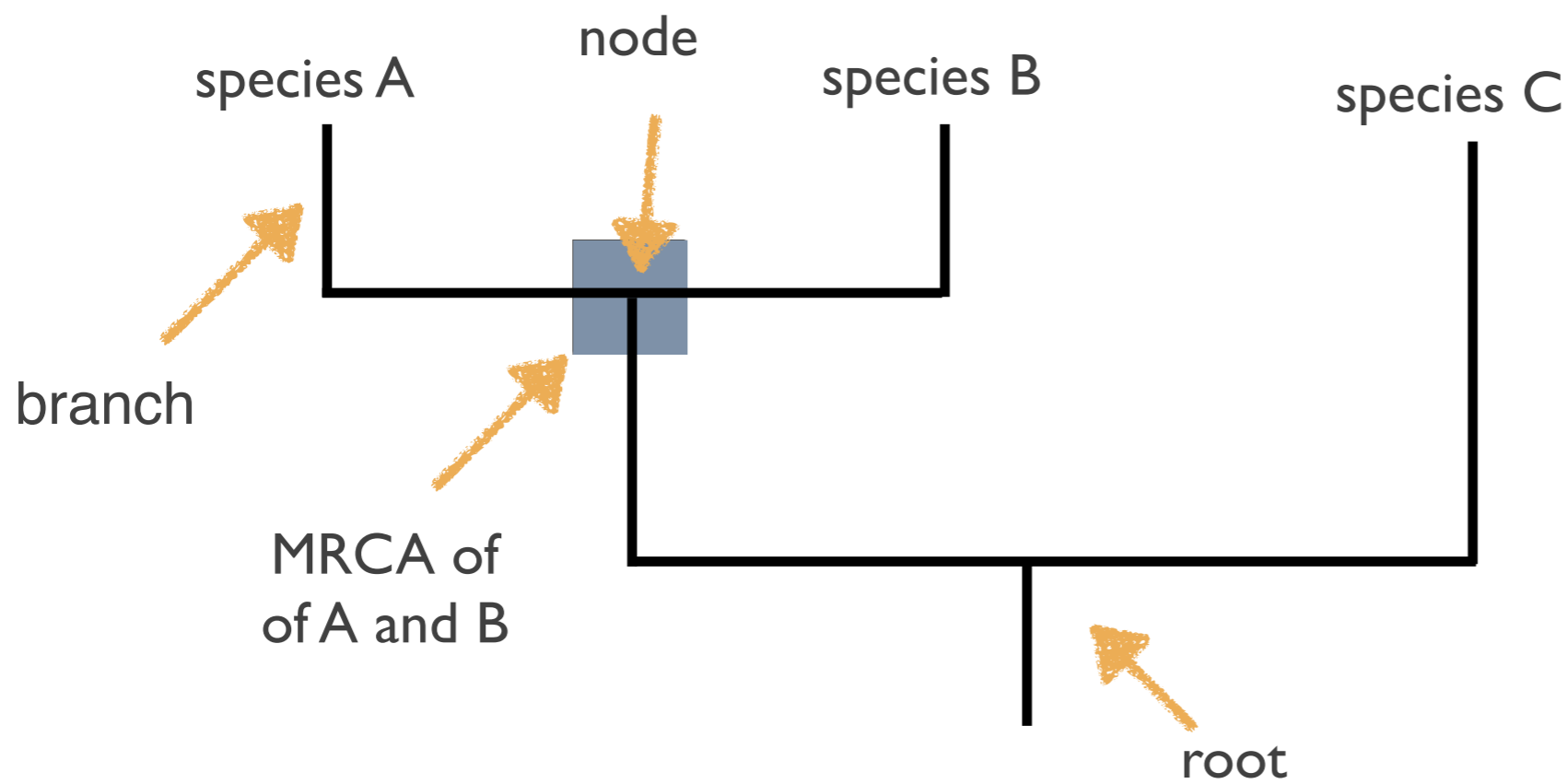
Model system: Cape Verde cone snails

I think



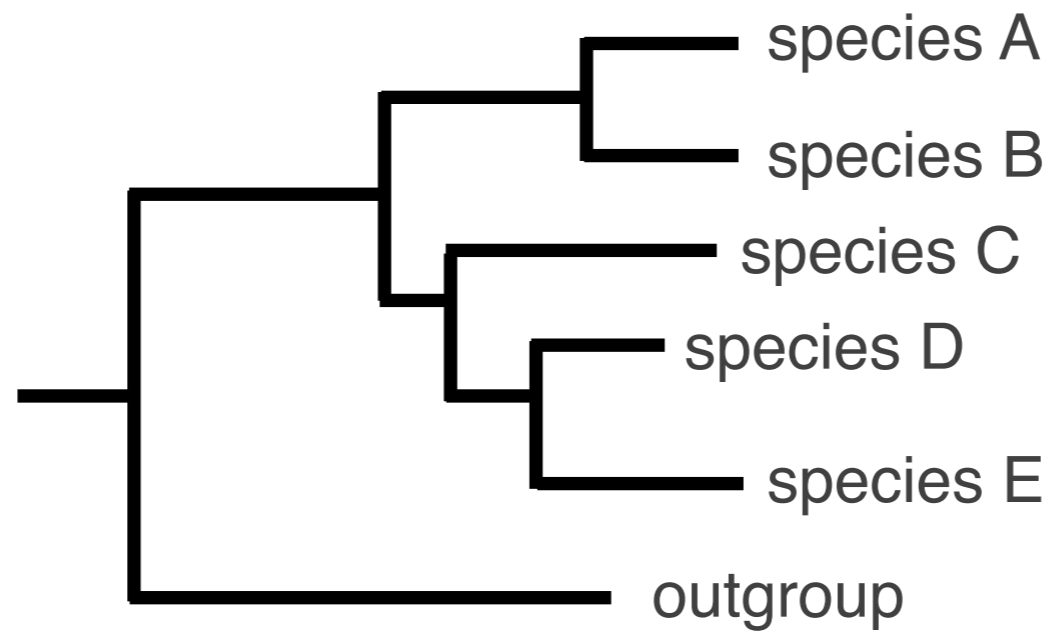
There between A & B. various
 sort of relation. C + B. The
 finest gradation, B & D
 rather greater distinction
 than genus would be
 formed. - bearing relation

A and B are **sister** groups



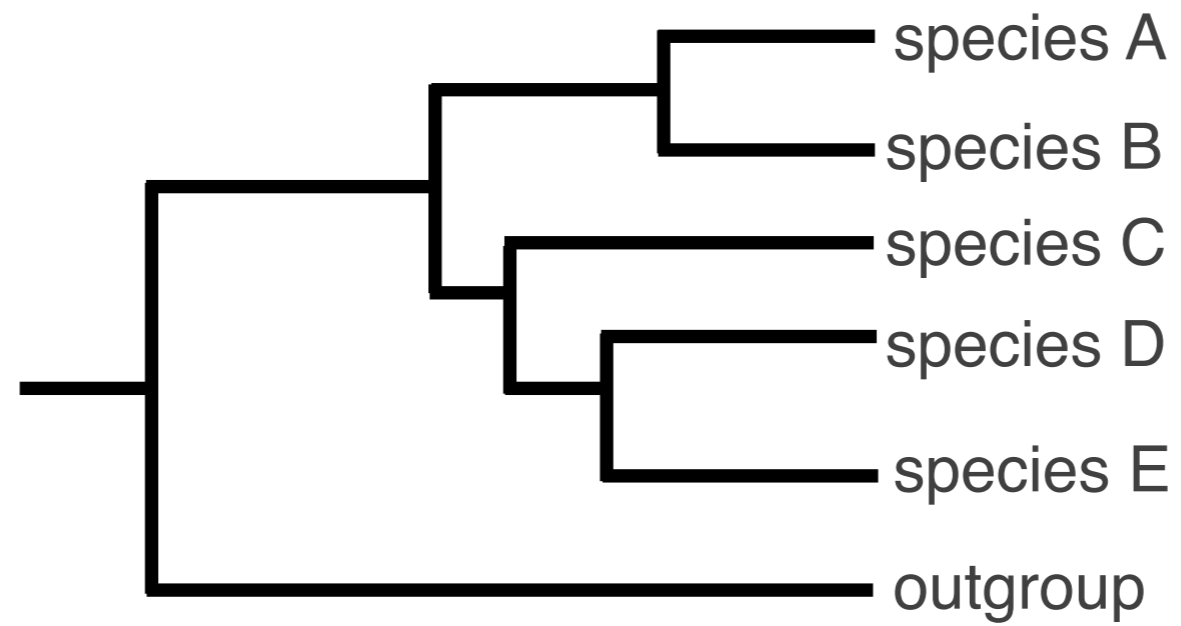
C is the **outgroup**
to A and B

Phylogram

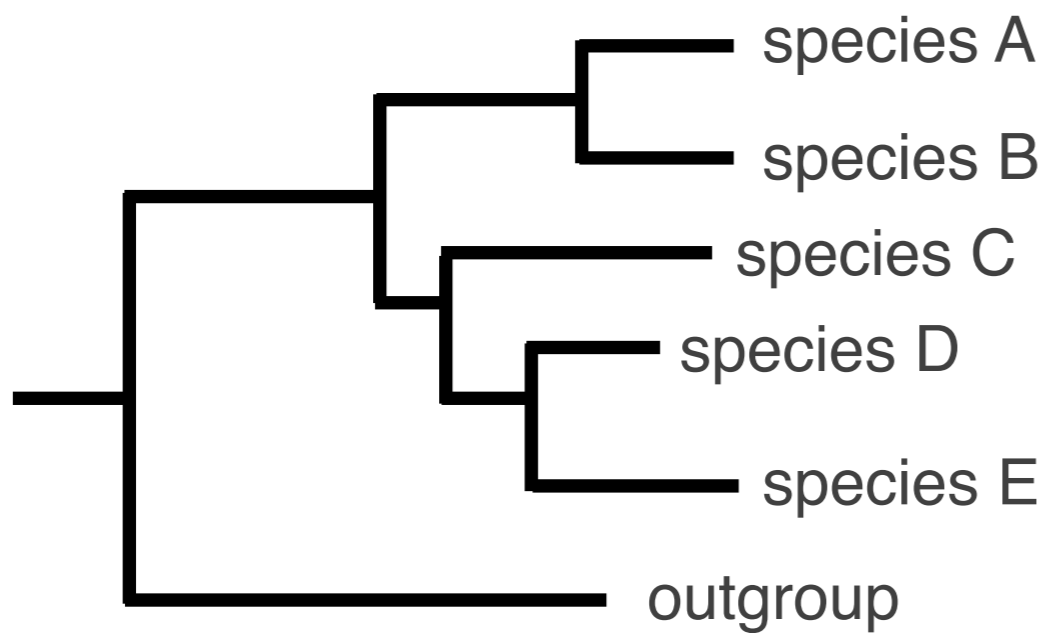


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0.002 subs. per site

Cladogram

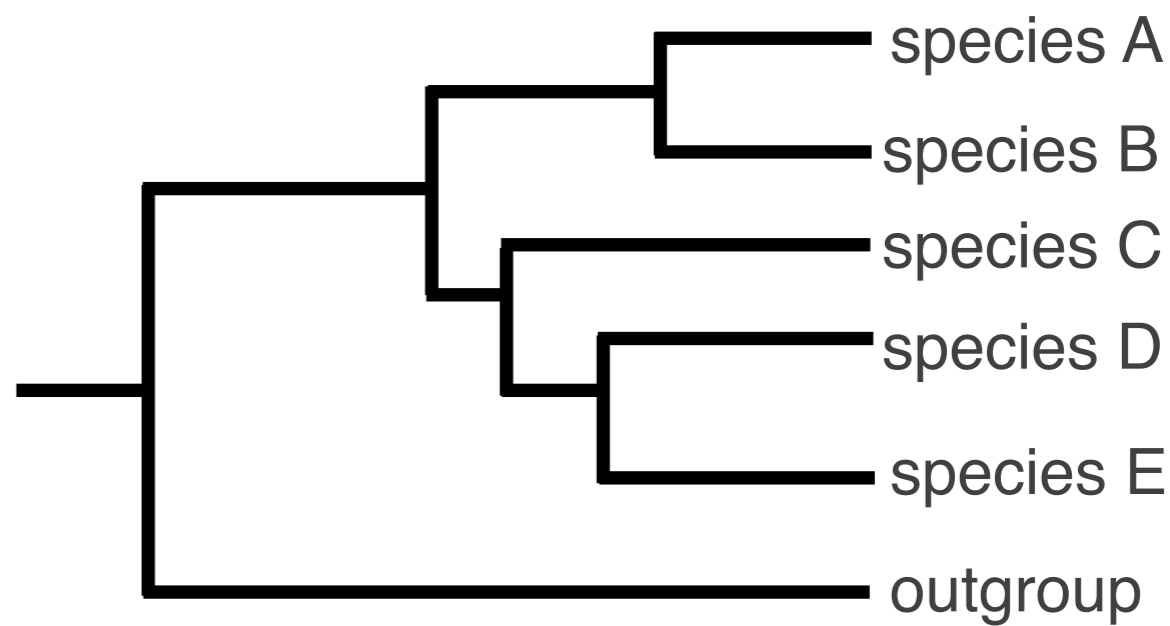


Phylogram

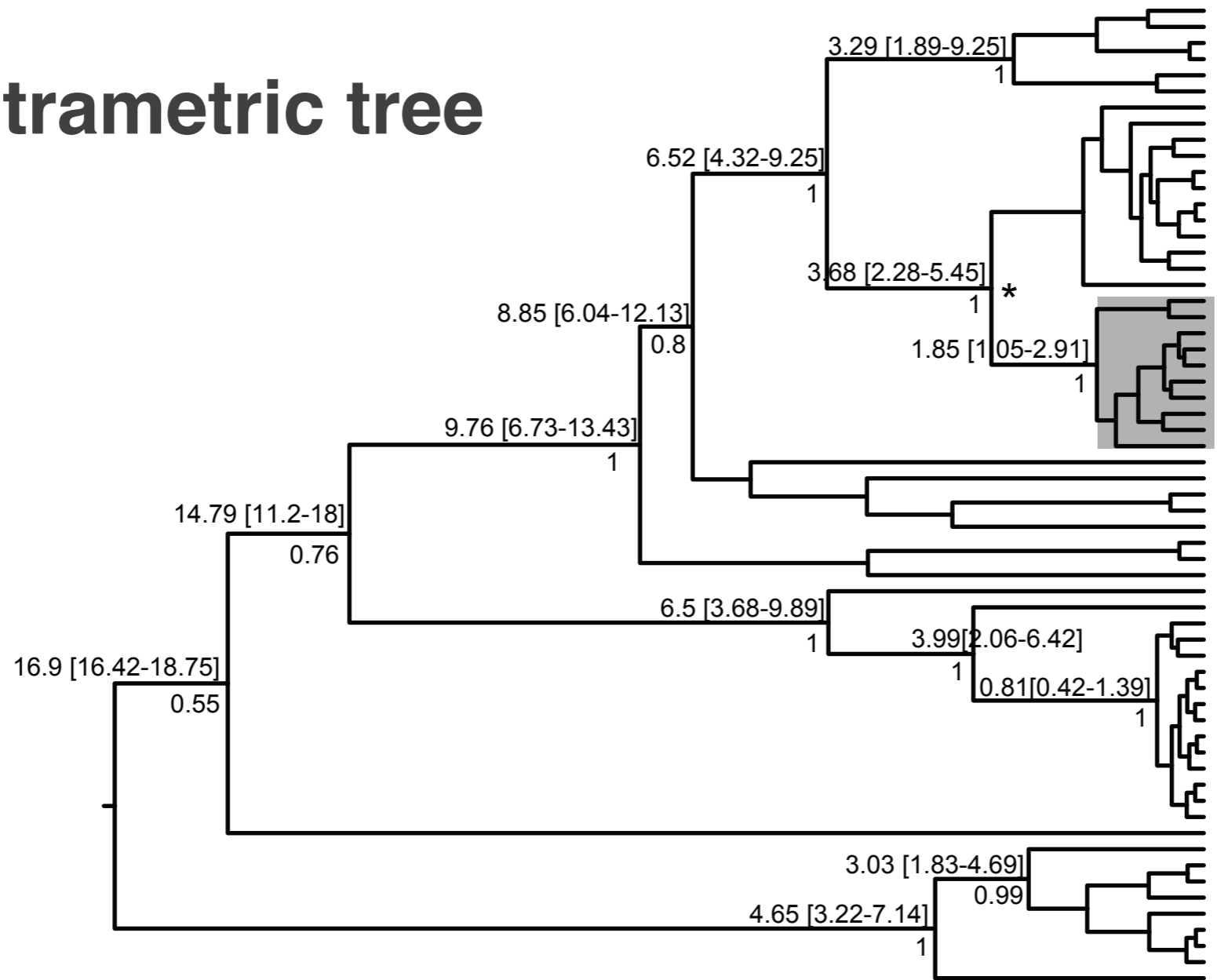


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0.002 subs. per site

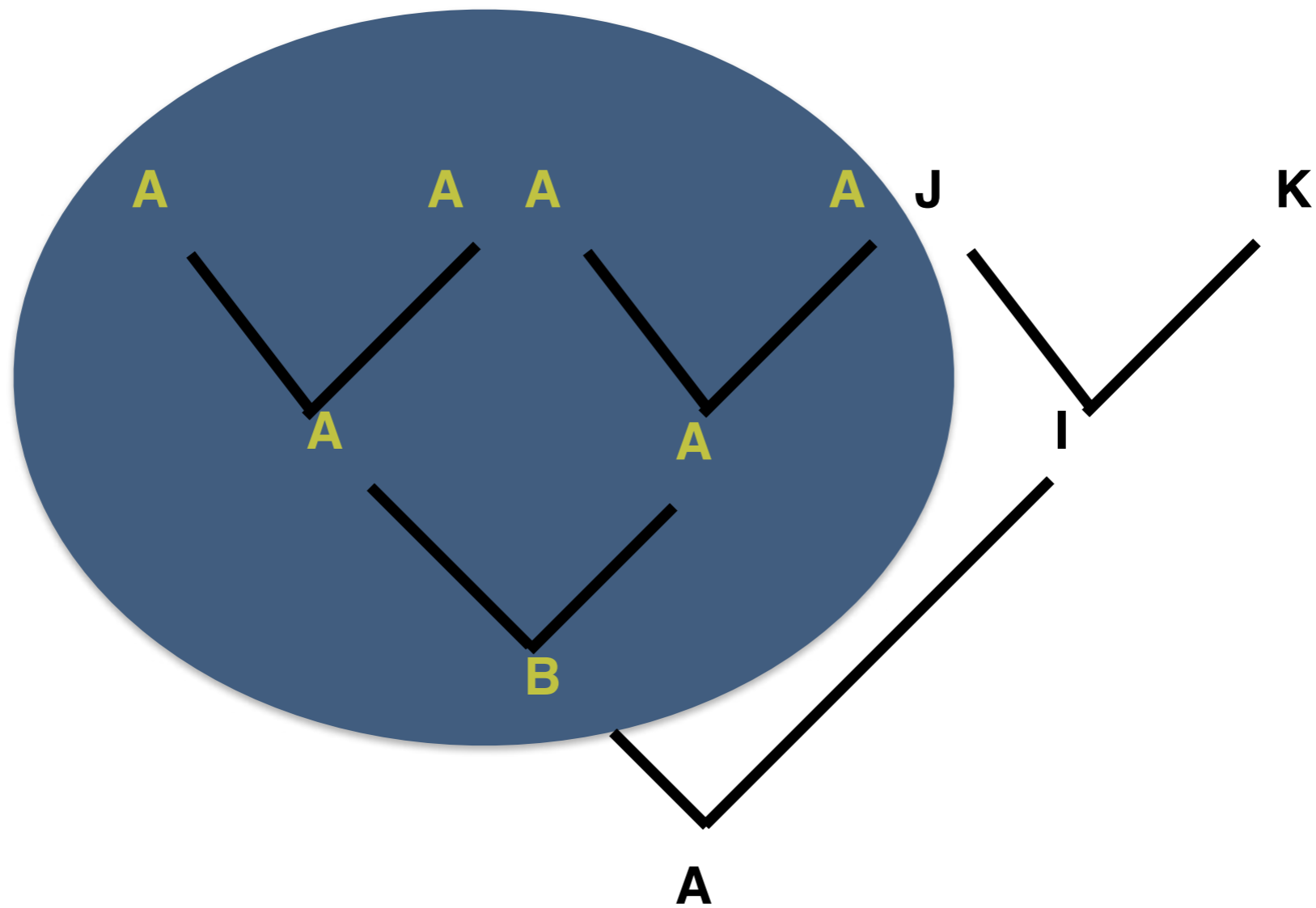
Cladogram



Ultrametric tree

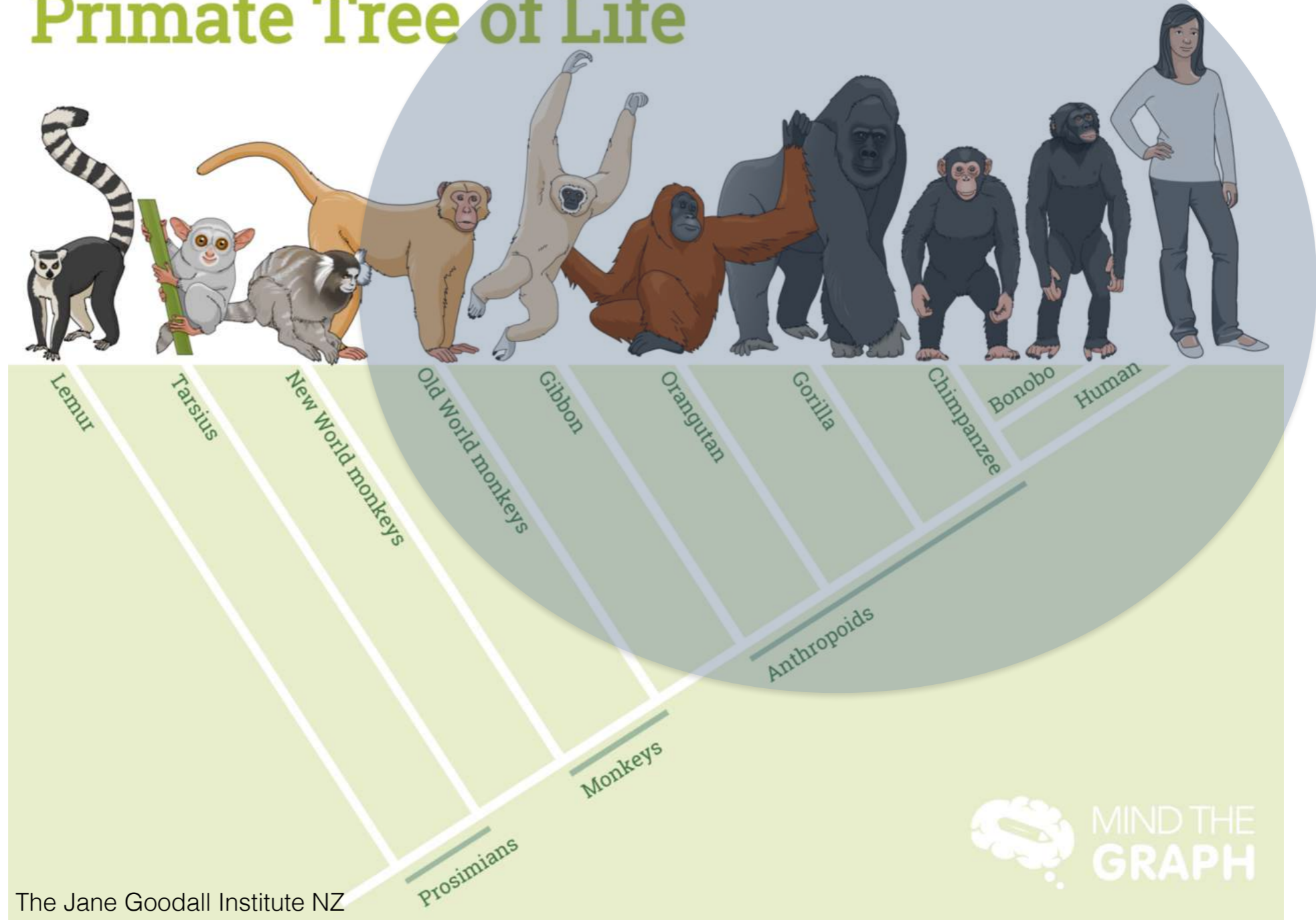


Taxon I



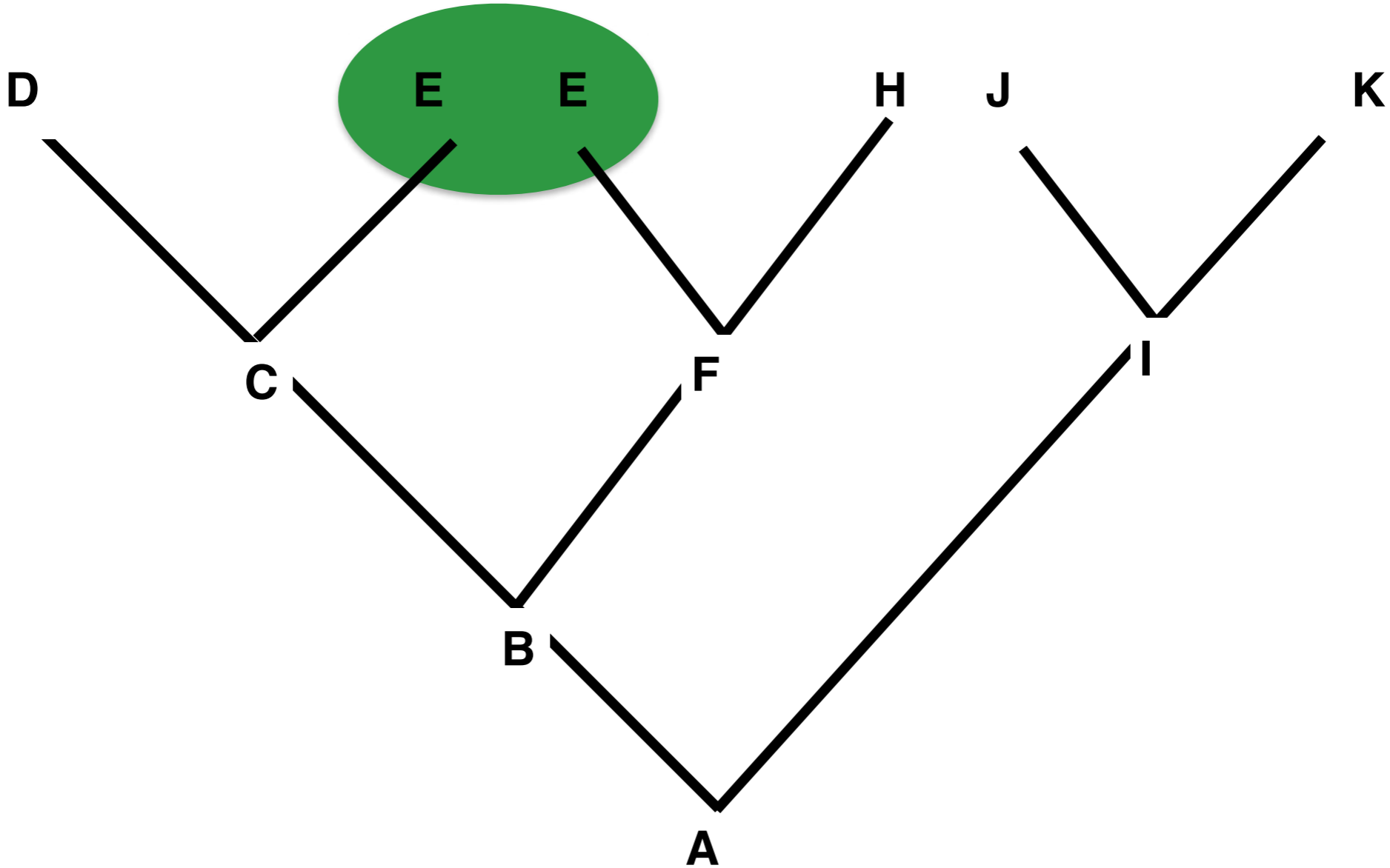
monophyletic

Primate Tree of Life

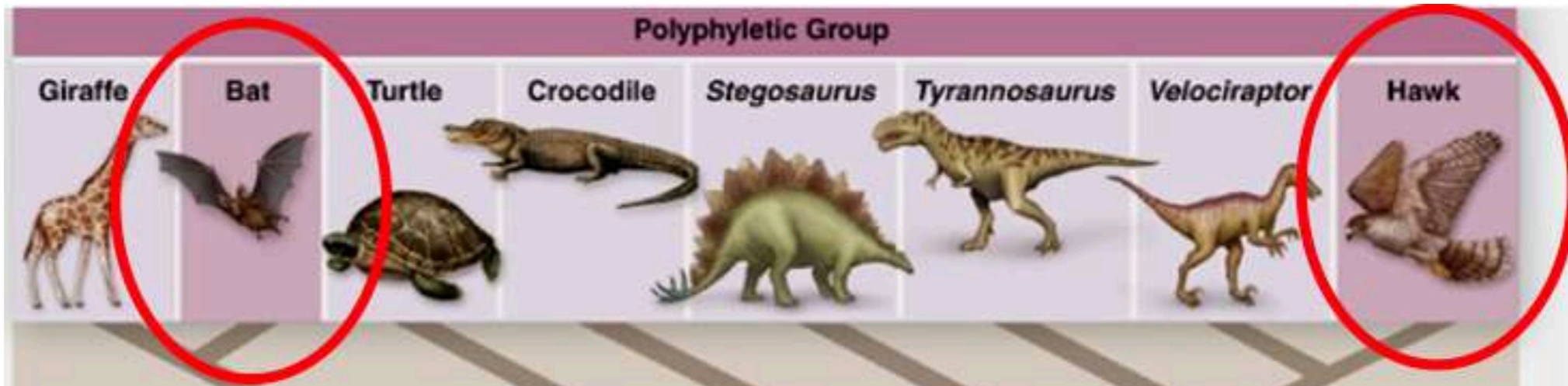


polyphyletic

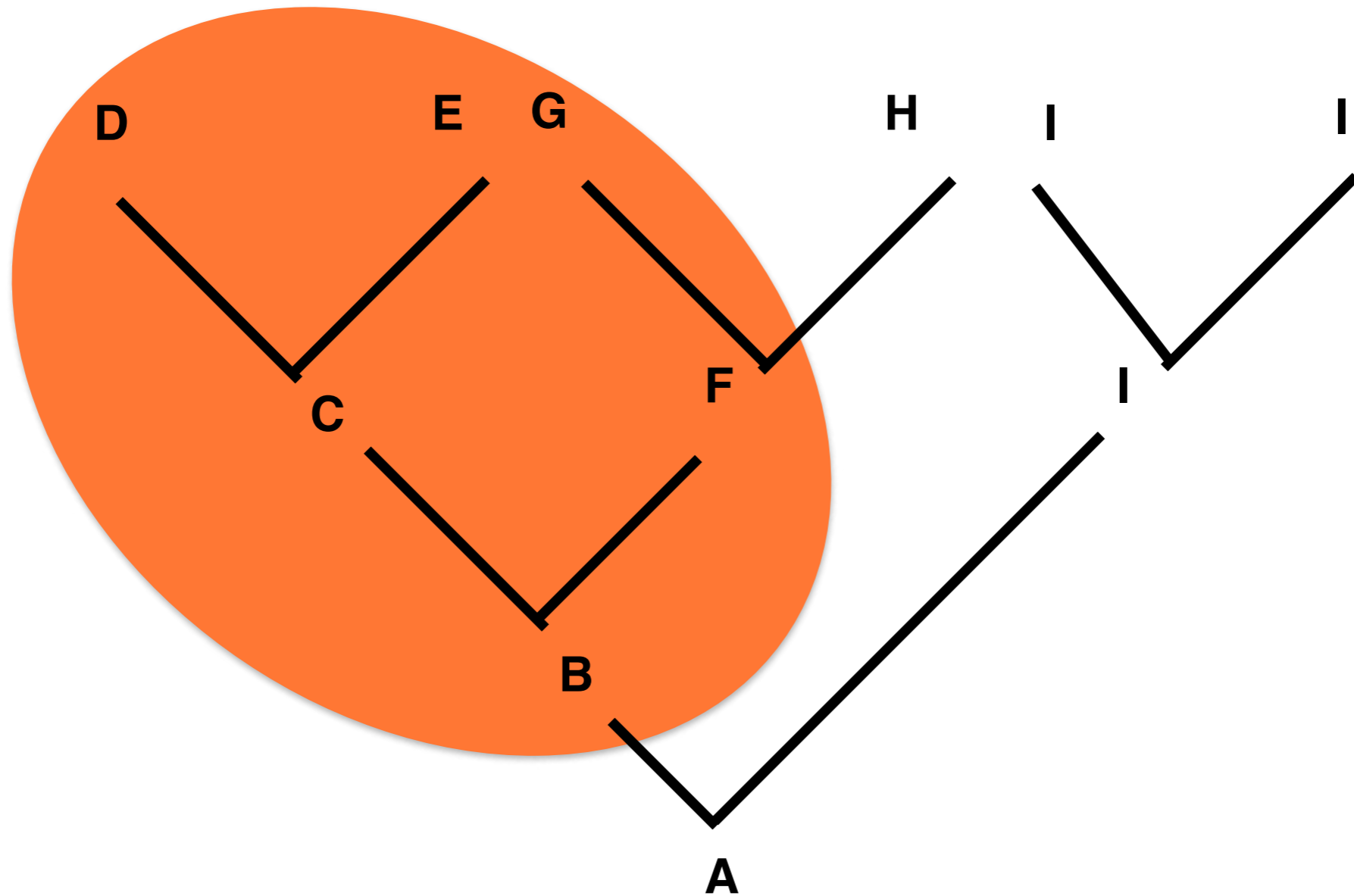
Taxon 2



polyphyletic

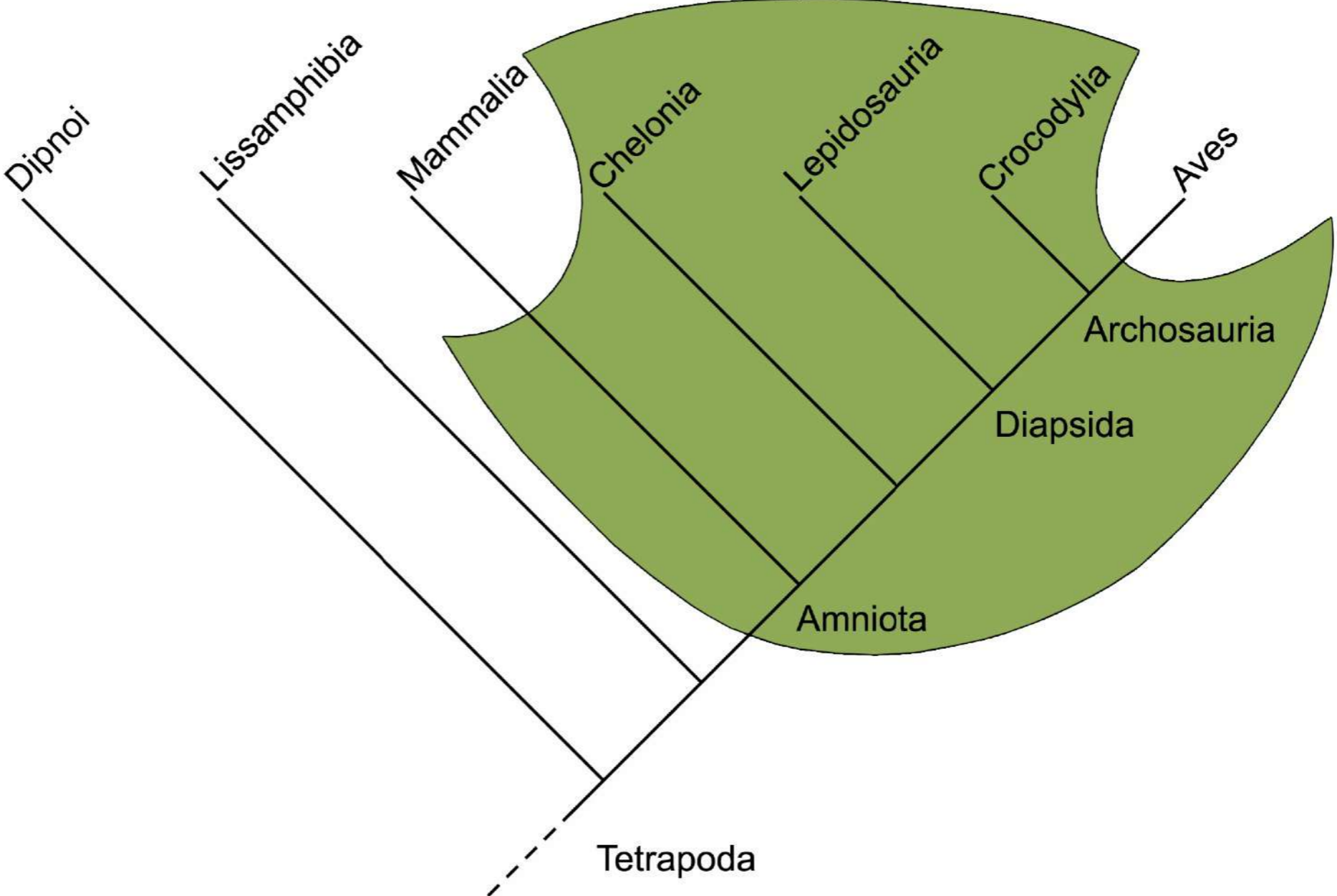


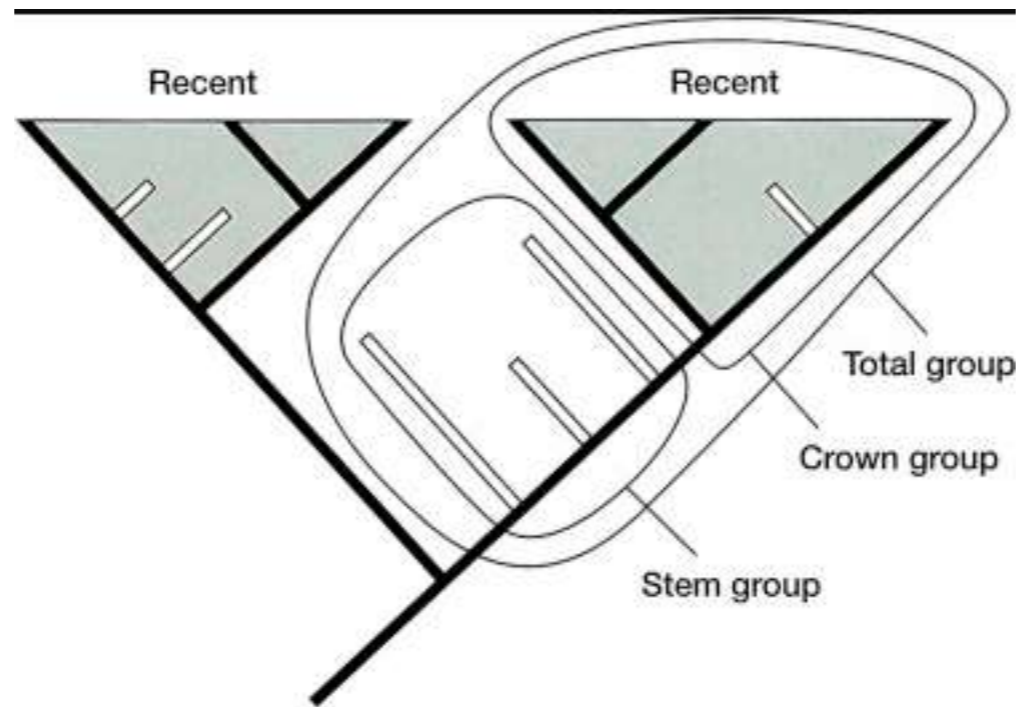
Taxon 3






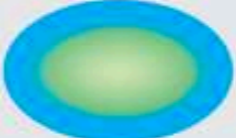








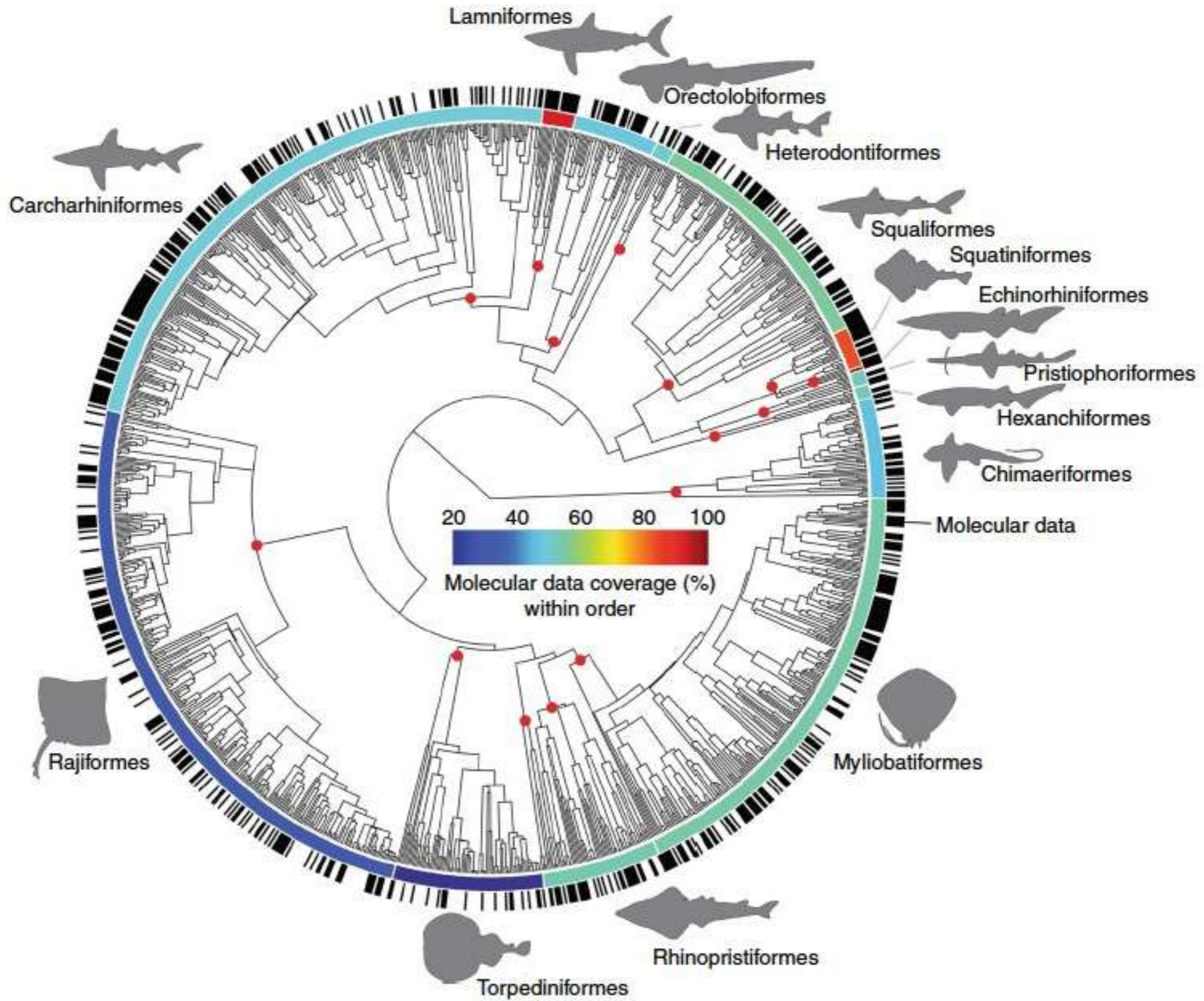
paraphyletic

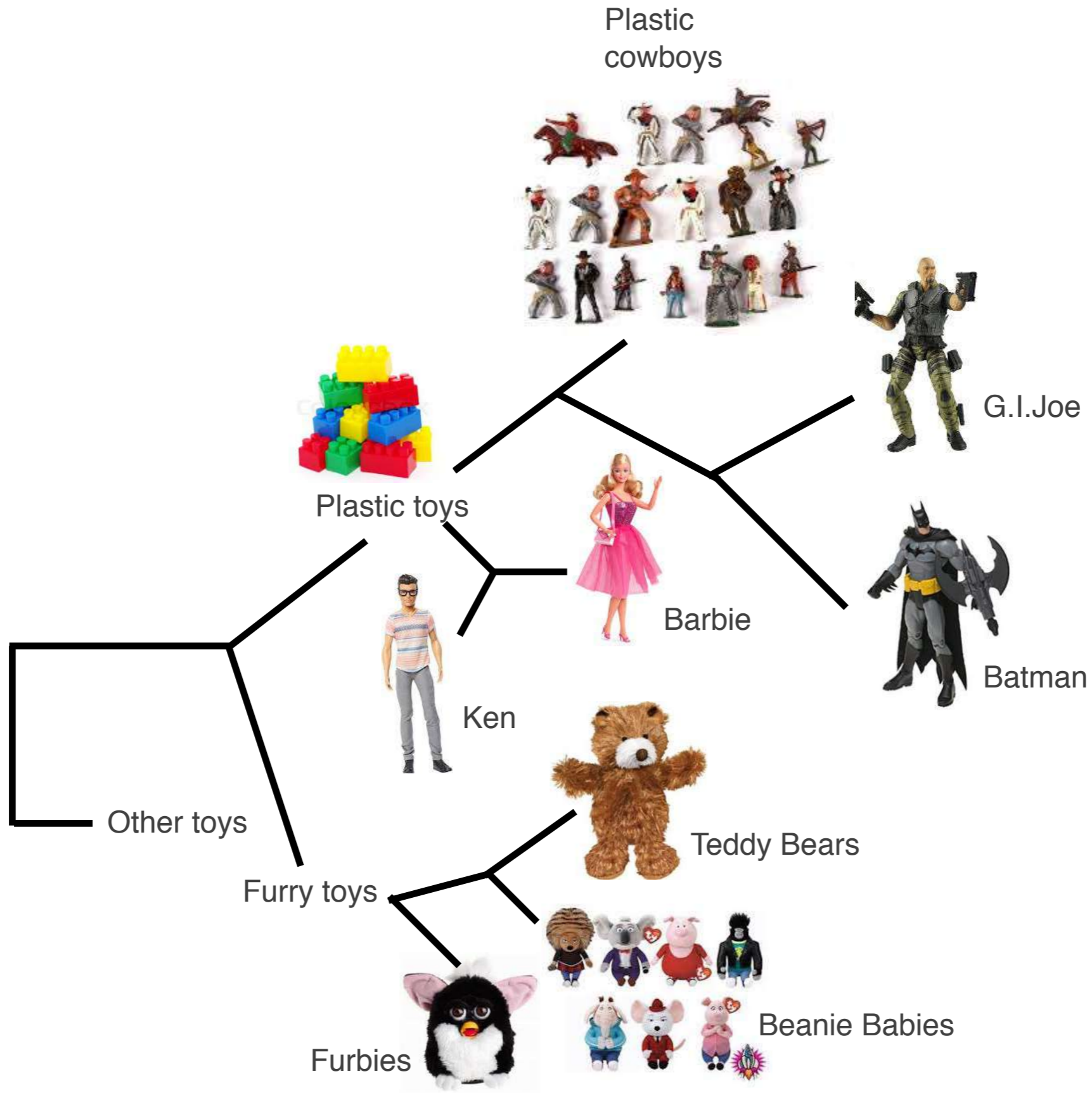
■ Reptilia





	Allopatric	Parapatric	Sympatric
Continuous population of one species			
Formation of barrier to gene flow	 Geographic barrier	 Adjacent habitat	 Trait polymorphism
Reproductive isolation occurs			
NO GENE FLOW			
Two new species are formed			





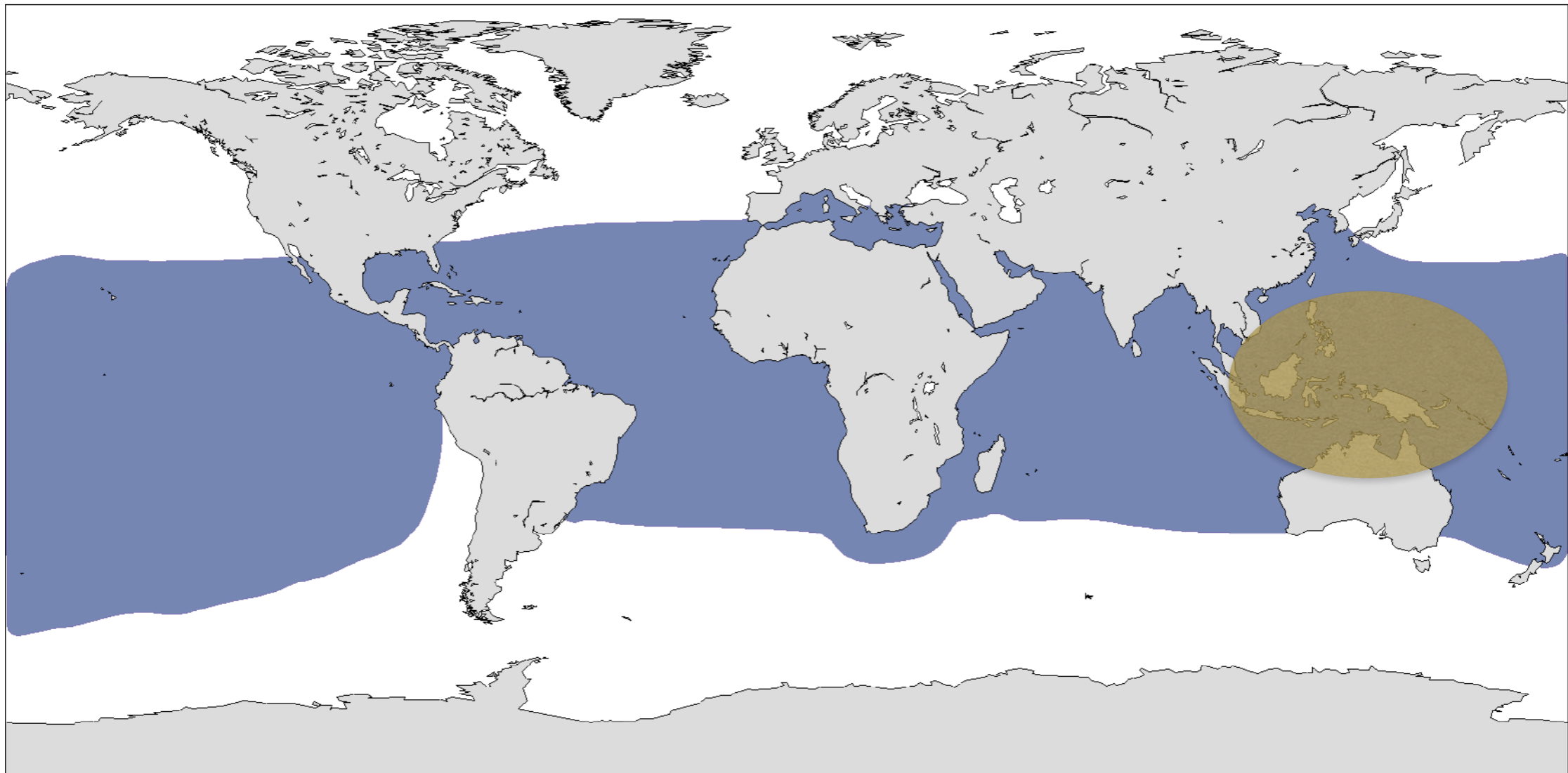
02

Model system: Cape Verde cone snails





Geographic distribution of the genus *Conus*



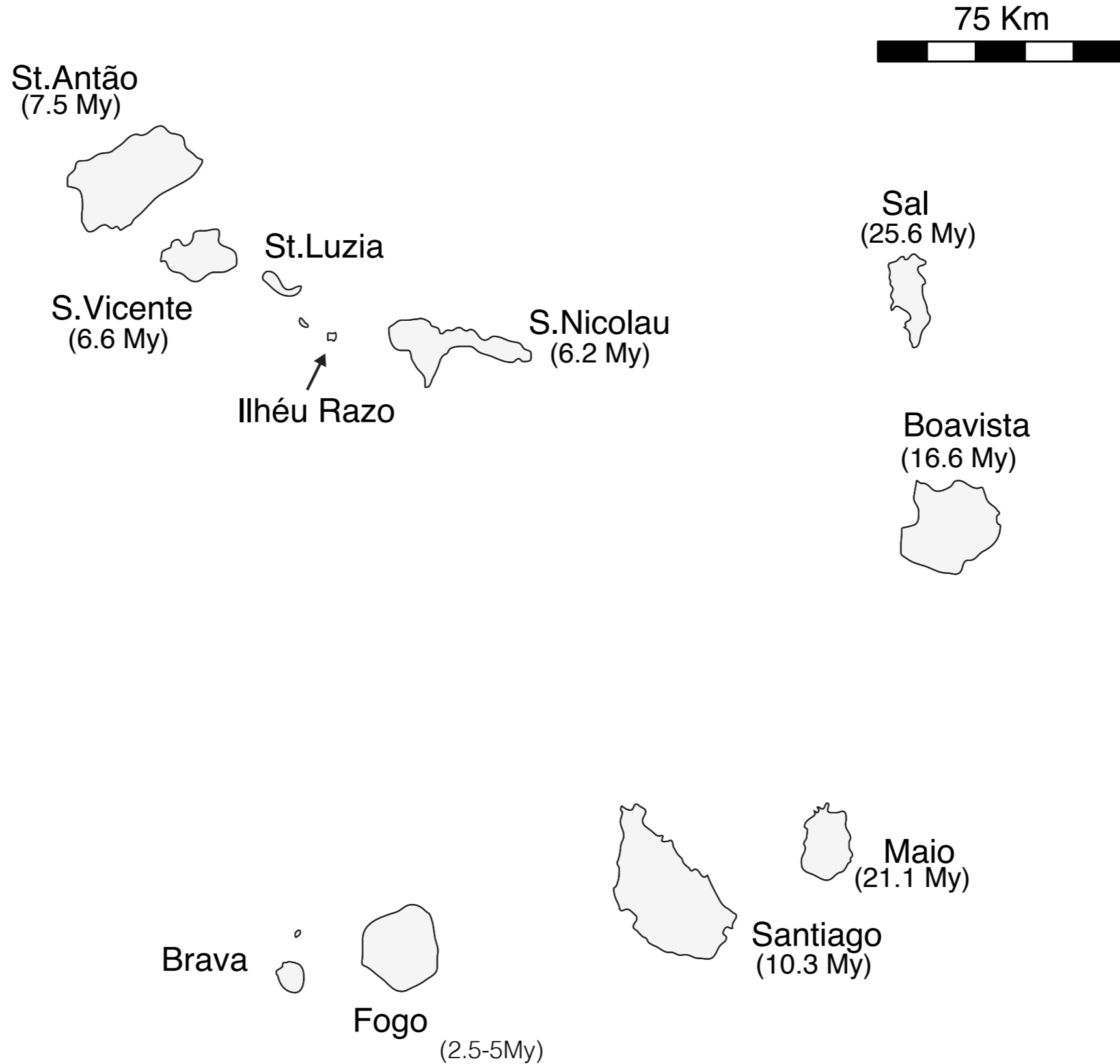
02

Model system: Cape Verde cone snails





Cape Verde Islands Geological ages



02

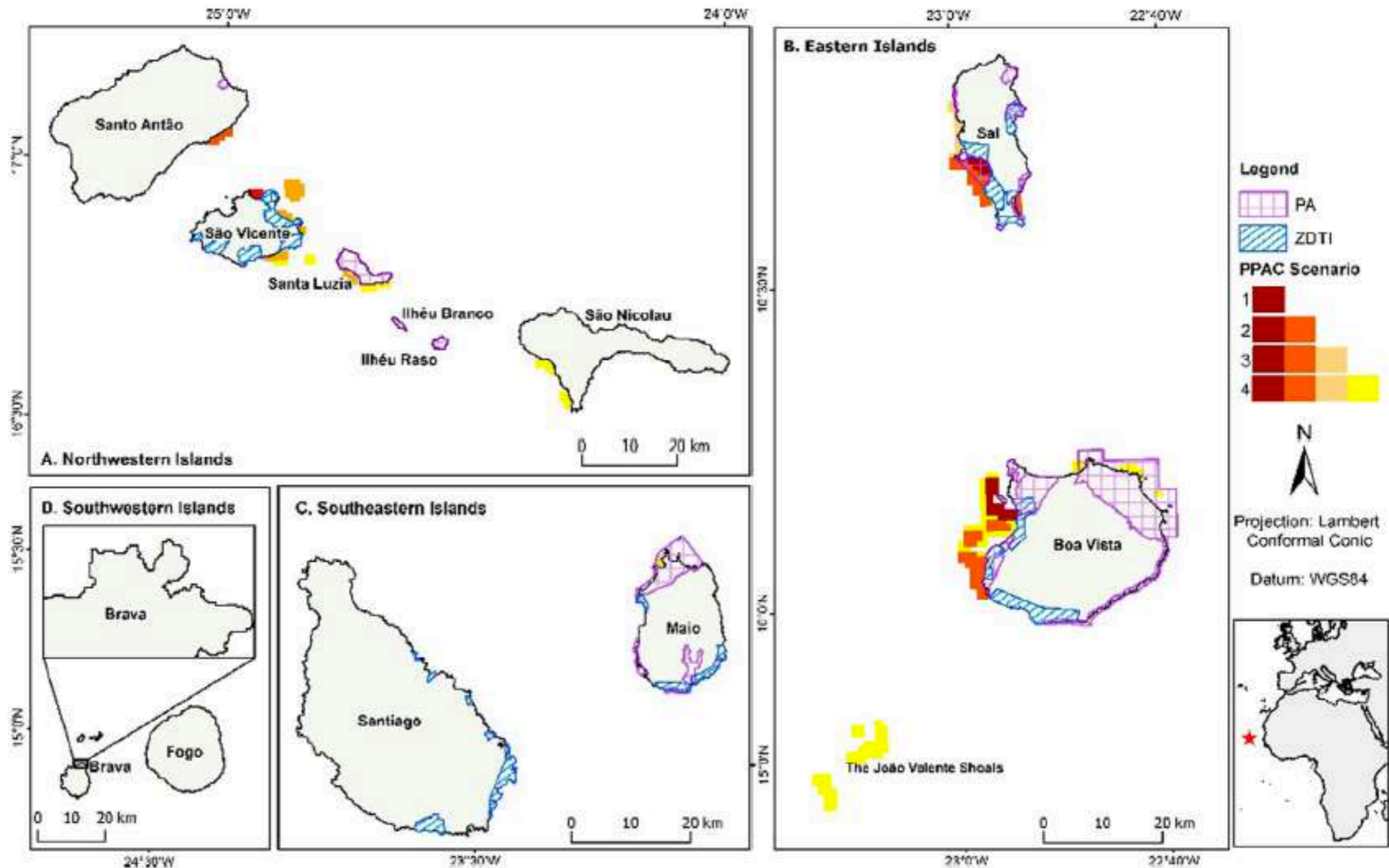
Fogo Island





Cape Verde Islands *Conus* PPACs

H. Peters et al. / *Global Ecology and Conservation* 7 (2016) 201–213



Cape Verde *Conus*

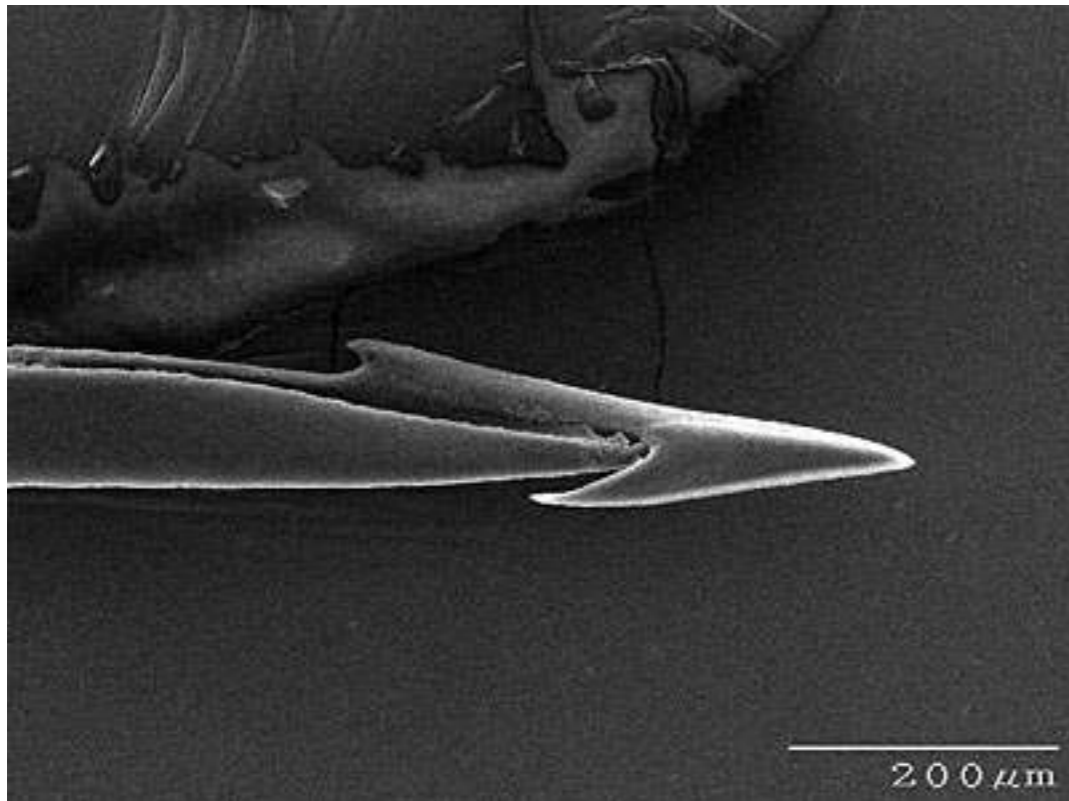
10%

≈ 60 endemics



The three main radula types in *Conus*

- a) vermivorous
- b) molluscivorous
- c) piscivorous



(a)



(b)



(c)



Larval development

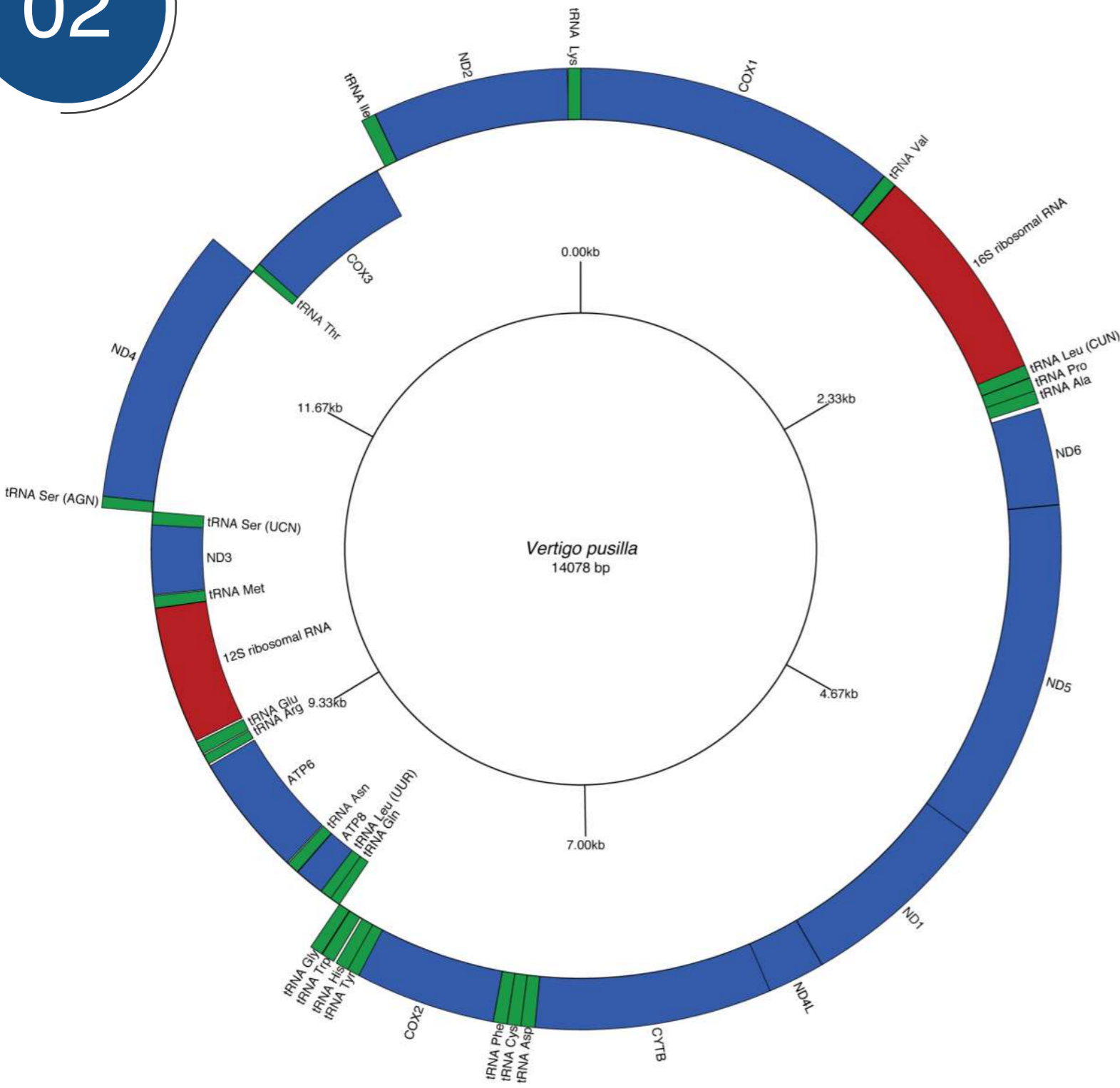


egg capsules

Habitat



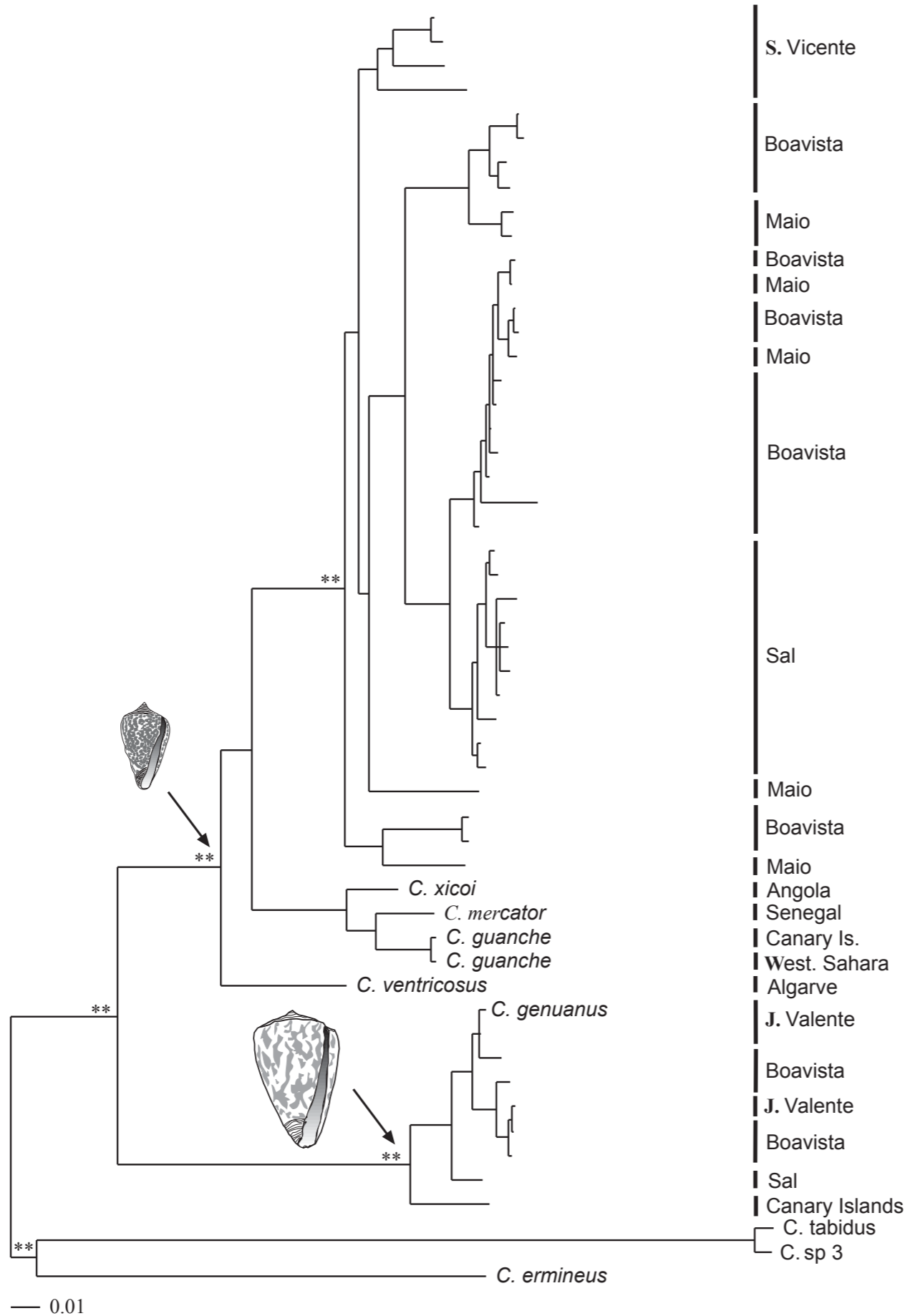
mtDNA circular molecule



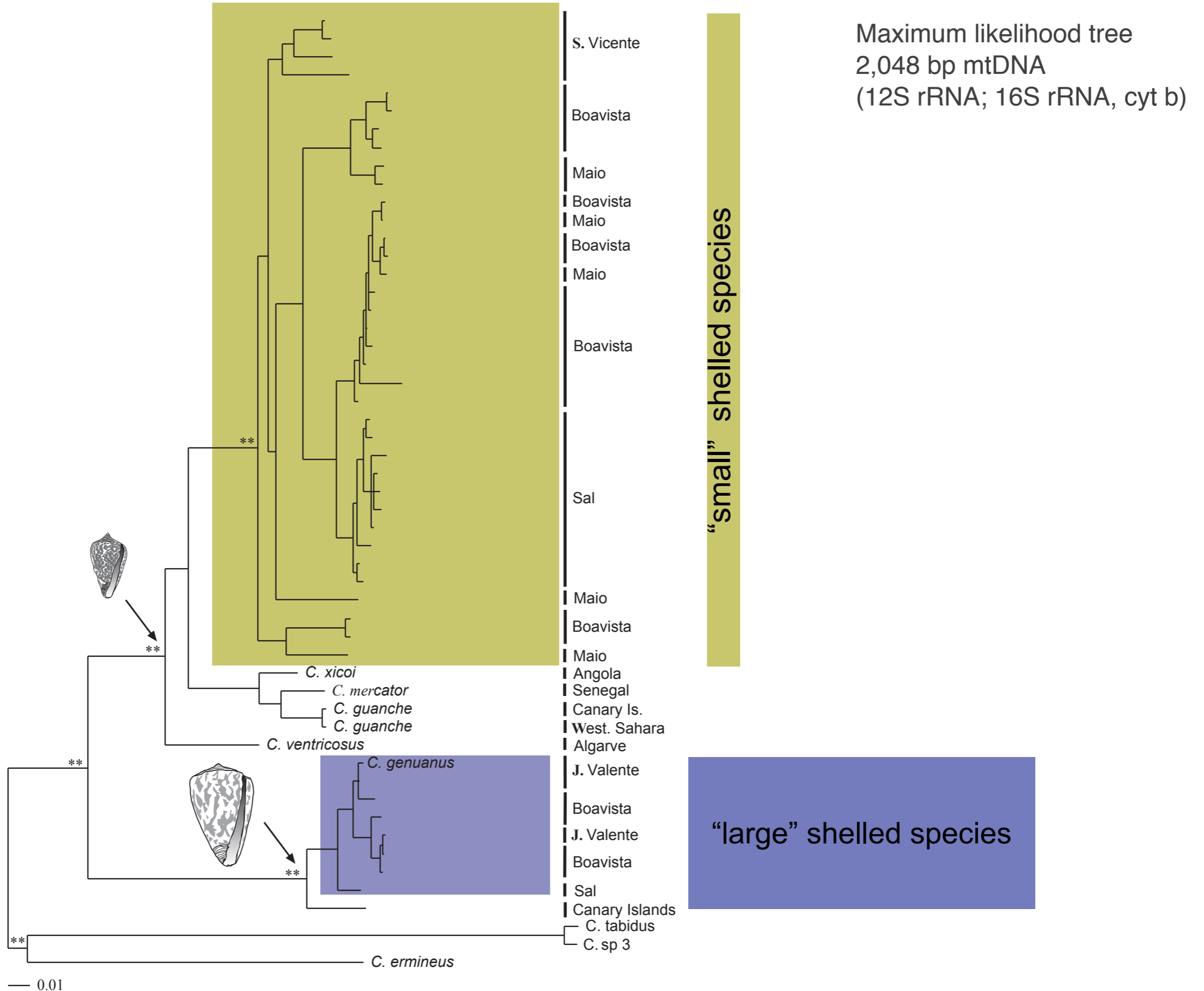
- 22 tRNAs
- 13 protein-coding genes
- 2 ribosomal RNAs

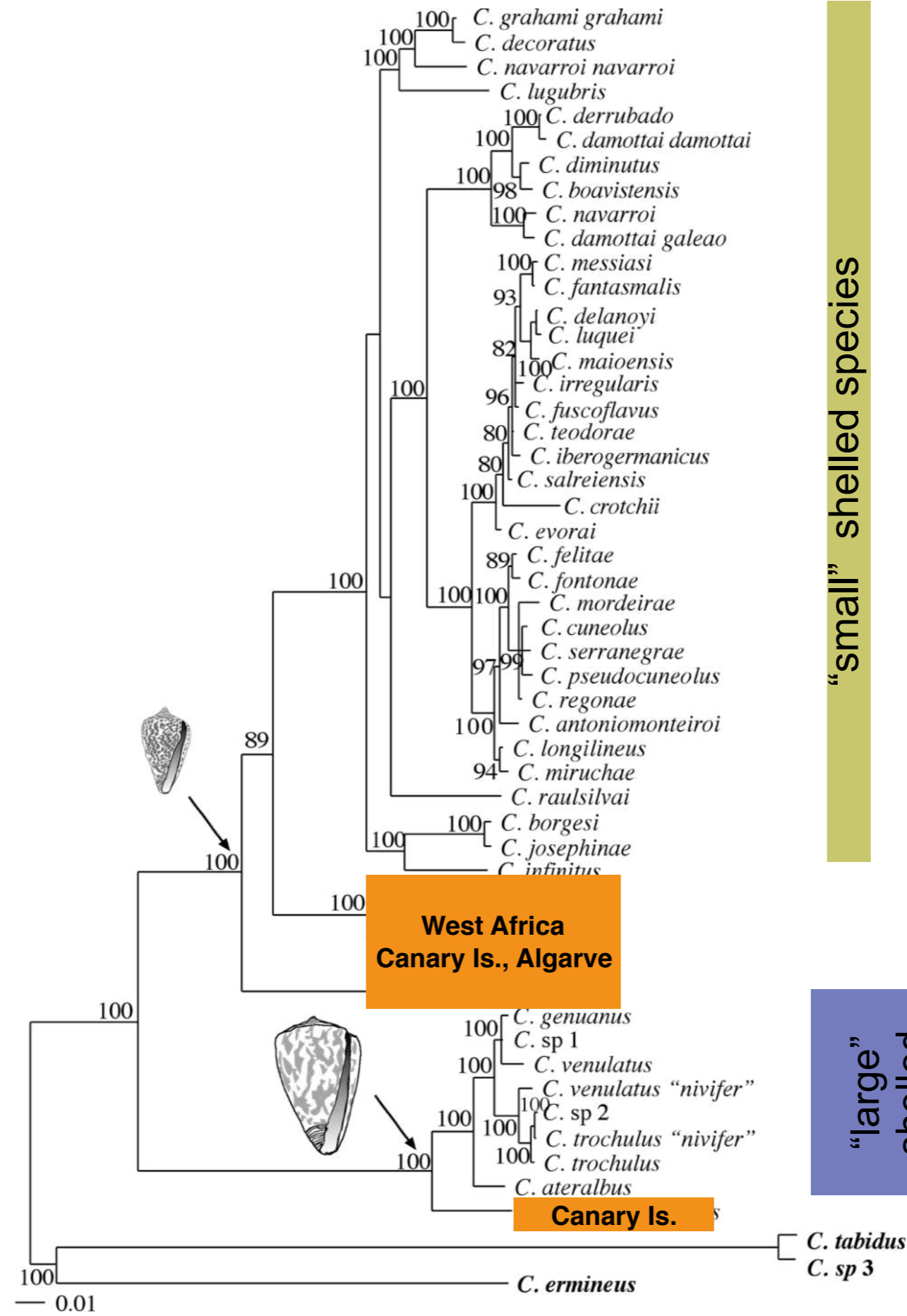
Molecular analyses

Maximum likelihood tree
 2,048 bp mtDNA
 (12S rRNA; 16S rRNA, cyt b)



Molecular analyses





Maximum likelihood tree
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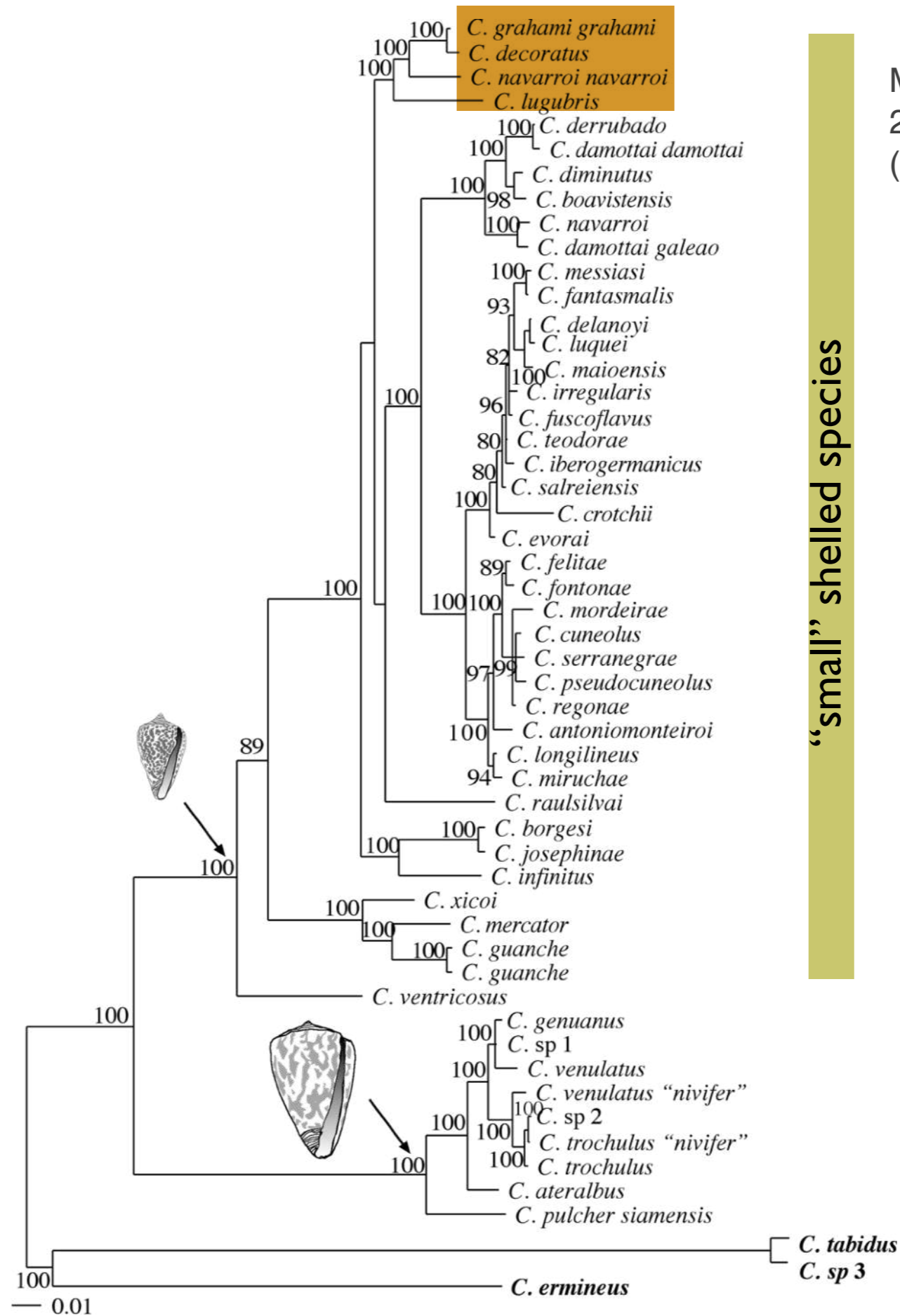
“small” shelled species

“large” shelled species

West Africa
 Canary Is., Algarve

Canary Is.

0.01

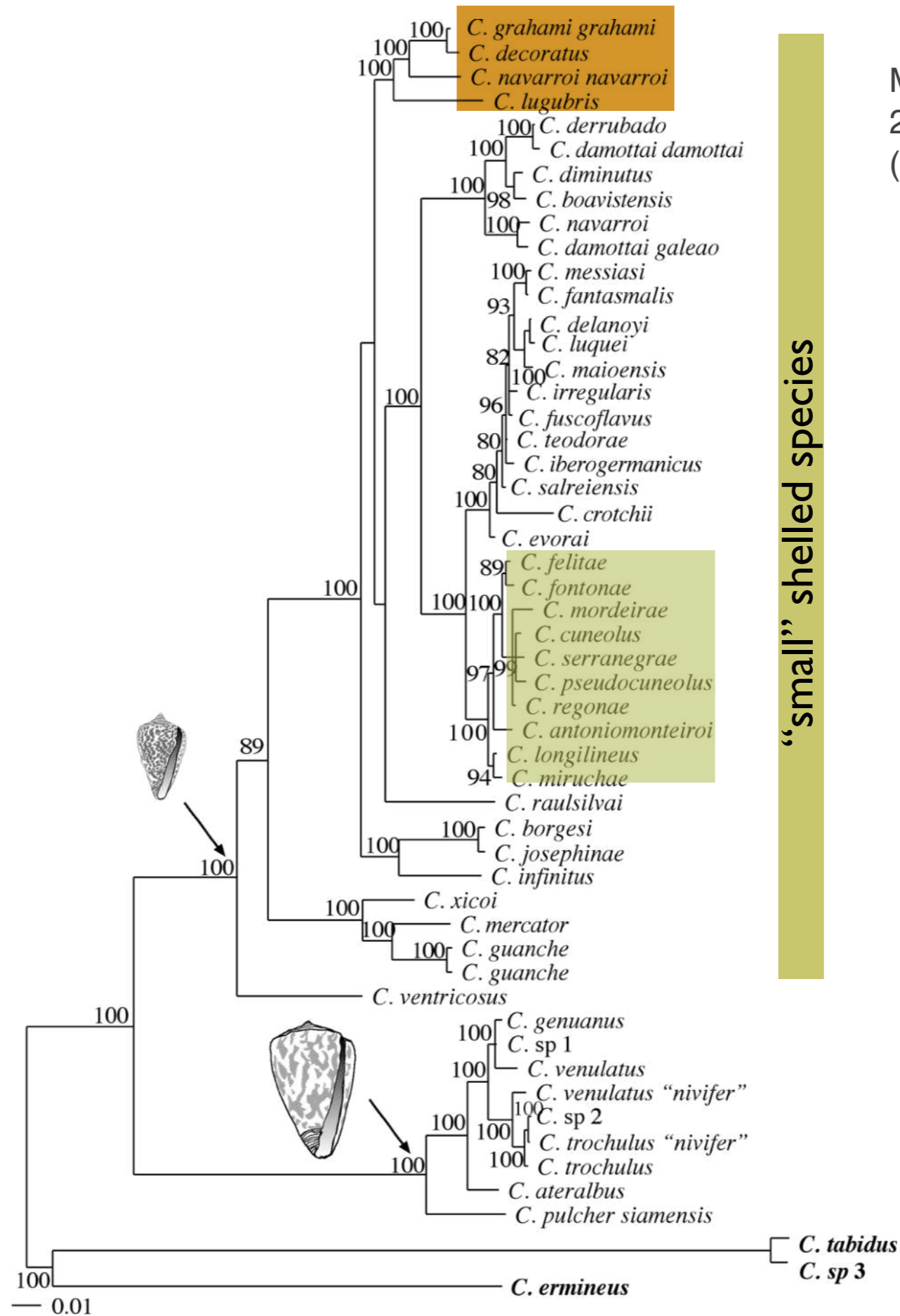


Maximum likelihood tree
2,048 bp mtDNA
(12S rRNA; 16S rRNA, cyt b)

“small” shelled species

S.Vicente

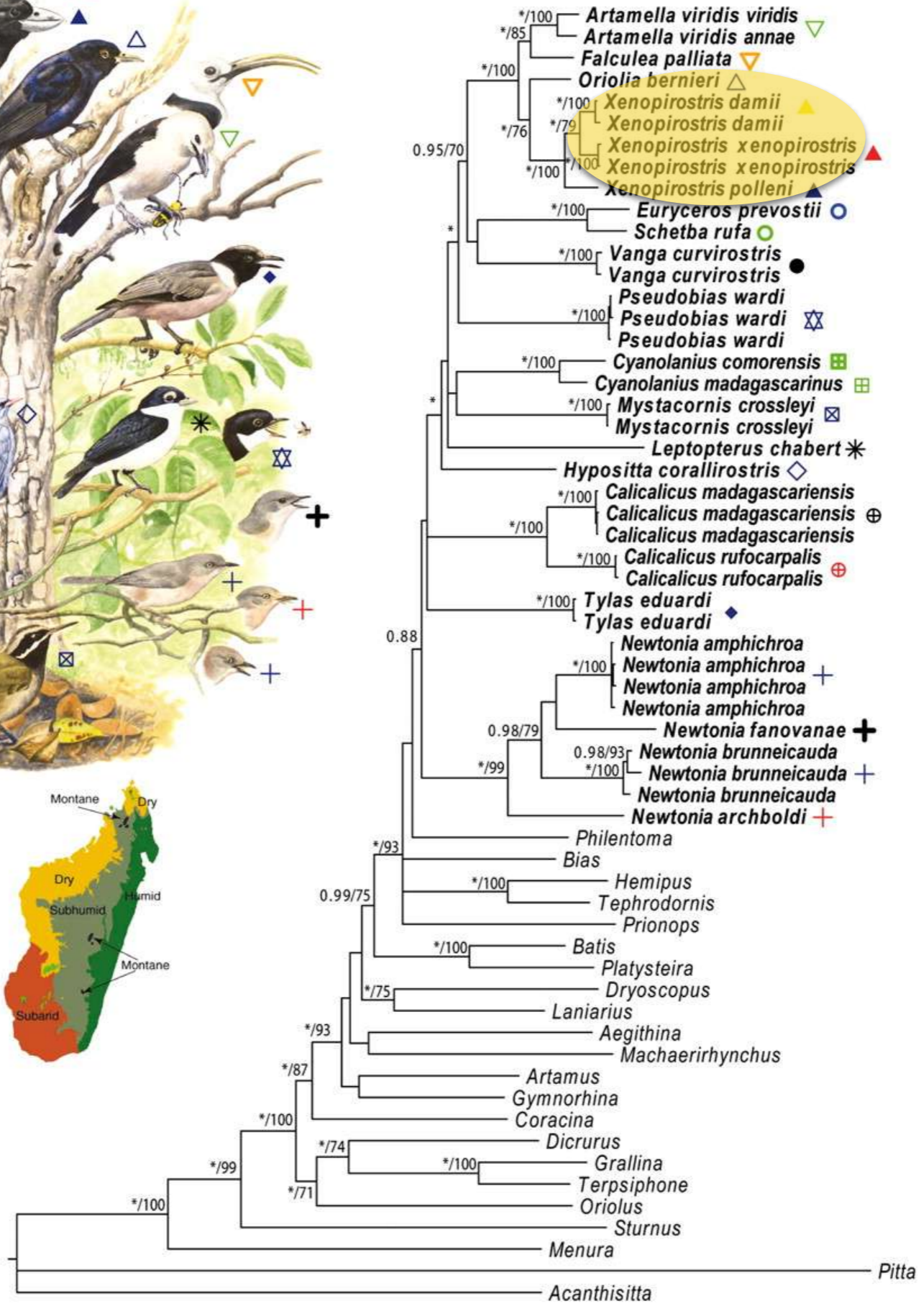
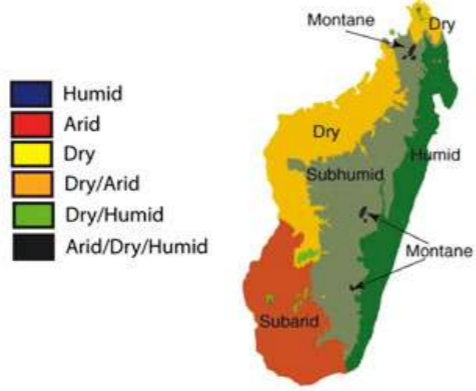
Sal

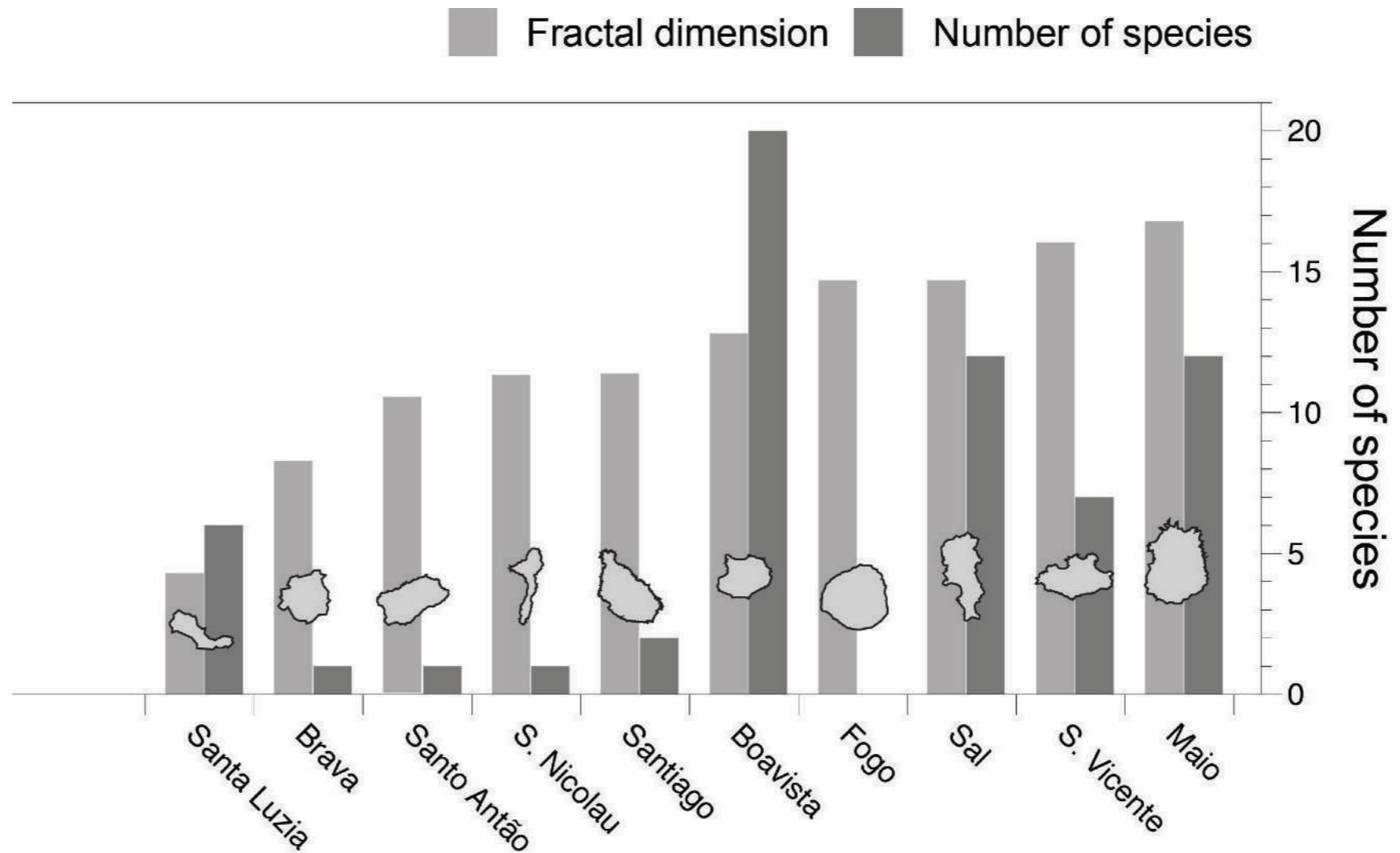


Maximum likelihood tree
2,048 bp mtDNA
(12S rRNA; 16S rRNA, cyt b)

“small” shelled species

Radiation of Madagascar birds of the family Vangidae



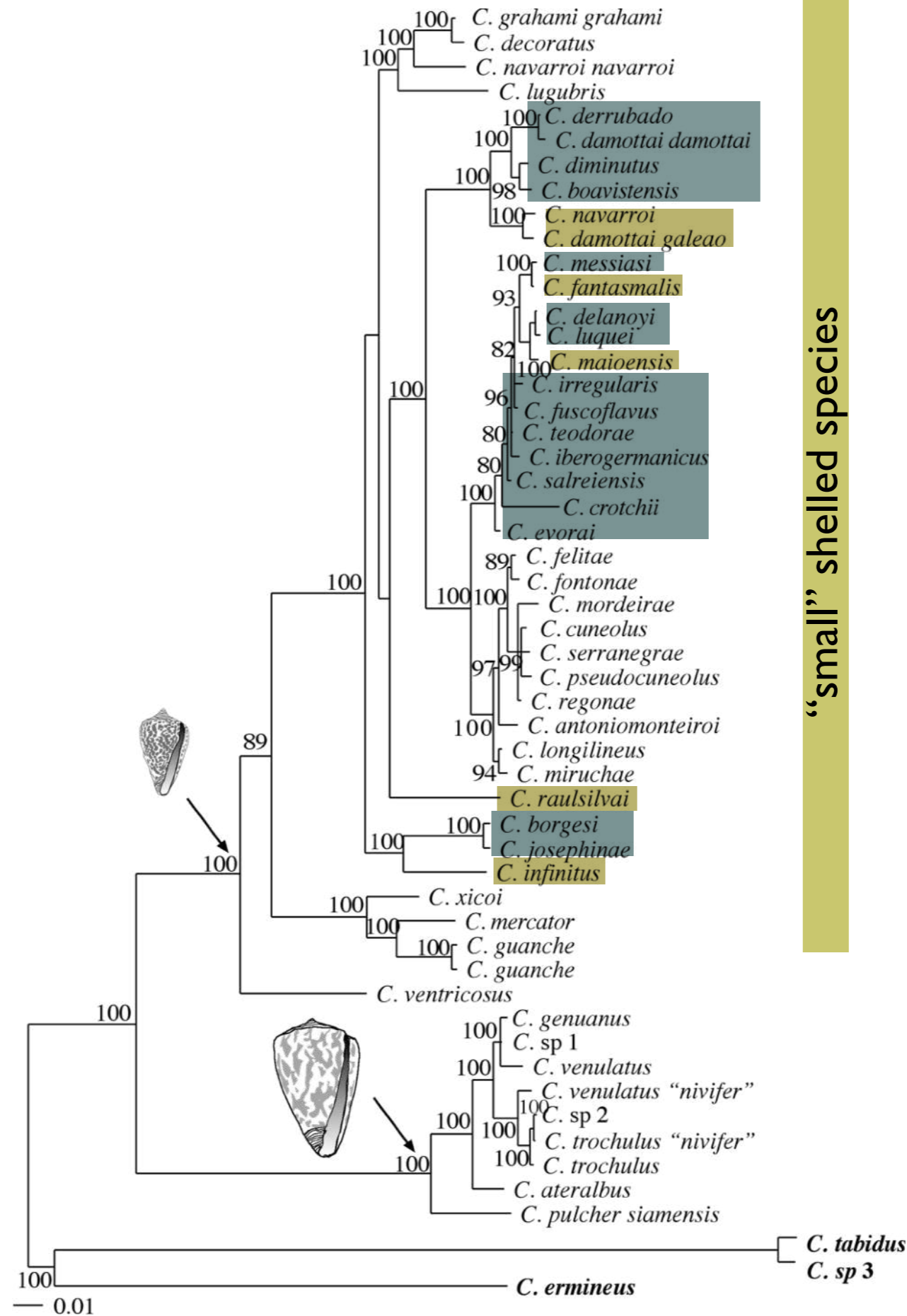


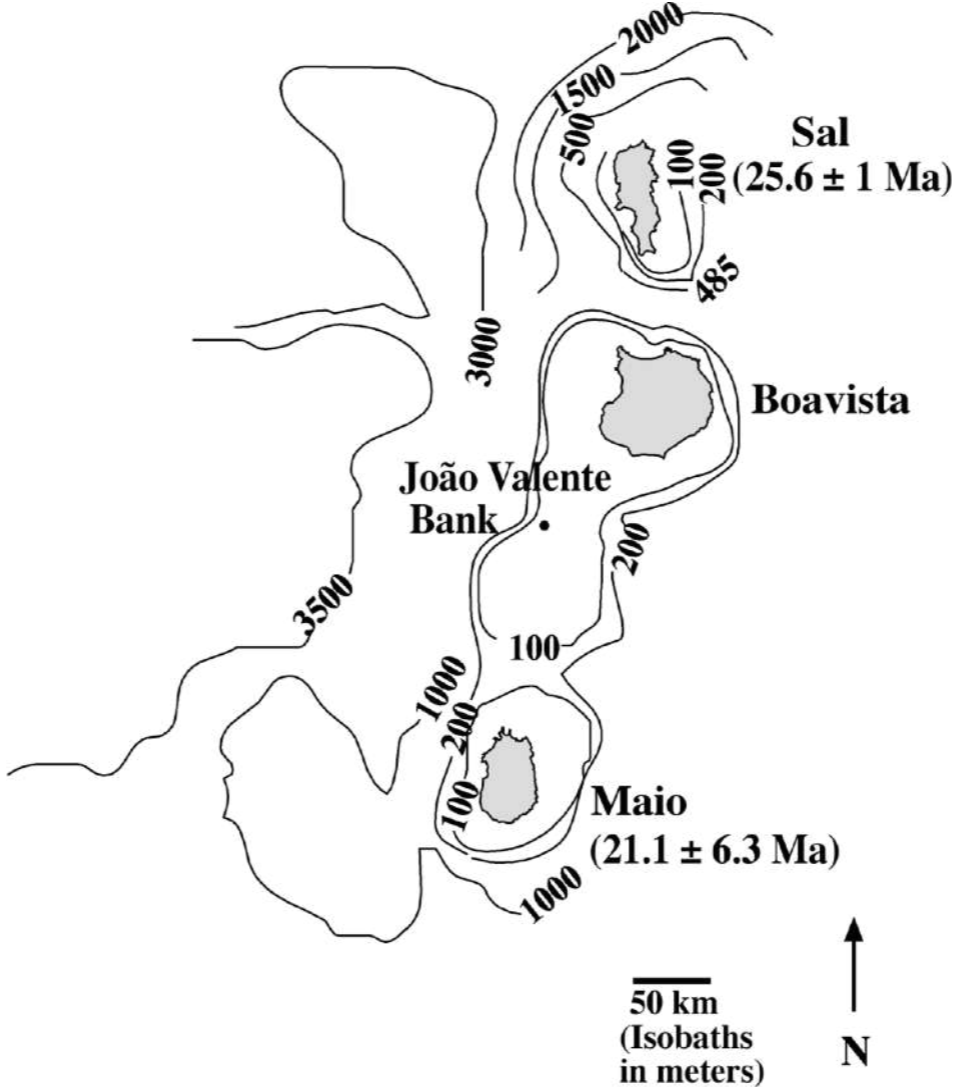
Cape Verde

Average fractal dimension = 1.432 ± 0.075

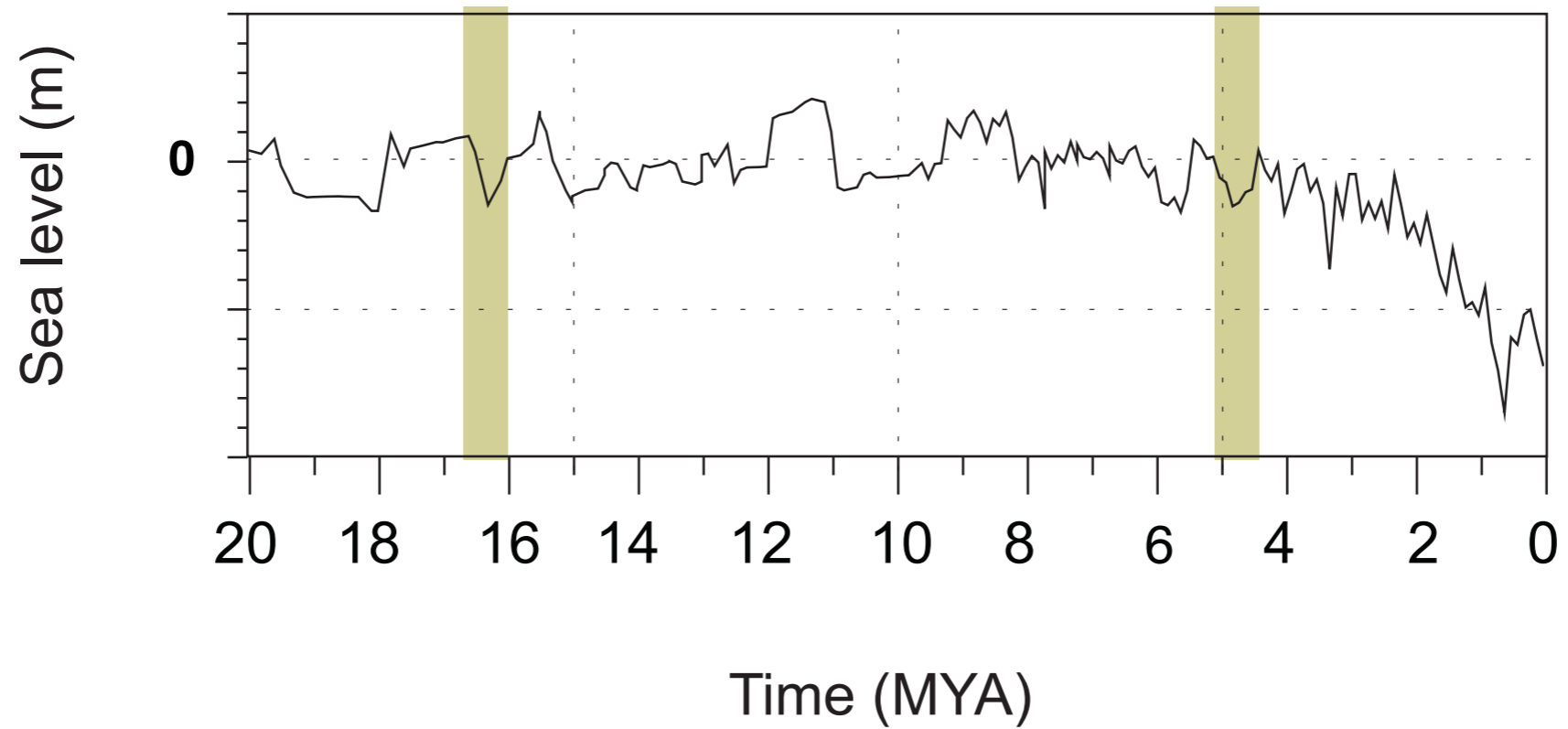
Boavista
Maio

Maximum likelihood tree
2,048 bp mtDNA
(12S rRNA; 16S rRNA, cyt b)



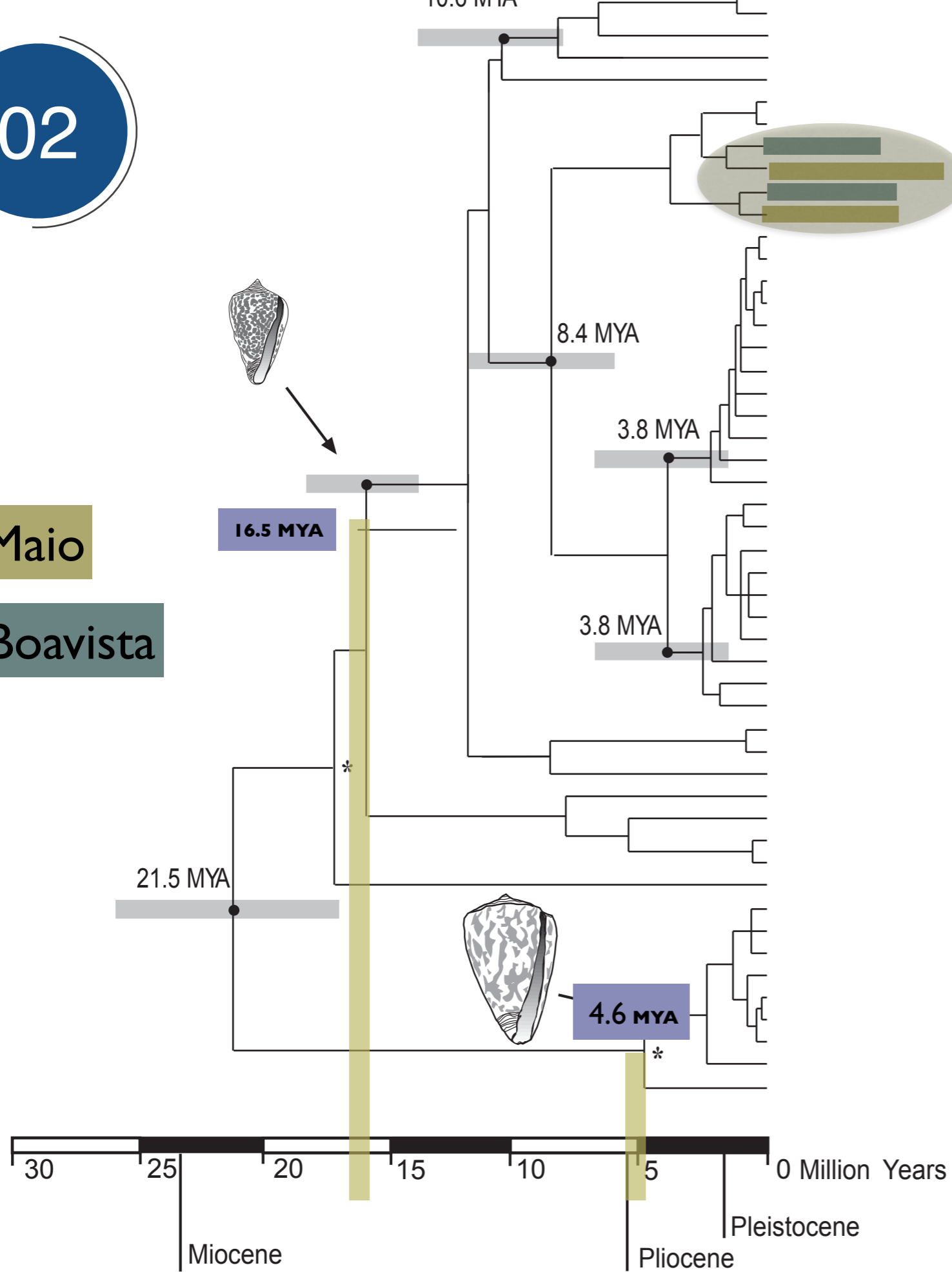


Eustatic sea level variations

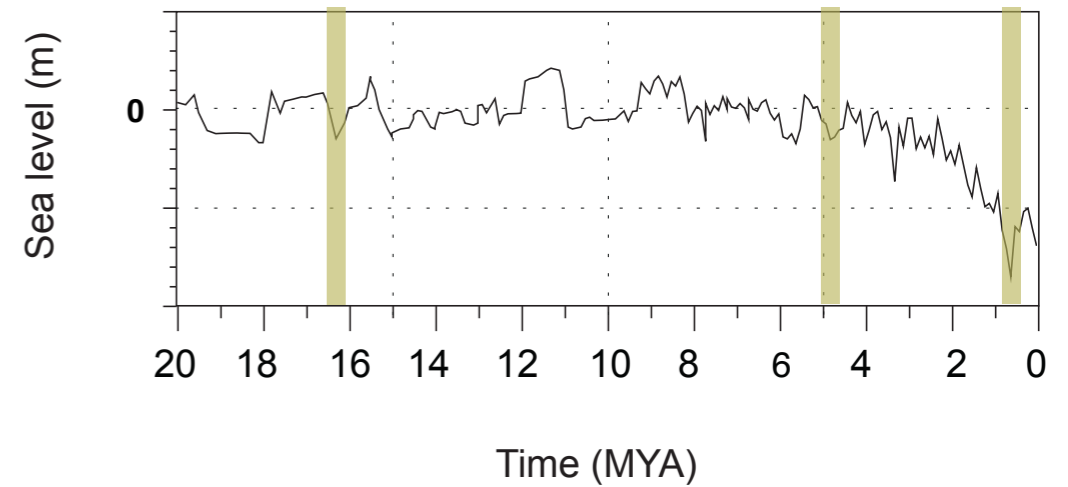


Dating analysis
2,048 bp mtDNA
(12S; 16S; cytB)

Maio
Boavista



Eustatic sea level variations



Why is Cape Verde so diverse?

- Isolation



- Allopatric speciation promoted by the reduced dispersal ability of the larvae

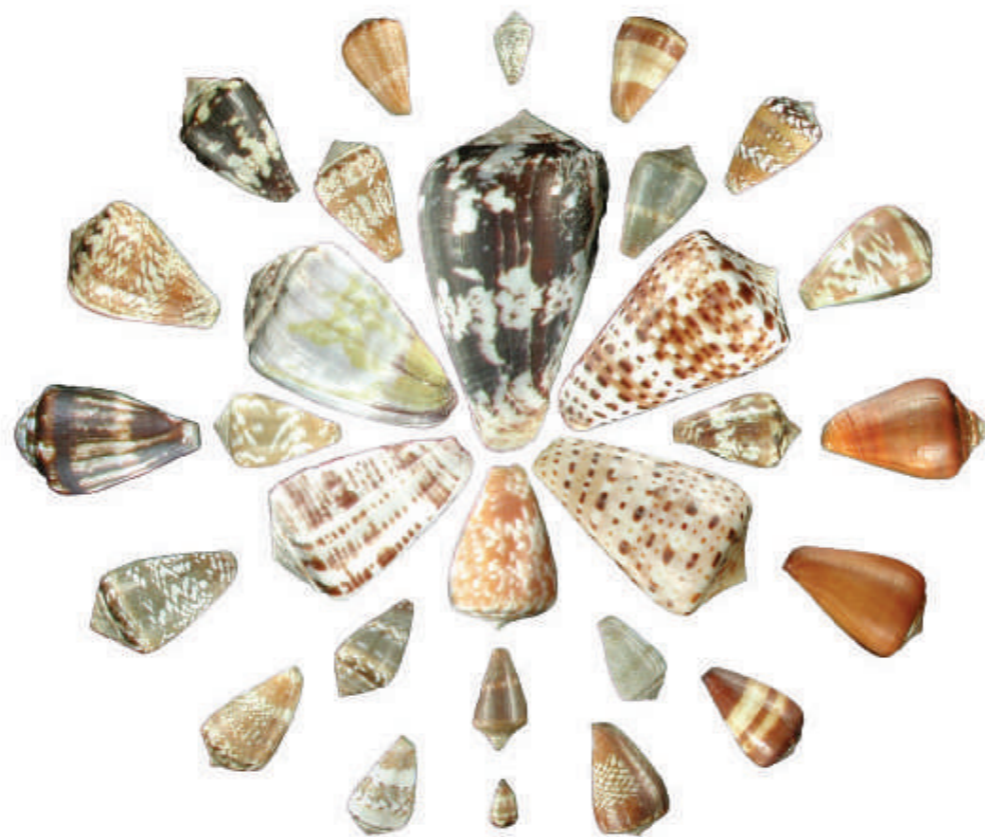


Patterns of Cladogenesis in the Venomous Marine Gastropod Genus *Conus* from the Cape Verde Islands

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