

stem ages, crown ages y SARS-CoV-2 en Colombia



Instituto Nacional de Salud
@INSColombia



Nextstrain @nextstrain · Mar 27

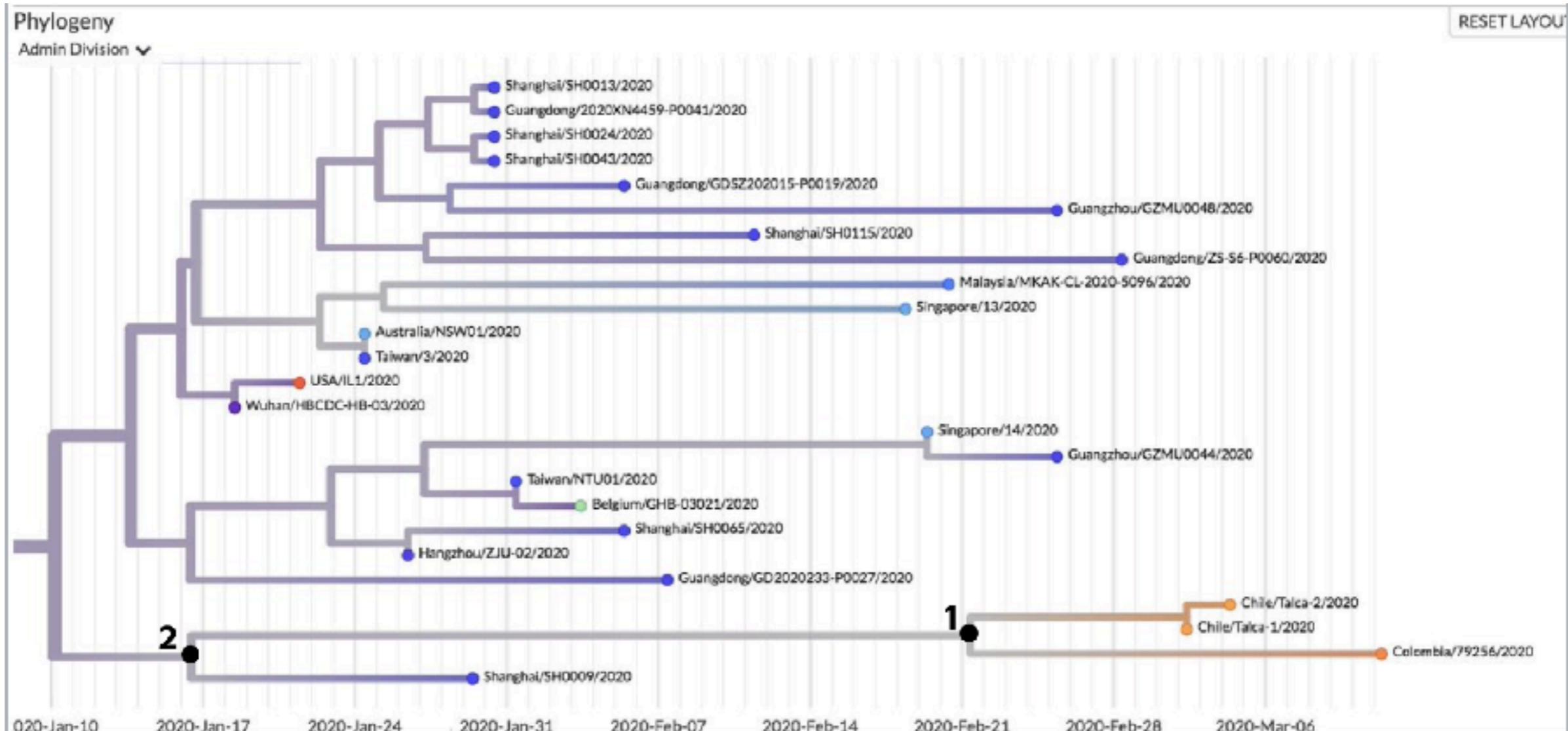
A huge thanks to @INSColombia, @UCooperativaCol, and data sharing from @GISaid, we now have our first genome from Colombia at nextstrain.org/nccv?f_country...! This virus nests with 2 viruses sampled from Chile, within a cluster otherwise containing viruses from China.

Investigadores del @INSColombia en alianza con @Inst_humboldt, @uccsm, @imperialcollege, @MRC_outbreak, @LSHTM, obtienen la primera secuencia de genoma de SARS-CoV2 circulante en #Colombia. Aporte al estudio de la pandemia de COVID-19.

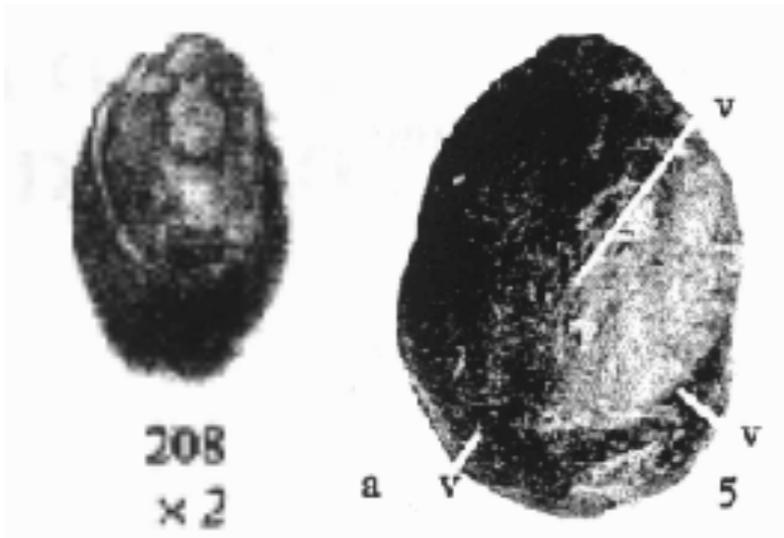
Hilo

[Translate Tweet](#)

9:17 AM · Mar 29, 2020 · Twitter for iPhone



¿y exactamente dónde pongo mi fósil?



P. Fine & F. Zapata

Review

TRENDS in Plant Science Vol.10 No.11 November 2005

Full text provided by www.ultrafind.com



Relaxed molecular clocks for dating historical plant dispersal events

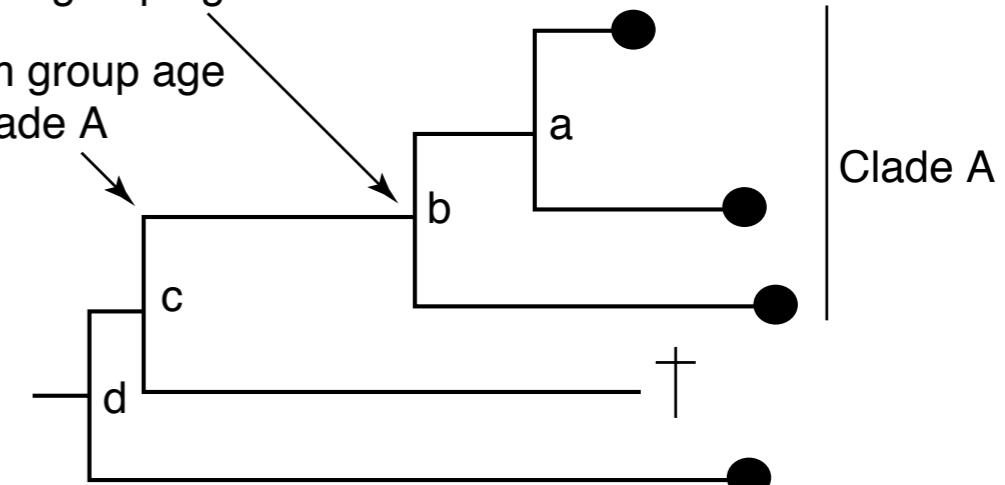
Susanne S. Renner

(a)

- Extant taxon
- + Extinct taxon

Crown group age of clade A

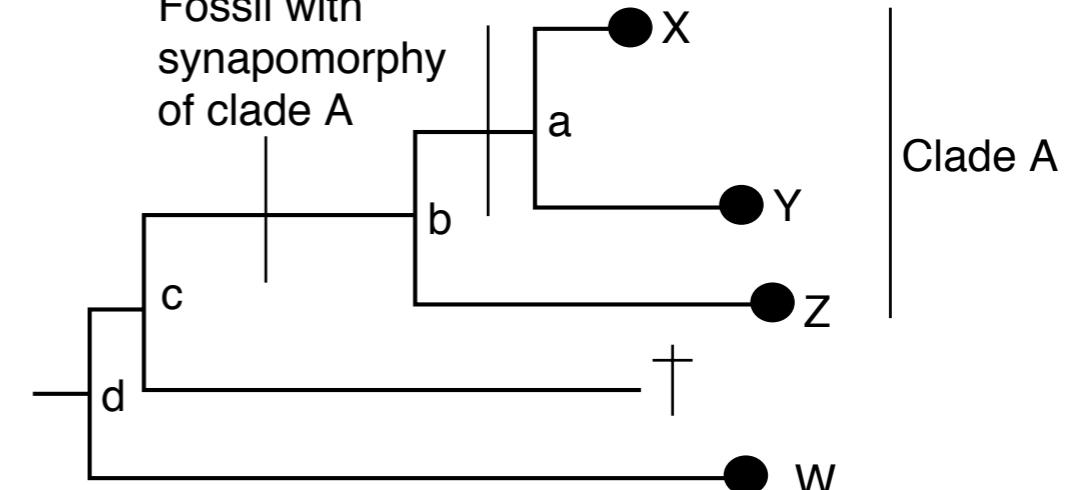
Stem group age
of clade A



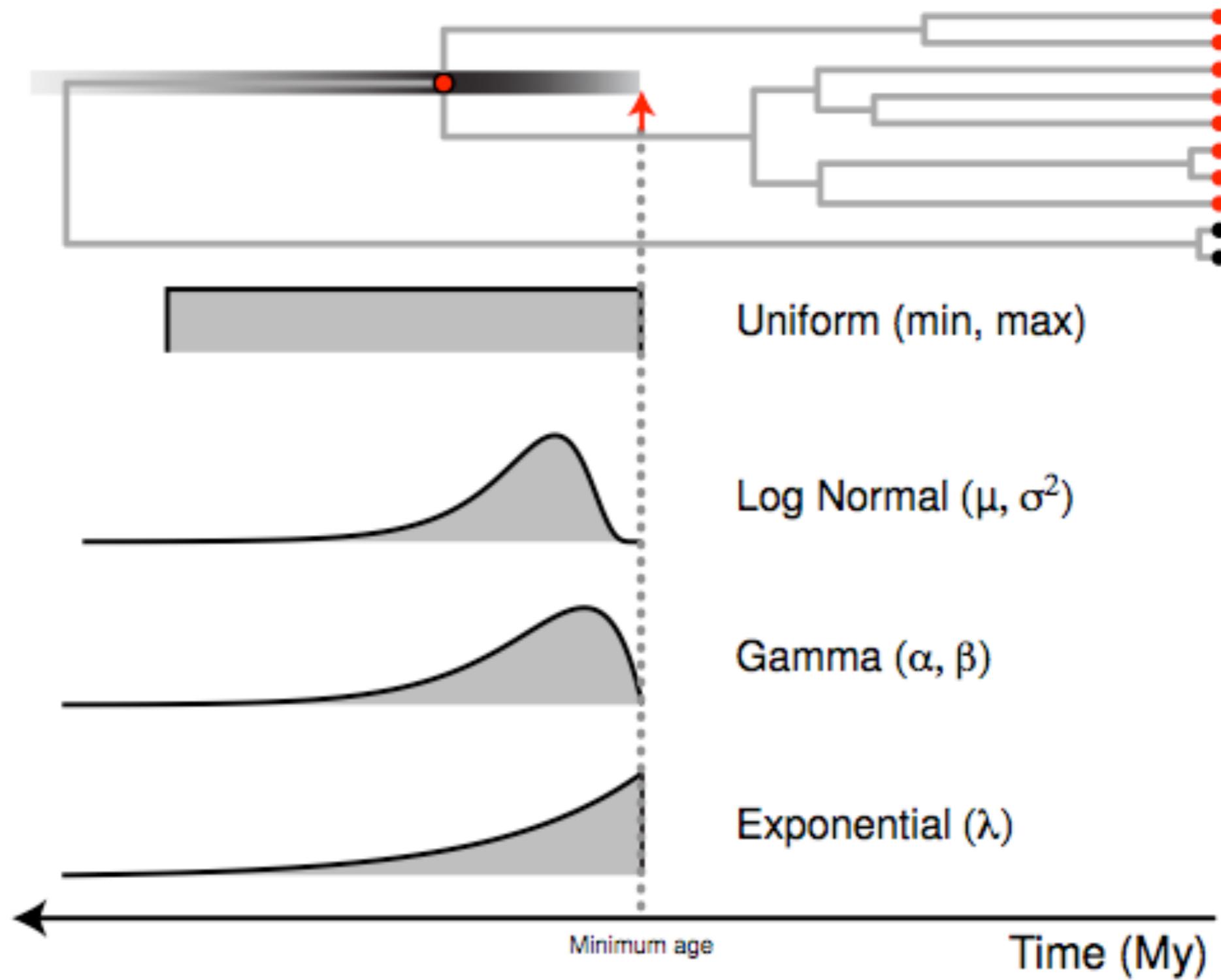
(c)

Fossil with
synapomorphy
of clade (X, Y)

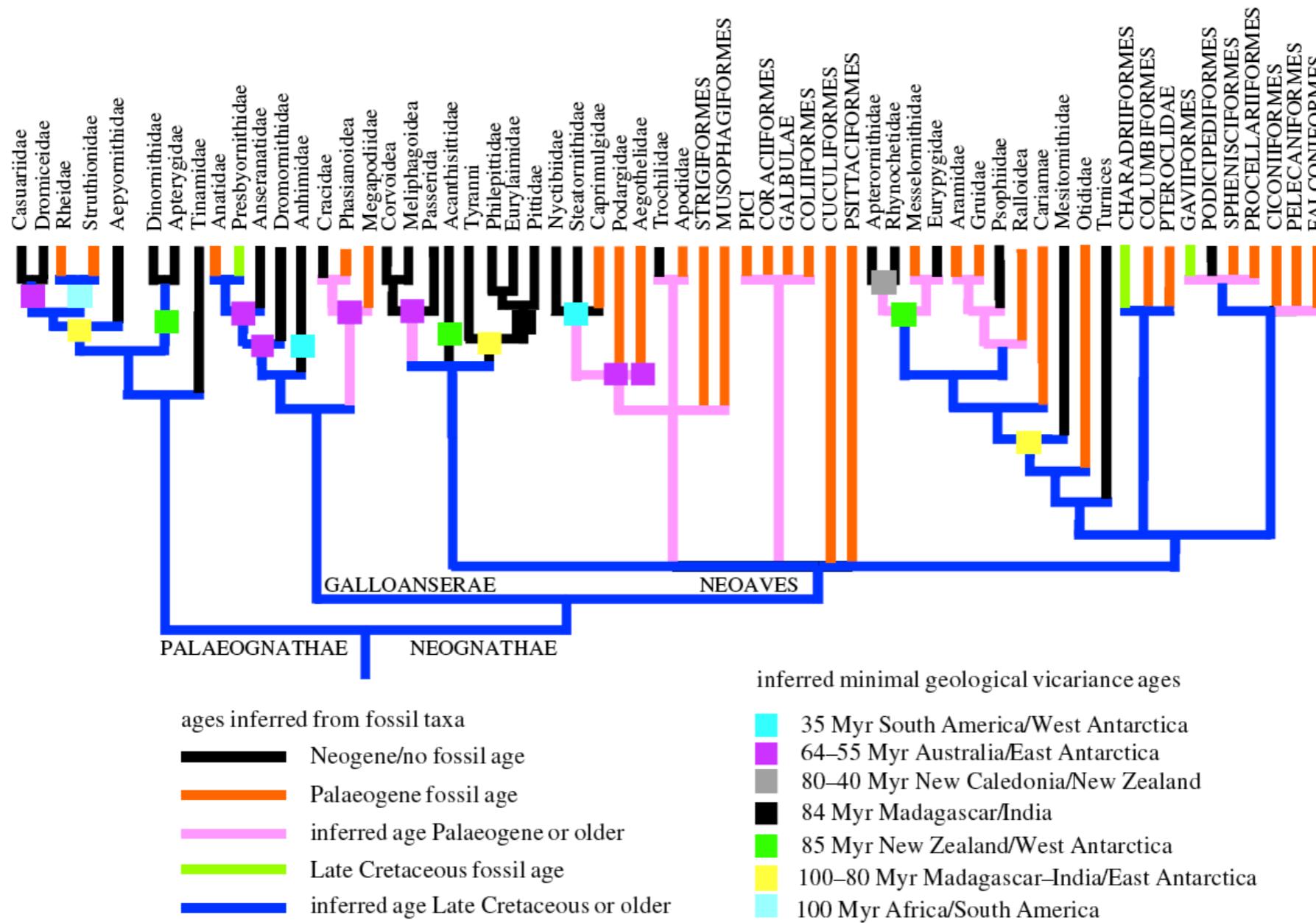
Fossil with
synapomorphy
of clade A



incorporación de incertidumbre en calibraciones fósiles



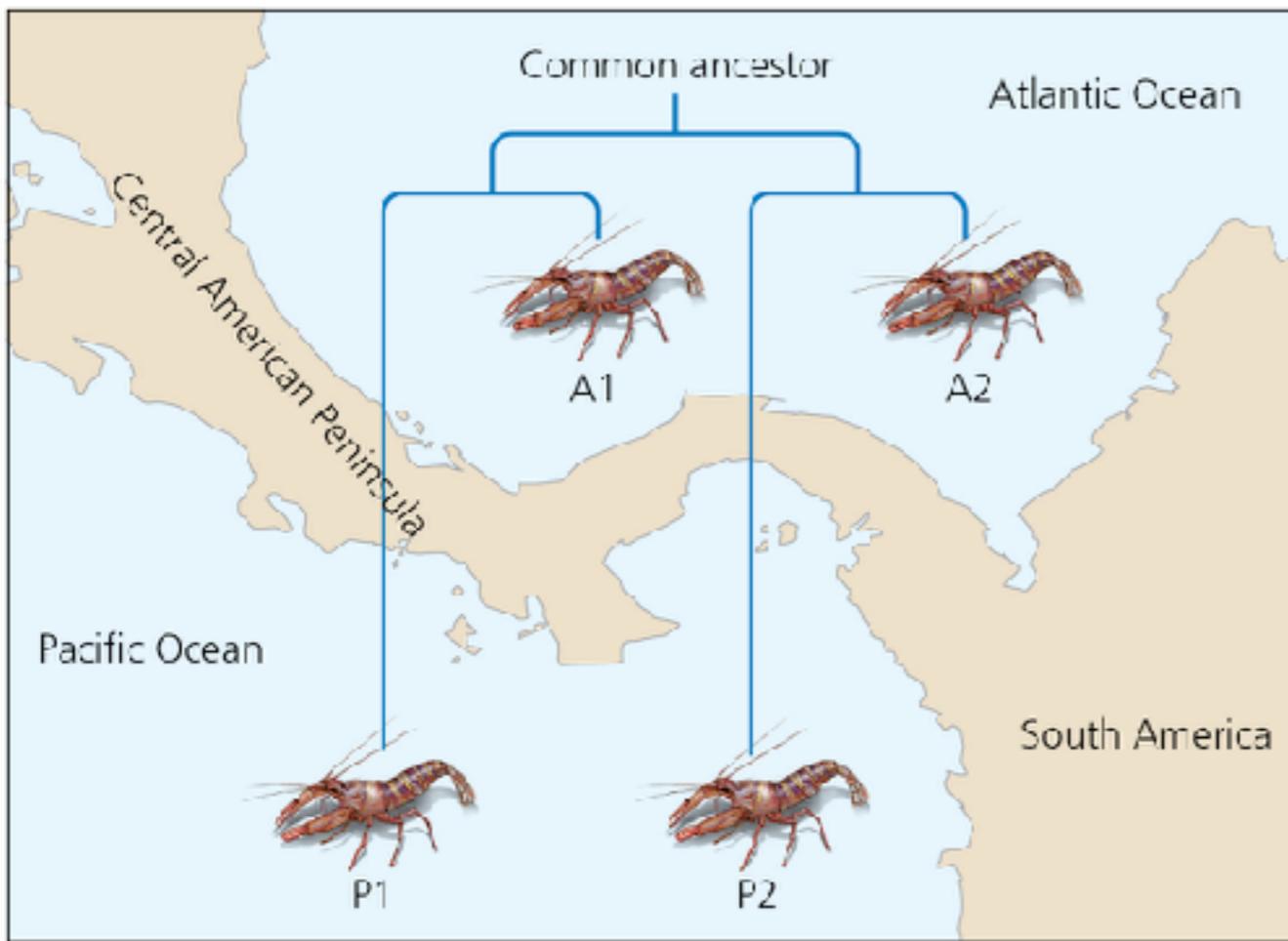
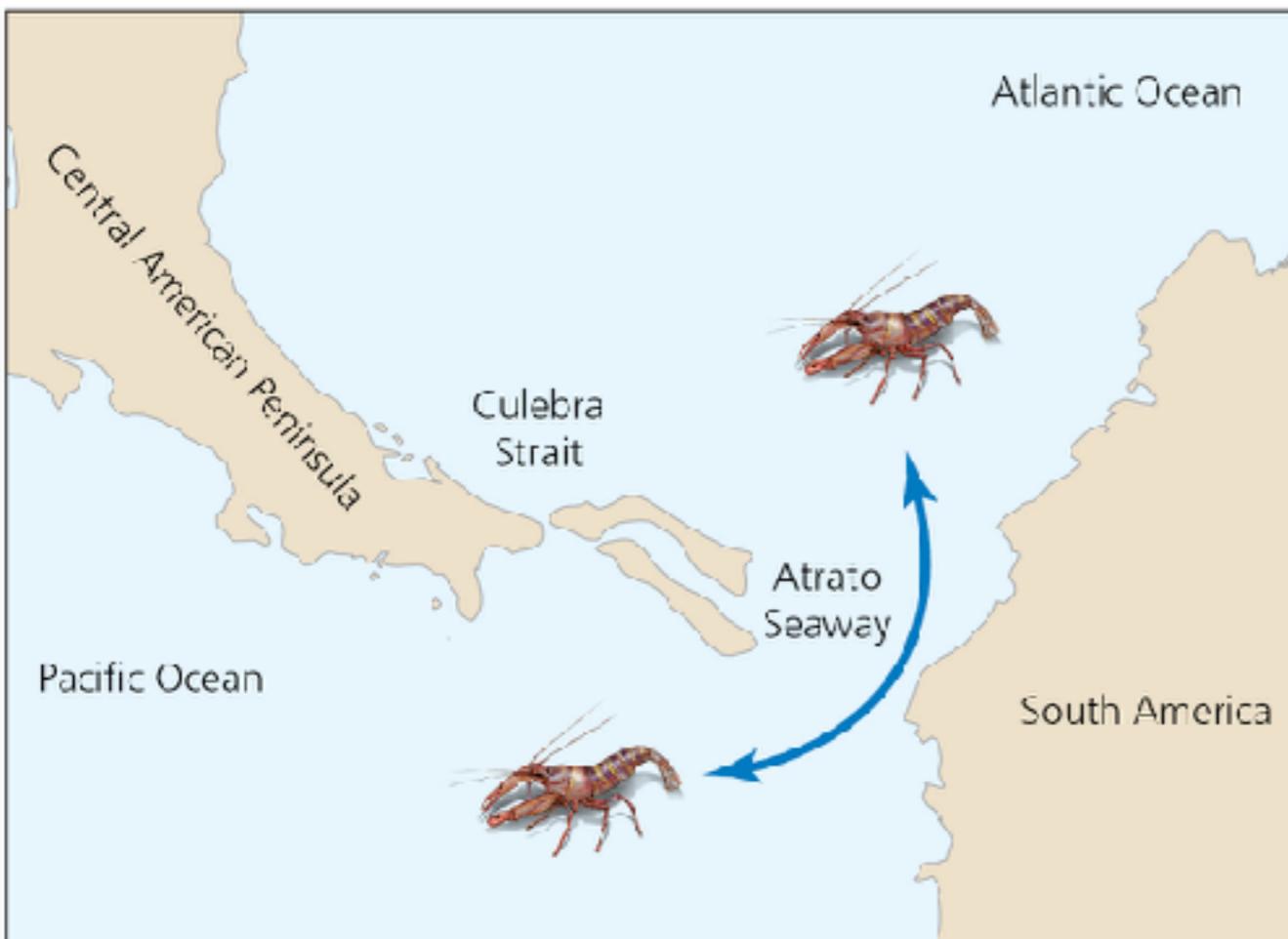
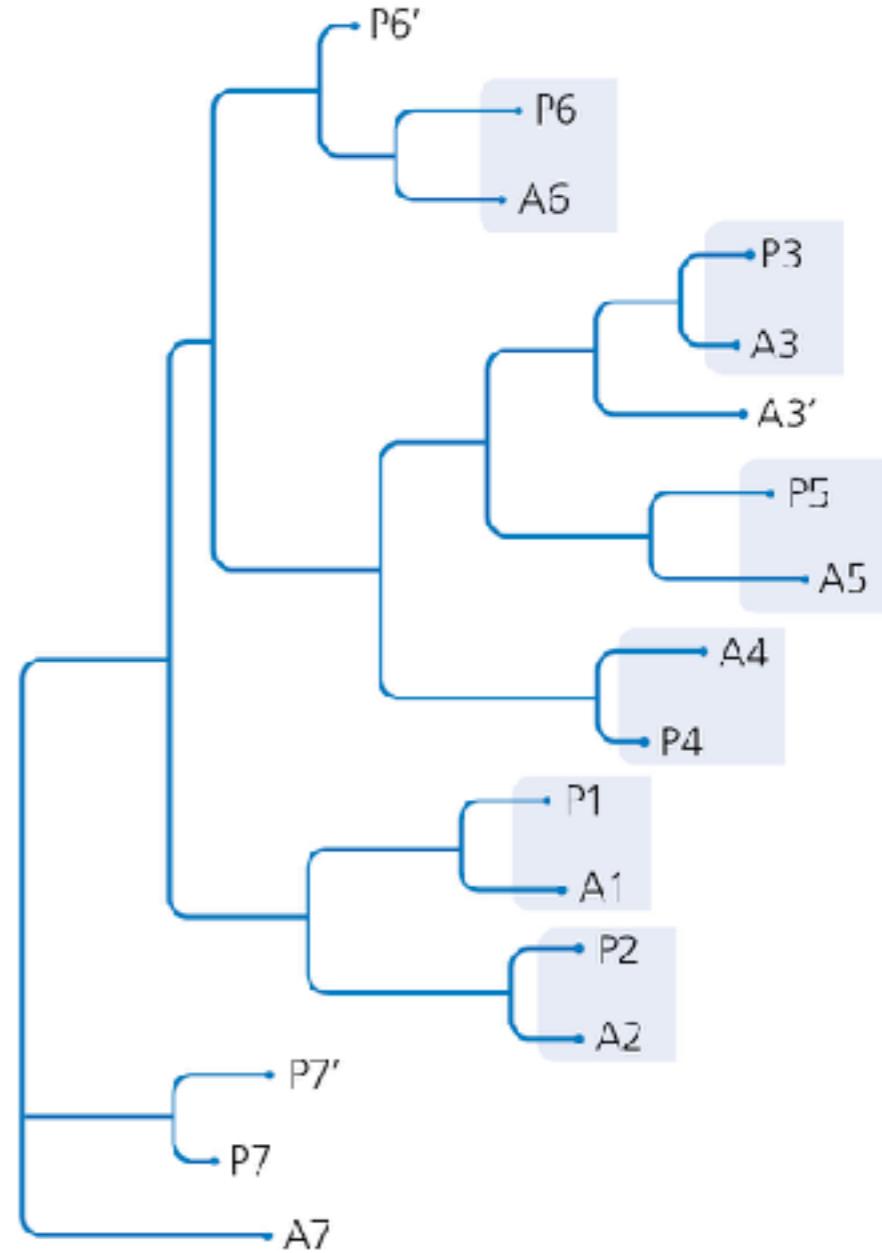
¿y cómo calibro el reloj si no hay muestras de distintos tiempos? 2. biogeografía



Avian evolution, Gondwana biogeography and the Cretaceous–Tertiary mass extinction event

Joel Cracraft

Proc. R. Soc. Lond. B (2001) 268, 459–469

A**B**

¿y cómo calibro el reloj si no hay muestras de distintos tiempos? 2. biogeografía

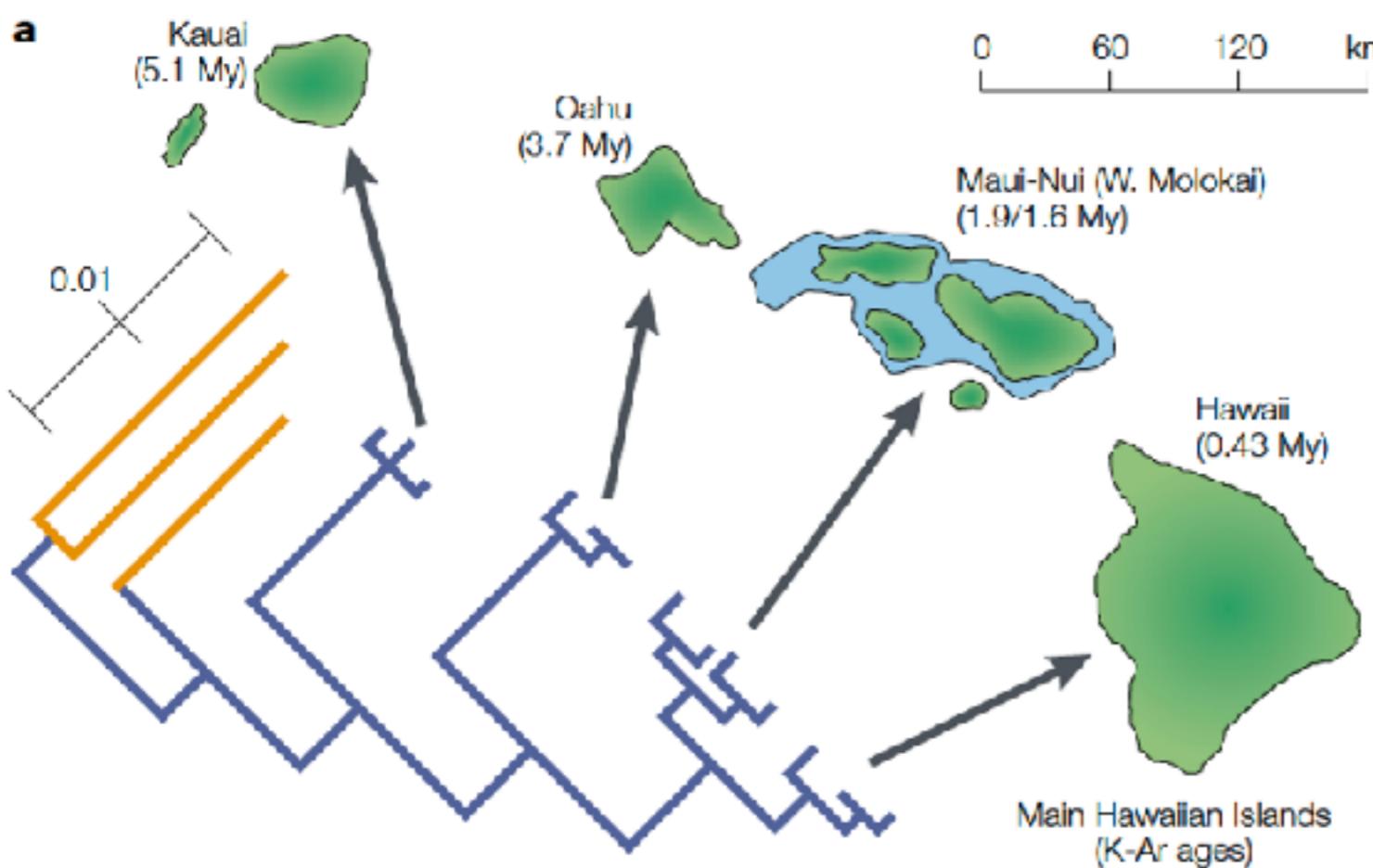
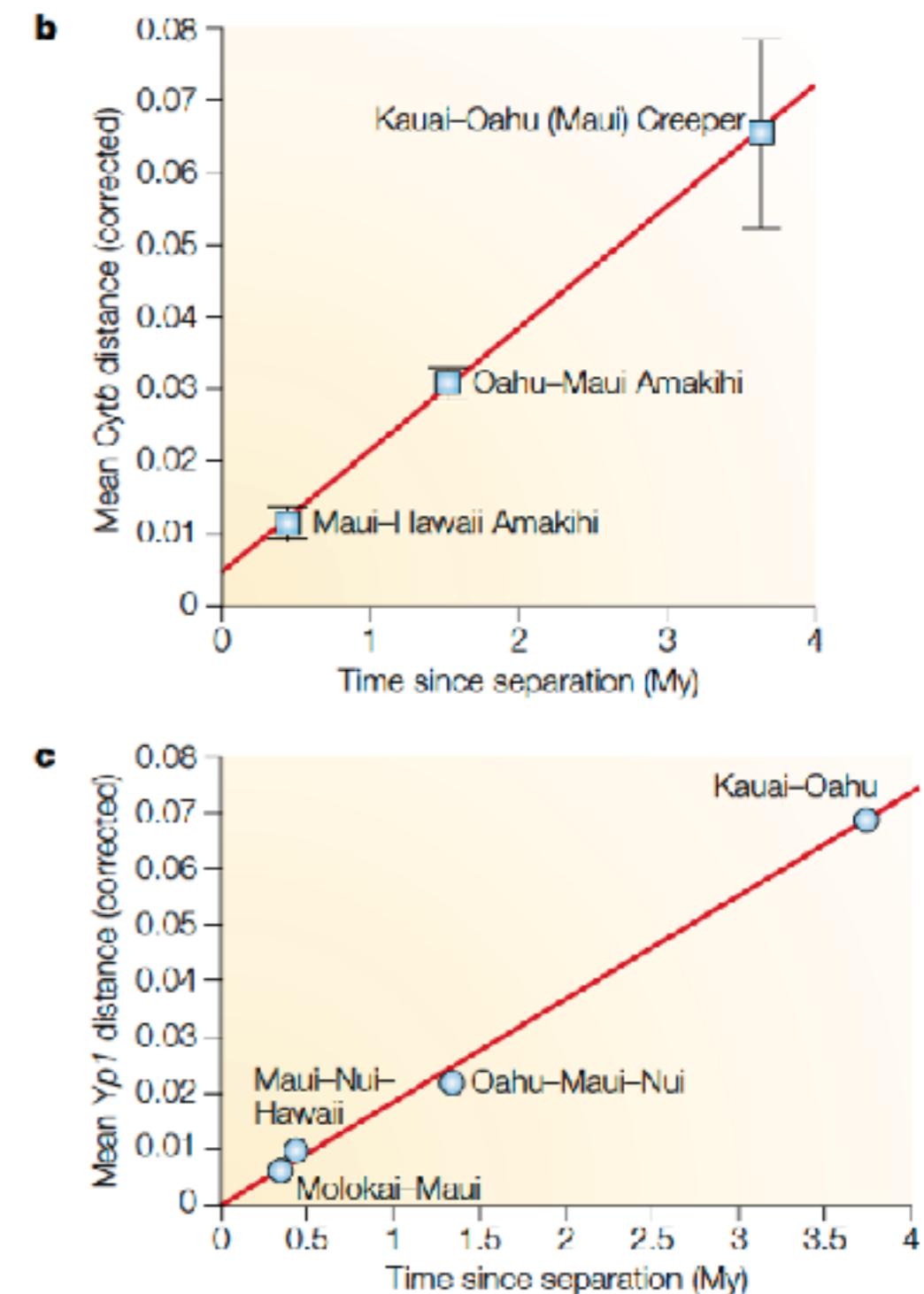


Figure 2 | A molecular clock for the Hawaiian islands. a | The volcanic origin of the Hawaiian islands has produced a chain of islands of increasing geological age. The phylogenetic relationships of island endemic birds (for example, the drepananine (honeycreeper) species such as the amakihi, *Hemignathus virens* and the akiapolaau / *Hemignathus wilsoni*, shown in the tree) and fruitflies (*Drosophila* spp.) reflect this volcanic ‘conveyer belt’, with the species of the oldest islands forming the deepest branch of the tree, and the younger islands on the tips of the tree. Orange lines represent the outgroups. b,c | Molecular dates for *Hemignathus* (panel b) and *Drosophila* (panel c) confirm this order of colonization, and produce a remarkably linear relationship between genetic divergence and time when DNA distance is plotted against island age. My, million years. Figures reproduced with permission from REE 10 © (1998) Blackwell Publishing.

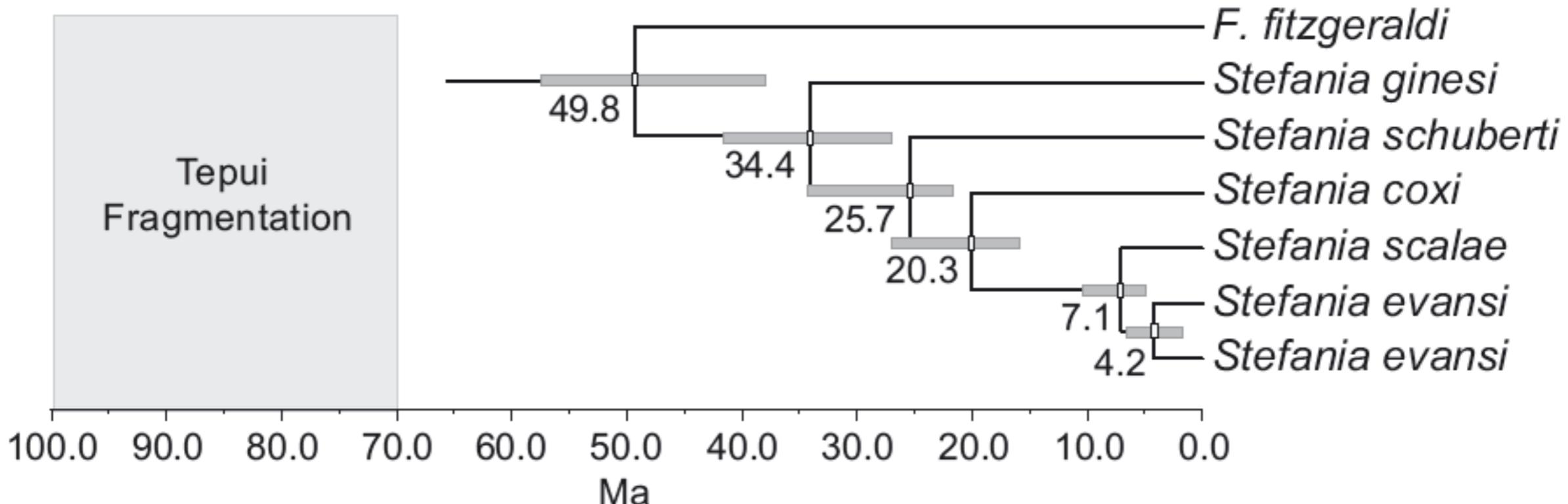




ANCIENT TEPUIS SUMMITS HARBOR YOUNG RATHER THAN OLD LINEAGES OF ENDEMIC FROGS

Patricia E. Salerno,^{1,2} Santiago R. Ron,³ J. Celsa Señaris,⁴ Fernando J. M. Rojas-Ruiz,⁴ Brice P. Noonan,⁵ and David C. Cannatella¹

Herpetologica, 58(3), 2002, 327–346



Middle Miocene closure of the Central American Seaway

C. Montes,^{1*} A. Cardona,² C. Jaramillo,³ A. Pardo,⁴ J. C. Silva,⁵ V. Valencia,⁶ C. Ayala,⁷ L. C. Pérez-Angel,¹ L. A. Rodriguez-Parra,¹ V. Ramírez,⁸ H. Niño⁸

Uranium-lead geochronology in detrital zircons and provenance analyses in eight boreholes and two surface stratigraphic sections in the northern Andes provide insight into the time of closure of the Central American Seaway. The timing of this closure has been correlated with Plio-Pleistocene global oceanographic, atmospheric, and biotic events. We found that a uniquely Panamanian Eocene detrital zircon fingerprint is pronounced in middle Miocene fluvial and shallow marine strata cropping out in the northern Andes but is absent in underlying lower Miocene and Oligocene strata. We contend that this fingerprint demonstrates a fluvial connection, and therefore the absence of an intervening seaway, between the Panama arc and South America in middle Miocene times; the Central American Seaway had vanished by that time.

ECOLOGY

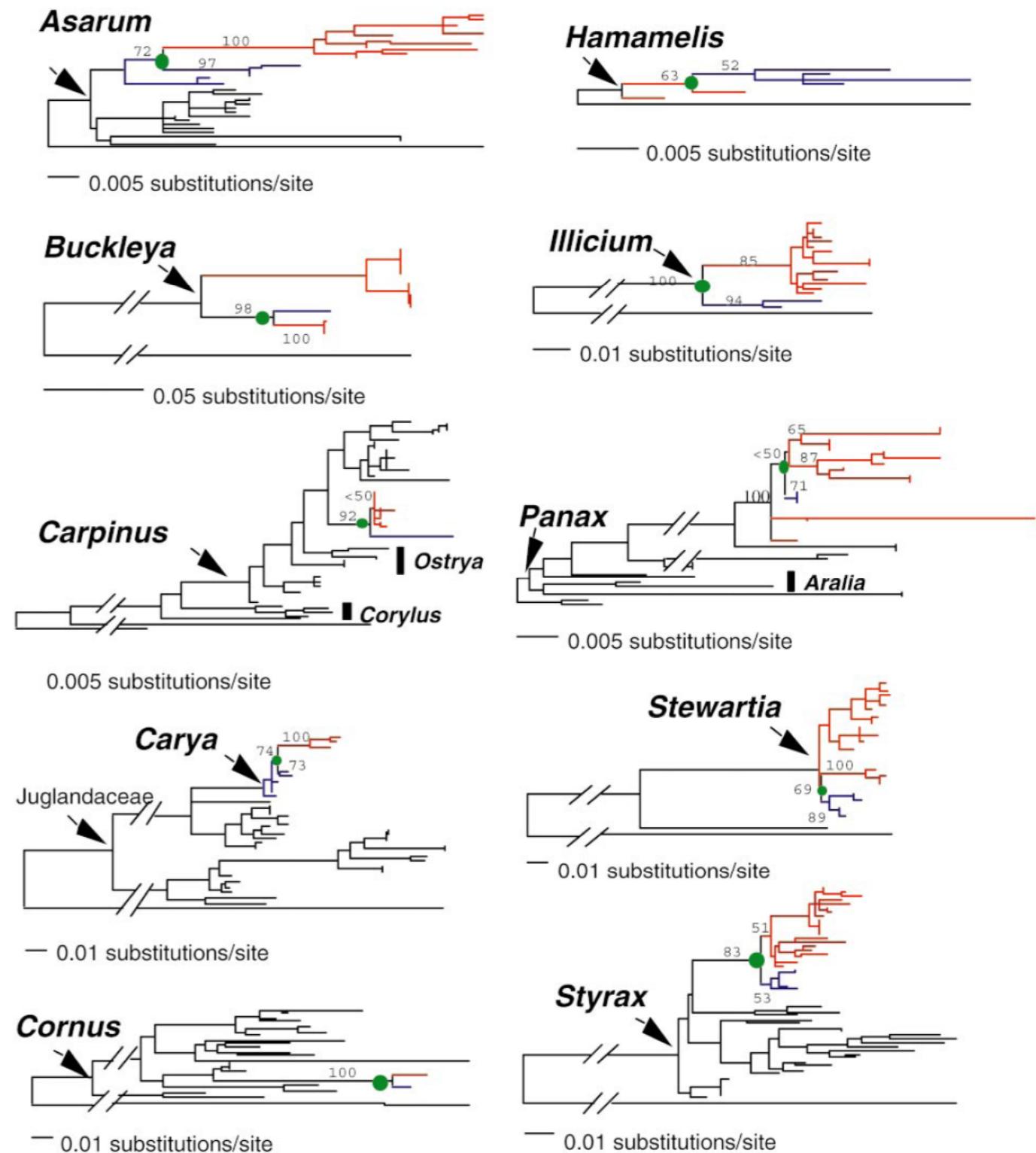
Formation of the Isthmus of Panama

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10.1126/sciadv.1600883

Aaron O'Dea,^{1*} Harilaos A. Lessios,¹ Anthony G. Coates,¹ Ron I. Eytan,² Sergio A. Restrepo-Moreno,^{3,4} Alberto L. Clorne,⁵ Laurel S. Collins,^{1,6} Alan de Queiroz,⁷ David W. Farris,⁸ Richard D. Norris,⁹ Robert F. Stallard,^{1,10} Michael O. Woodburne,¹¹ Orangel Aguilera,¹² Marie-Pierre Aubry,¹³ William A. Berggren,¹³ Ann F. Budd,¹⁴ Mario A. Cozzuol,¹⁵ Simon E. Coppard,¹⁶ Herman Duque-Caro,^{17†} Seth Finnegan,¹⁸ Germán M. Gasparini,⁵ Ethan L. Grossman,¹⁹ Kenneth G. Johnson,²⁰ Lloyd D. Keigwin,²¹ Nancy Knowlton,²² Egbert G. Leigh,¹ Jill S. Leonard-Pingel,²³ Peter B. Marko,²⁴ Nicholas D. Pyenson,²⁵ Paola G. Rachello-Dolmen,^{1,19} Esteban Soibelzon,⁵ Leopoldo Soibelzon,⁵ Jonathan A. Todd,²⁰ Geerat J. Vermeij,²⁶ Jeremy B. C. Jackson^{1,9,25}

The formation of the Isthmus of Panama stands as one of the greatest natural events of the Cenozoic, driving profound biotic transformations on land and in the oceans. Some recent studies suggest that the Isthmus formed many millions of years earlier than the widely recognized age of approximately 3 million years ago (Ma), a result that if true would revolutionize our understanding of environmental, ecological, and evolutionary change across the Americas. To bring clarity to the question of when the Isthmus of Panama formed, we provide an exhaustive review and reanalysis of geological, paleontological, and molecular records. These independent lines of evidence converge upon a cohesive narrative of gradually emerging land and constricting seaways, with formation of the Isthmus of Panama *sensu stricto* around 2.8 Ma. The evidence used to support an older isthmus is inconclusive, and we caution against the uncritical acceptance of an isthmus before the Pliocene.

¿y qué hago si el reloj no funciona...?



Evolution, 58(10), 2004, pp. 2175–2184

REGIONAL DIFFERENCES IN RATES OF PLANT SPECIATION AND MOLECULAR EVOLUTION: A COMPARISON BETWEEN EASTERN ASIA AND EASTERN NORTH AMERICA

QIU-YUN (JENNY) XIANG,^{1,2} WEN HENG ZHANG,^{1,3} ROBERT E. RICKLEFS,⁴ HONG QIAN,⁵ ZHI DUAN CHEN,⁶ JUN WEN,⁷ AND JIAN HUA LI⁸

Evolution, 58(10), 2004, pp. 2175–2184

Nothofagus

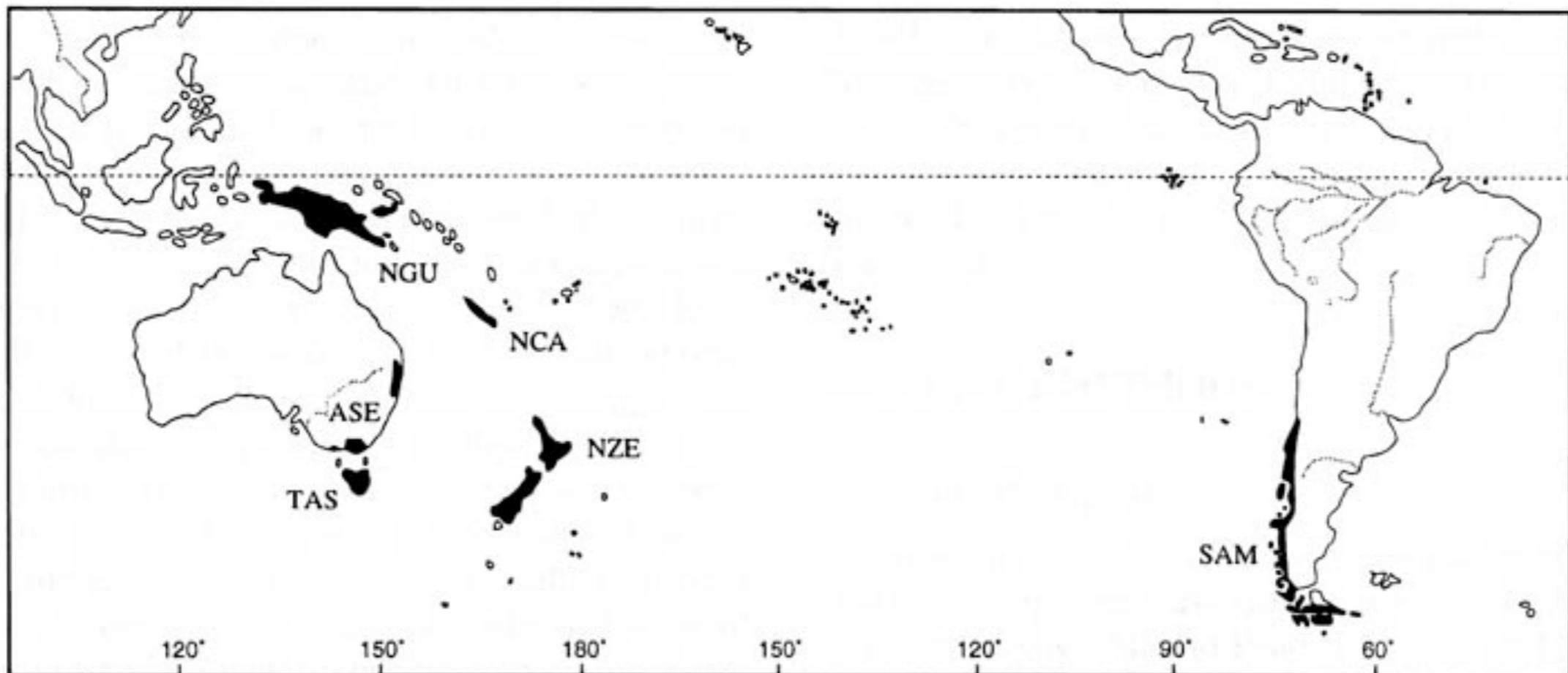
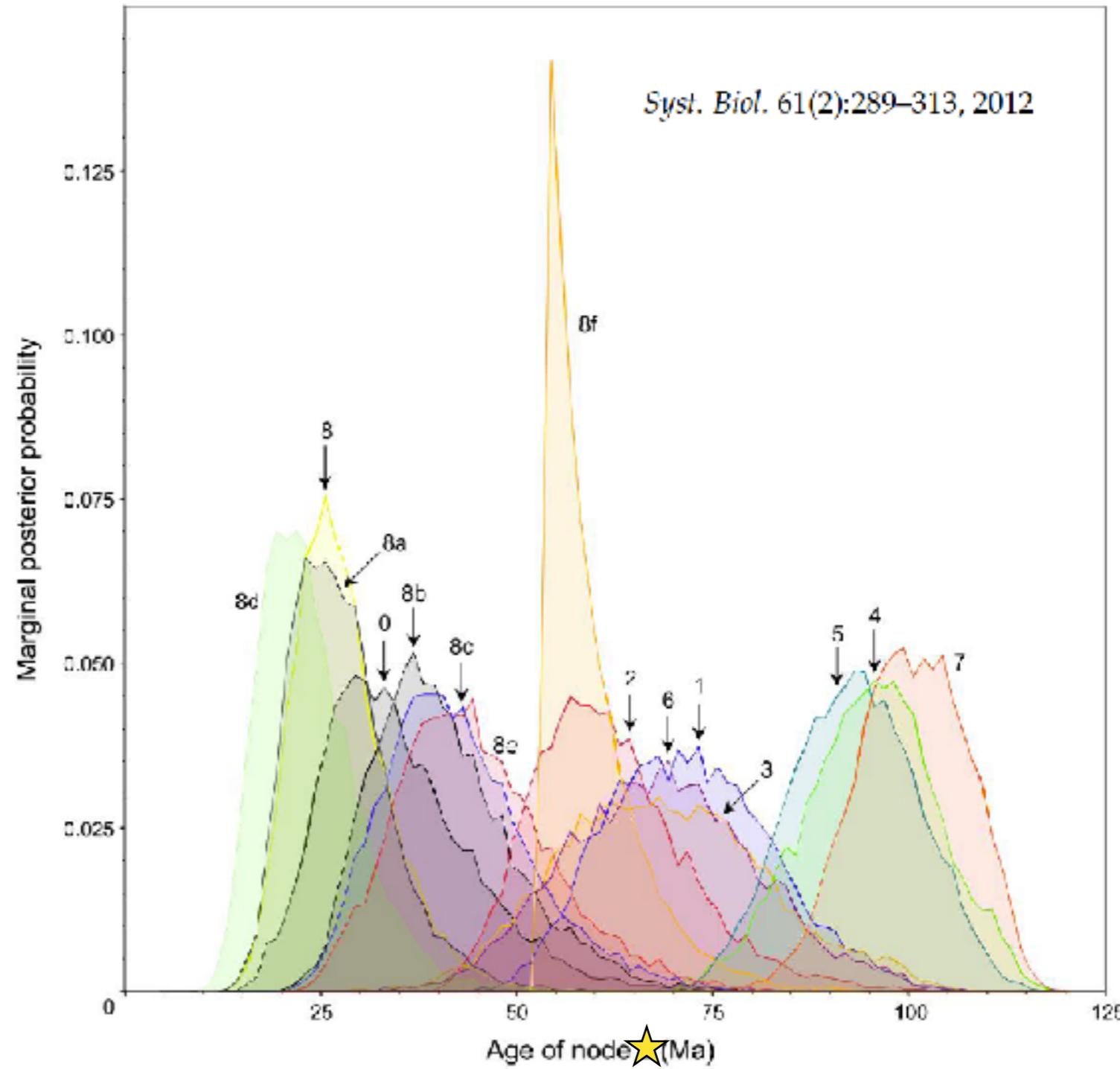
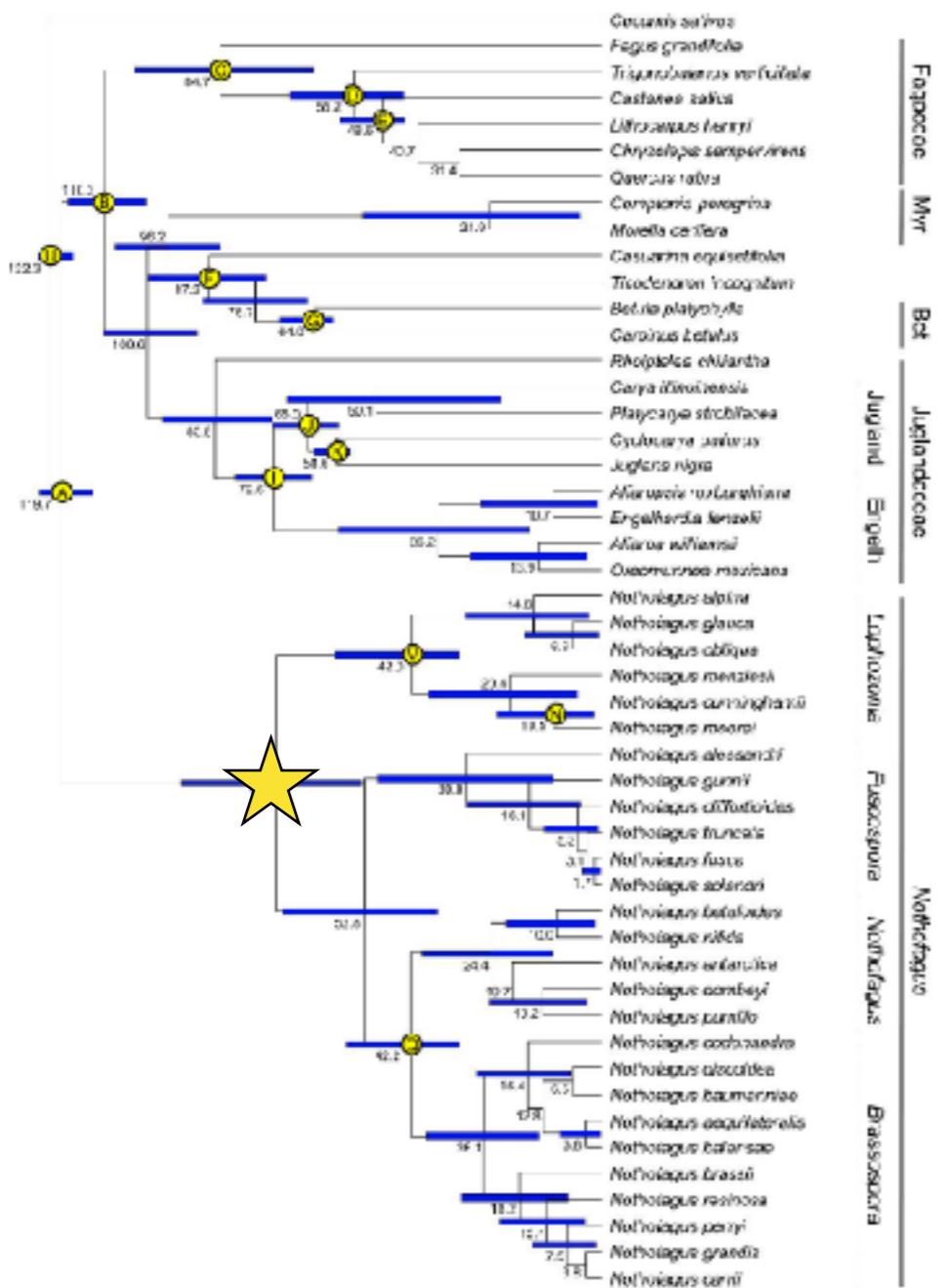


FIG. 1. Distribution of extant *Nothofagus* species showing the southern Pacific area. ASE, Southeast Australia; NCA, New Caledonia; NGU, New Guinea; NZE, New Zealand; SAM, South America; TAS, Tasmania.

¡jojo con el “reloj”!

Testing the Impact of Calibration on Molecular Divergence Times Using a Fossil-Rich Group: The Case of *Nothofagus* (Fagales)

HERVÉ SAUQUET^{1,*}, SIMON Y. W. HO^{2,3}, MARIA A. GANDOLFO⁴, GREGORY J. JORDAN⁵, PETER WILF⁶, DAVID J. CANTRELL⁷, MICHAEL J. BAYLY⁸, LINDELL BROMHAM², GILLIAN K. BROWN^{7,8}, RAYMOND J. CARPENTER⁹, DAPHNE M. LEE¹⁰, DANIEL J. MURPHY⁷, J. M. KALE SNIDERMAN¹¹, AND FRANK UDVICIC⁷



Syst. Biol. 61(2):289–313, 2012

Review

Six Impossible Things before Breakfast: Assumptions, Models, and Belief in Molecular Dating

Lindell Bromham^{1,*}

Confidence in molecular dating analyses has grown with the increasing sophistication of the methods. Some problematic cases where molecular dates disagreed with paleontological estimates appear to have been resolved with a growing agreement between molecules and fossils. But we cannot relax just yet. The growing analytical sophistication of many molecular dating methods relies on an increasingly large number of assumptions about evolutionary history and processes. Many of these assumptions are based on statistical tractability rather than being informed by improved understanding of molecular evolution, yet changing the assumptions can influence molecular dates. How can we tell if the answers we get are driven more by the assumptions we make than by the molecular data being analyzed?

Molecular Dating Analyses Rely on Assumptions

Alice laughed: "There's no use trying," she said; "one can't believe impossible things."

"I daresay you haven't had much practice," said the Queen. "When I was younger, I always did it for half an hour a day. Why, sometimes I've believed as many as six impossible things before breakfast."

Lewis Carroll (1871) *Through the Looking-Glass: And What Alice Found There*, Macmillan

In the age of big data, there is a tendency to view molecular dating as primarily a computational challenge. How can we upgrade our bioinformatic tools to handle the ever-increasing amounts of sequence data and the growing sophistication of analytical methods? Less attention is paid to phylogenetic inference in terms of its place in the broader context of historical inference. Molecular dating – estimating dates of evolutionary events from comparative analysis of DNA or protein – shares with other 'historical sciences', including evolutionary biology, astronomy, archaeology, and geology, the challenge of reconstructing a plausible narrative of past events that we cannot directly witness, using only observations made in the present day [1]. The process of inferring dates from molecular data has special features that set it apart from other estimation procedures (Box 1). Most importantly, historical inference is dependent on assumptions about the processes that produced the data, and is not guaranteed to converge on the right answer given more data. If our assumptions are wrong, then our inference could be misleading, however much data we have.

Of course, we all know that molecular dating analyses rely on assumptions, but the nature and number of those assumptions is changing. In early molecular dating studies the assumptions were relatively few and simple (Box 2). It was possible to state what we had to believe in order

Highlights

Estimating dates of divergence from DNA sequence data is a methodological and computational challenge as the amount of data explodes, and as models and methods become more statistically sophisticated.

The focus on methodological advances distracts from deeper challenges associated with historical inference: how can we construct plausible narratives for events long-past and long-term processes that we cannot directly observe?

As molecular dating methods grow more sophisticated, the number of assumptions we must make about the evolutionary process increases, so that it becomes difficult to keep track of what we must believe in order to believe the molecular dates.

Some disagreements between molecular dating studies should primarily be interpreted as a debate about assumptions and prior beliefs, such as the interpretation of fossil evidence.

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evolución molecular, transmisión críptica del coronavirus y por qué tiene sentido estar encerrados en la casa

Cryptic transmission of novel coronavirus revealed by genomic epidemiology

2 Mar 2020 by Trevor Bedford

The field of genomic epidemiology focuses on using the genetic sequences of pathogens to understand patterns of transmission and spread. Viruses mutate very quickly and accumulate changes during the process of transmission from one infected individual to another. The novel coronavirus which is responsible for the emerging COVID-19 pandemic mutates at an average of about **two mutations per month**. After someone is exposed they will generally incubate the virus for ~5 days before symptoms develop and transmission occurs. Other research has shown that the "serial interval" of SARS-CoV-2 is ~7 days. You can think of a transmission chain as looking something like:



where, on average, we have 7 days from one infection to the next. As the virus transmits, it will mutate at this rate of two mutations per month. This means, that on average every other step in the transmission chain will have a mutation and so would look something like:

