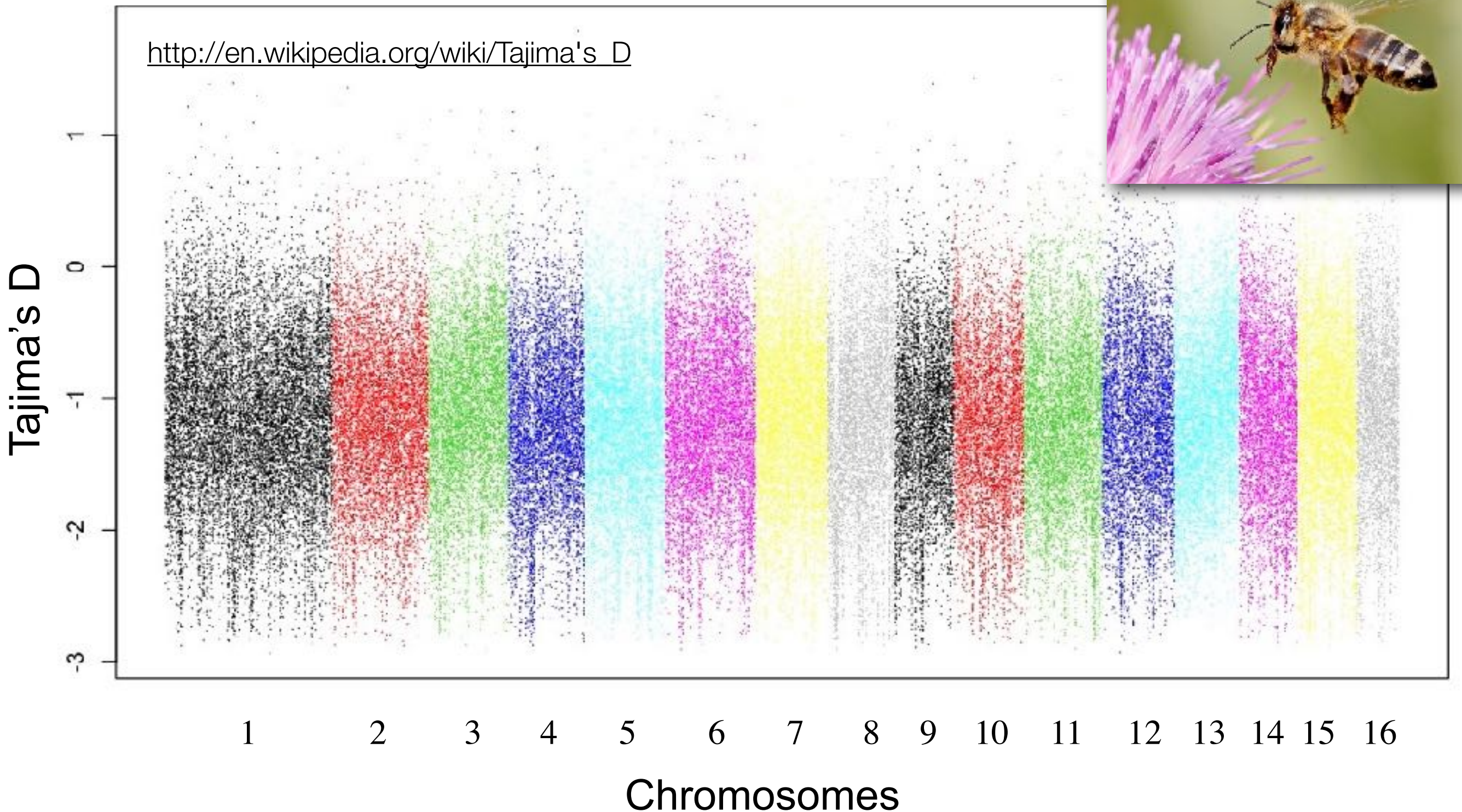# *scans* del genoma y búsqueda de señales de selección

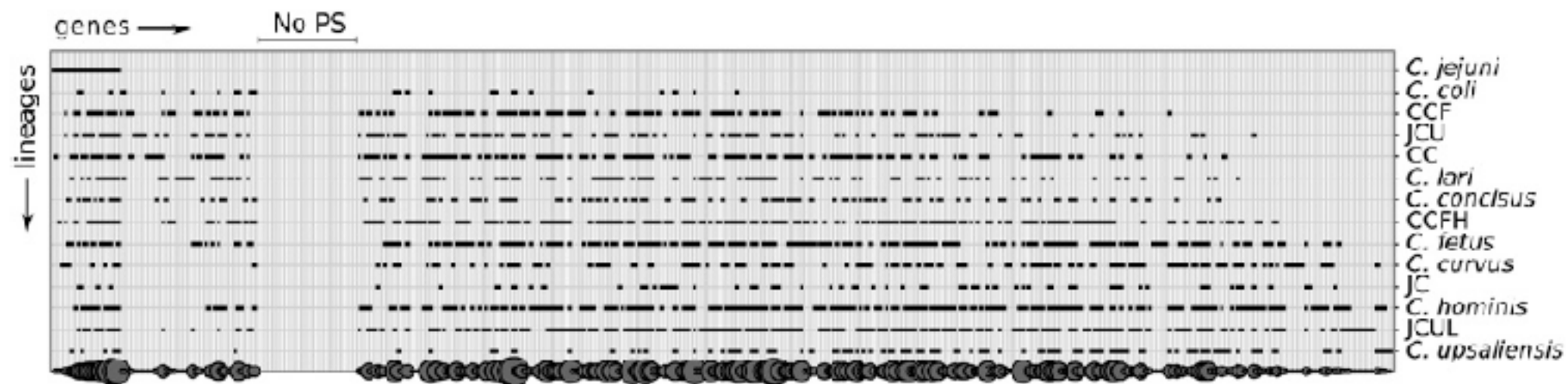S. Ramírez et al. (In prep.)

http://en.wikipedia.org/wiki/Tajima's_D

evidencia en contra de la teoría neutral:
genomas fuertemente moldeados por selección positiva

Figure 2. Distribution of the positively selected genes in the 14 tested lineages of *Campylobacter*. The genes and lineages were sorted following a correspondence analysis. (Black dots) Genes under positive selection, (gray circles of different diameters, *bottom*) number of lineages under positive selection (PS) for a specific gene. (CCF) *C. consisus, C. curvus,* and *C. fetus* ancestral lineage; (JCU) *C. jejuni, C. coli,* and *C. upsaliensis* ancestral lineage; (CC) *C. consisus* and *C. curvus* ancestral lineage; (CCFH) *C. consisus, C. curvus, C. fetus,* and *C. hominis* ancestral lineage; (JC) *C. jejuni* and *C. coli* ancestral lineage; (JCUL) *C. jejuni, C. coli, C. upsaliensis,* and *C. lari* ancestral lineage.

Pervasive, genome-wide positive selection leading to functional divergence in the bacterial genus *Campylobacter*

Tristan Lefébure and Michael J. Stanhope[1]
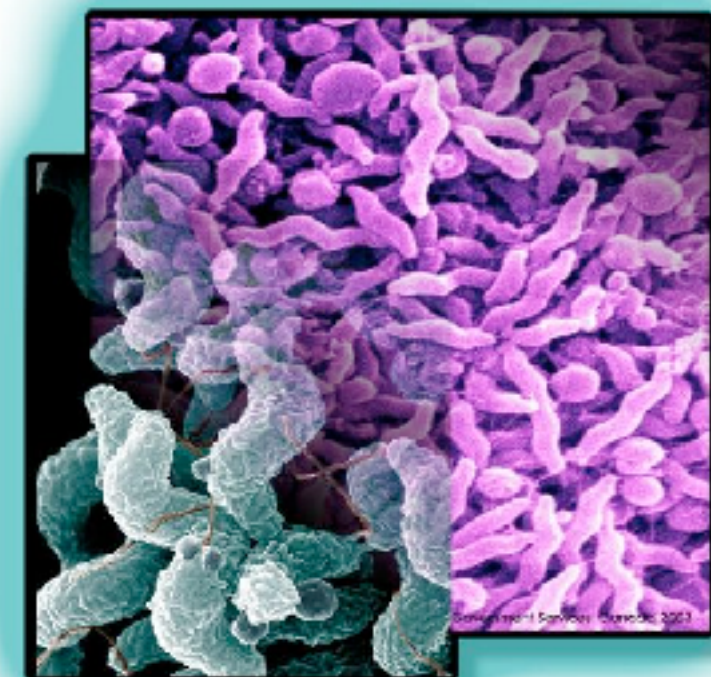
The Neutral Theory in Light of Natural Selection

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Abstract

In this perspective, we evaluate the explanatory power of the neutral theory of molecular evolution, 50 years after its introduction by Kimura. We argue that the neutral theory was supported by unreliable theoretical and empirical evidence from the beginning, and that in light of modern, genome-scale data, we can firmly reject its universality. The ubiquity of adaptive variation both within and between species means that a more comprehensive theory of molecular evolution must be sought.

*Key words:* natural selection, neutral theory, population genetics.

https://www.molecularecologist.com/2018/05/is-the-neutral-theory-dead/

lo que se puede aprender cuando se rechaza evolución neutral
cómo el estudio de genes y árboles permite evaluar hipótesis de selección natural
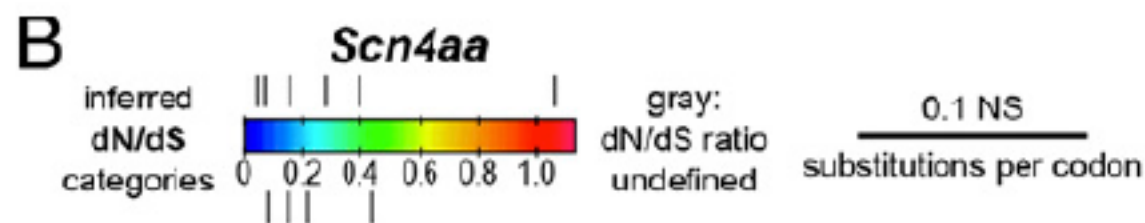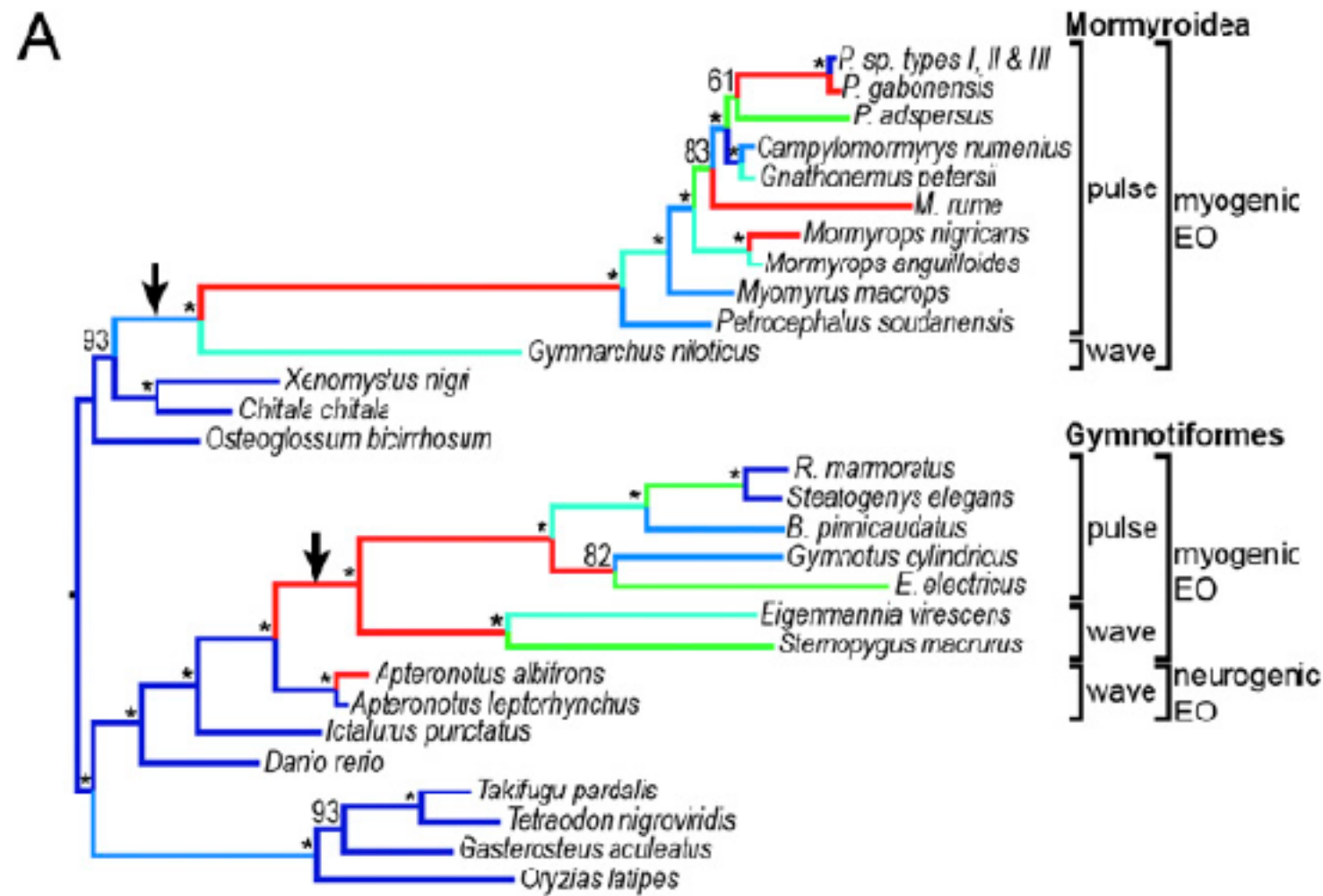
Adaptive evolution of voltage-gated sodium channels:
The first 800 million years

Harold H. Zakon[1]

evolución neutral y el "reloj" molecular
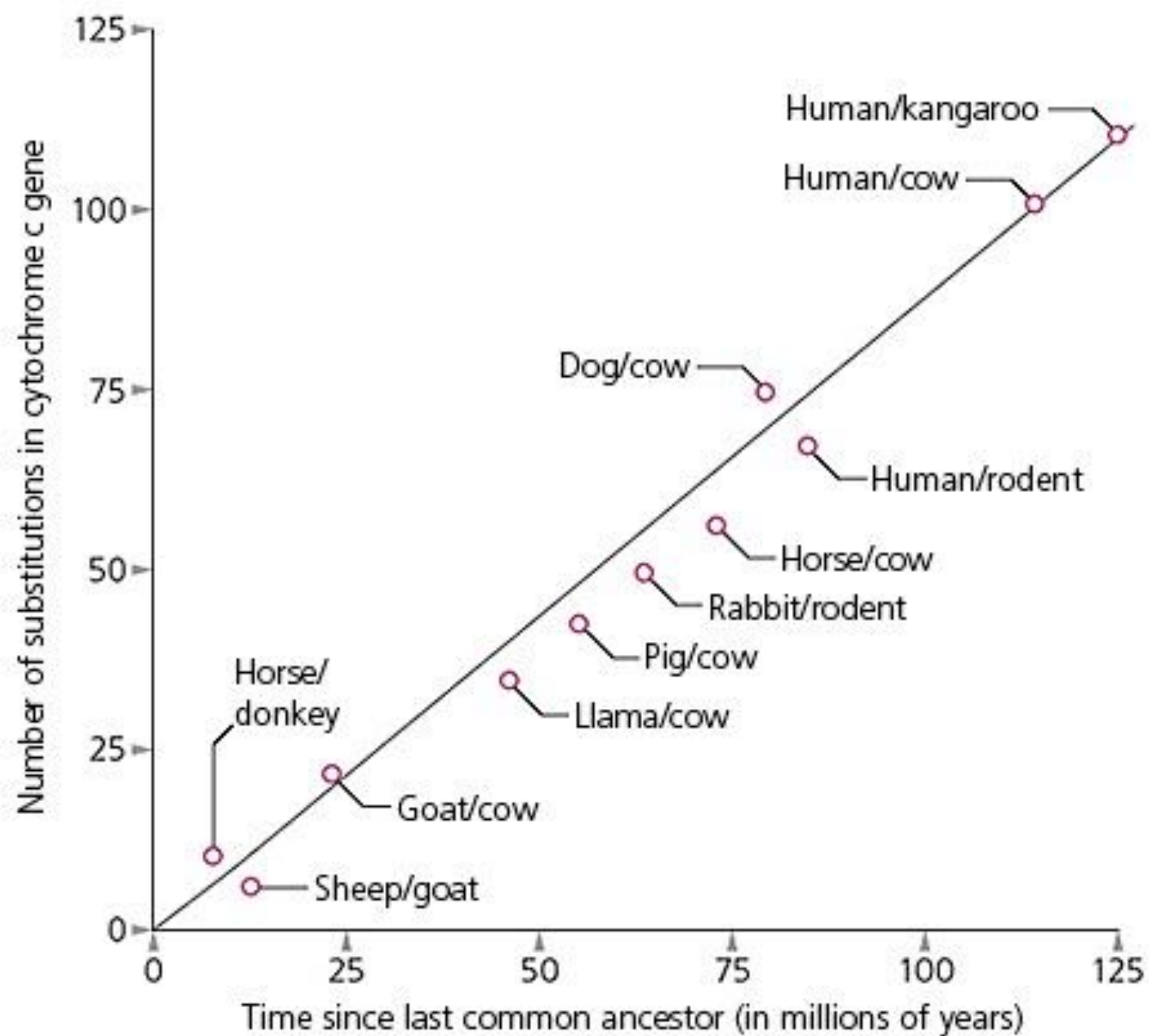
el "reloj" molecular y su validación

## Box 2 | Analysing rates of nucleotide substitution in HIV

Numerous methods have been described for estimating the rate of genetic change in viruses[105]. The common feature of these techniques is the use of viral sequences sampled over time to directly observe evolutionary change. This is possible owing to the exceptional rate of nucleotide substitution of RNA viruses, such as the human immunodeficiency virus (HIV). One of the most straightforward methods — a linear regression of genetic divergence against the time of isolation of the viruses — was used to estimate the date of the most recent common ancestor of HIV-1 group M to the 1930s (REF. 17). Although this study has been criticized for not adequately accounting for recombination, which could affect its accuracy[75], and for flaws in the statistical methods, which could affect its precision[105], it remains our best estimate so far. Reassuringly, the inferred regression slope (shown in the figure) almost exactly predicts the position of the oldest HIV sequence, a 1959 sample from the Democratic Republic of Congo (DRC). Figure modified with permission from REF. 17 © (2000) American Association for the Advancement of Science.
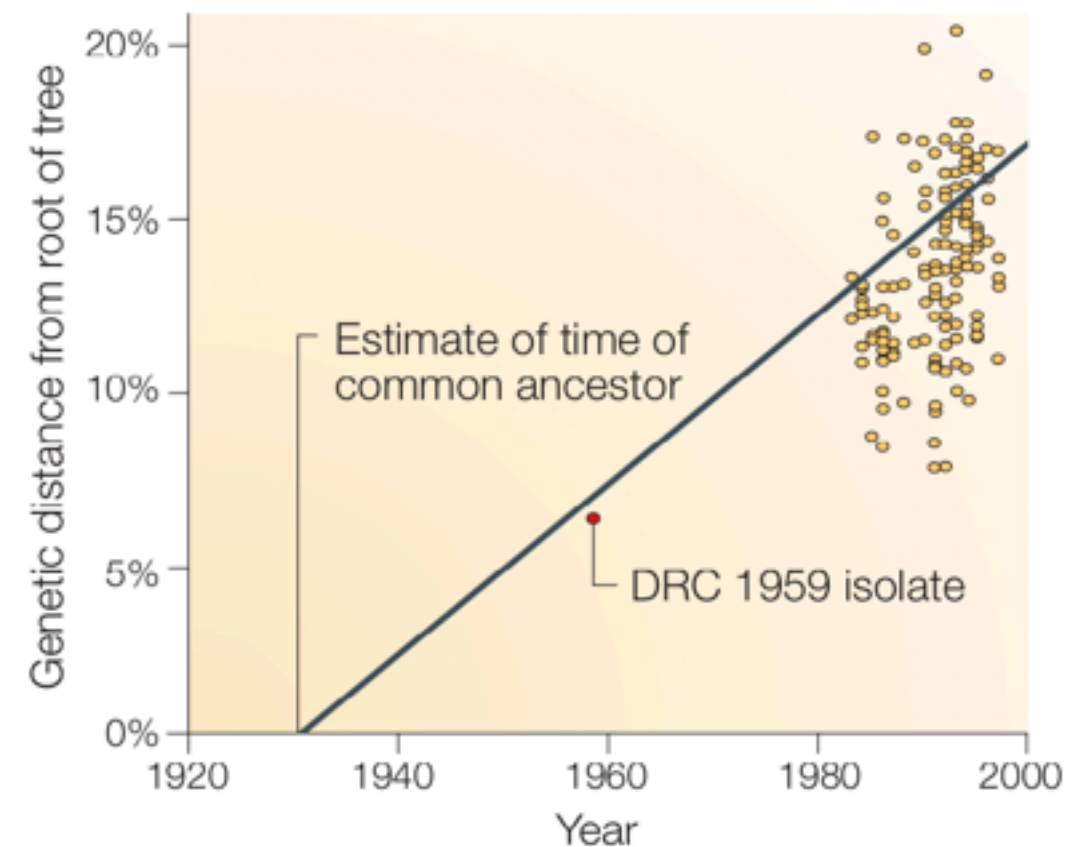
THE CAUSES AND CONSEQUENCES
OF HIV EVOLUTION

Andrew Rambaut*, David Posada†, Keith A. Crandall‡ and Edward C. Holmes*

virus, filogenias y la temporalidad de epidemias: HIV-1 M subtipo B en USA
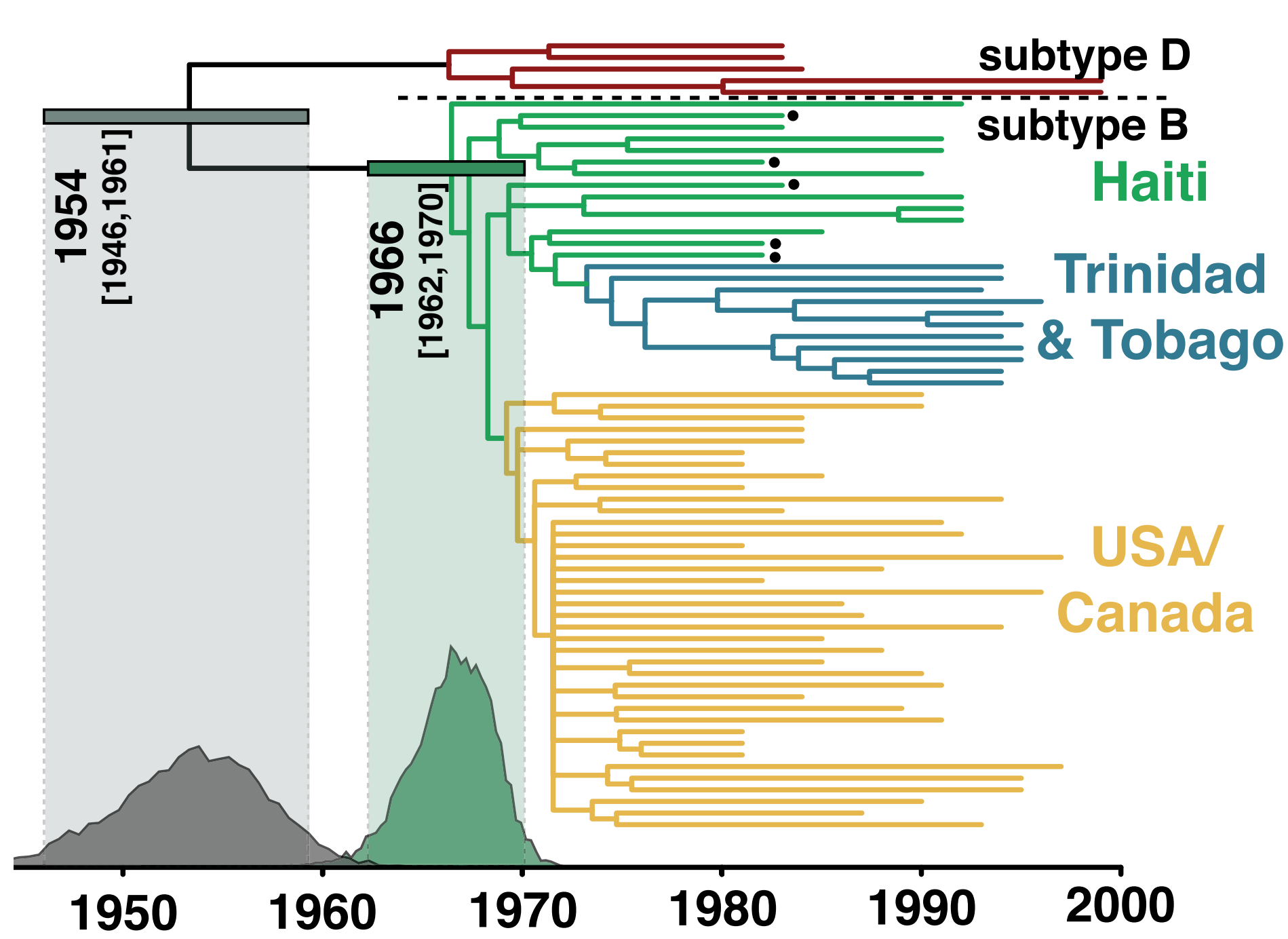
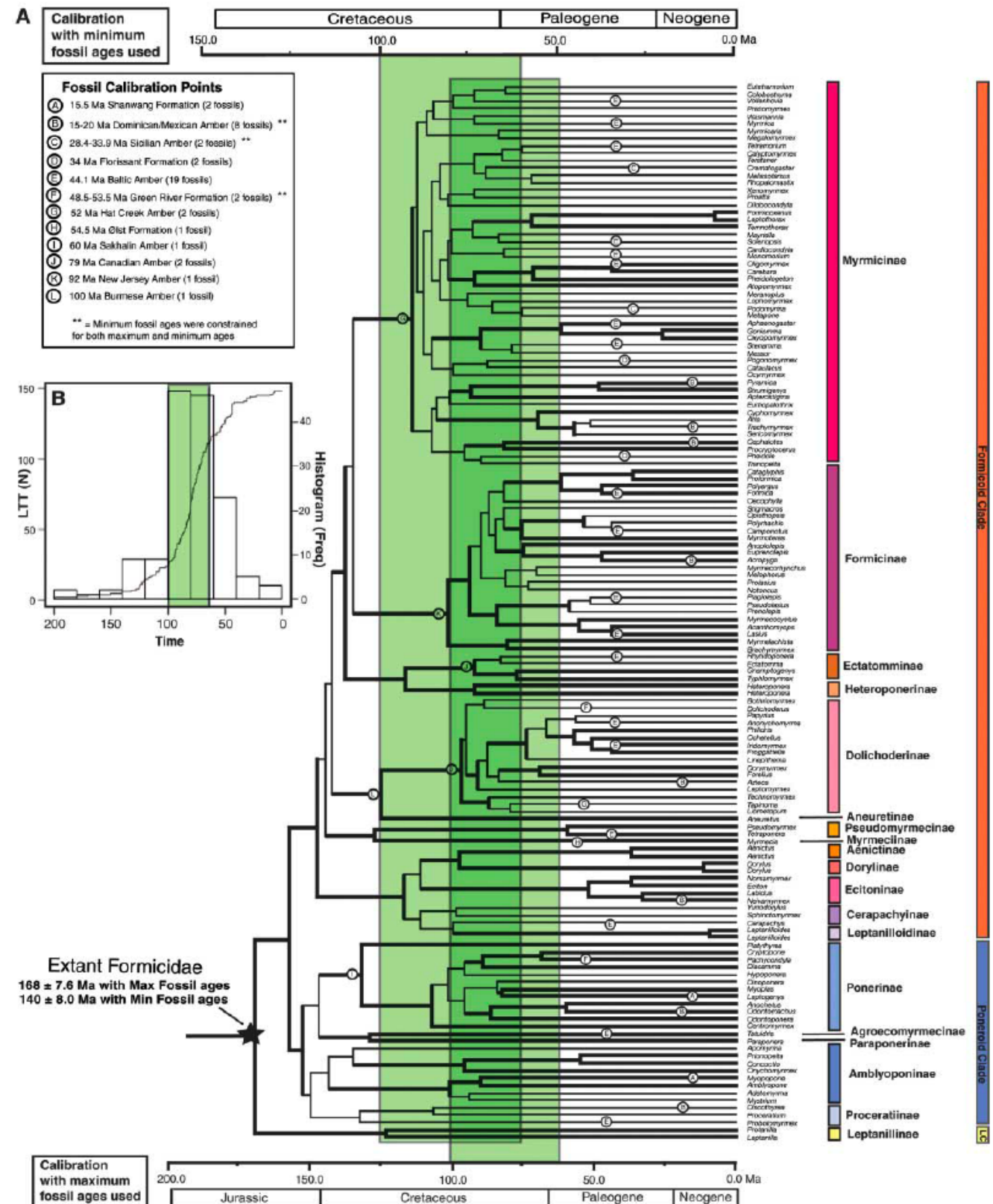http://www.wired.com/wiredscience/2011/05/giant-ant-fossils/

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Phylogeny of the Ants: Diversification in the Age of Angiosperms

Corrie S. Moreau,[1]* Charles D. Bell,[2] Roger Vila,[1] S. Bruce Archibald,[1] Naomi E. Pierce[1]
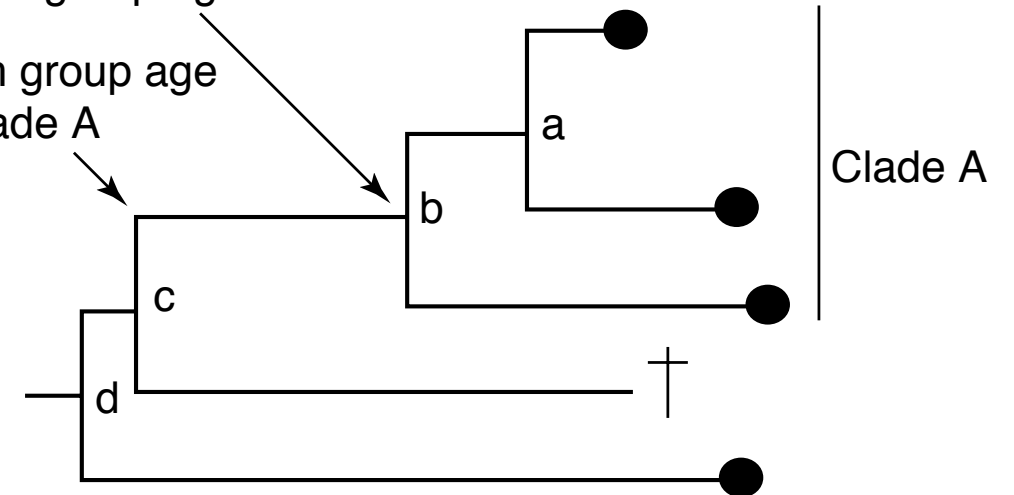
¿y exactamente dónde pongo mi fósil?

(a)
● Extant taxon
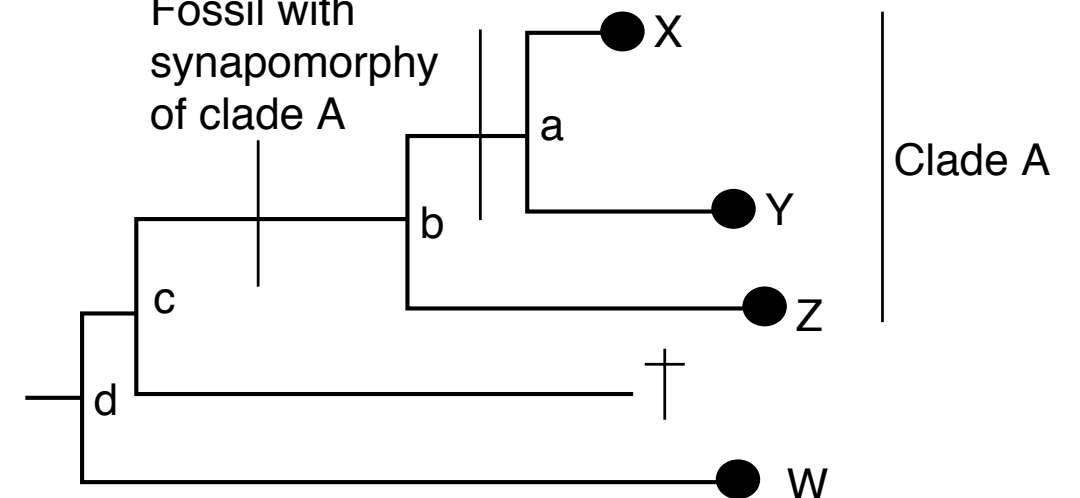† Extinct taxon

Crown group age of clade A

Stem group age of clade A

Clade A

(c)
Fossil with synapomorphy of clade (X, Y)

Fossil with synapomorphy of clade A
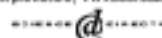
Clade A

Relaxed molecular clocks for dating historical plant dispersal events

Susanne S. Renner

¿y exactamente dónde pongo mi fósil?

P. Fine & F. Zapata
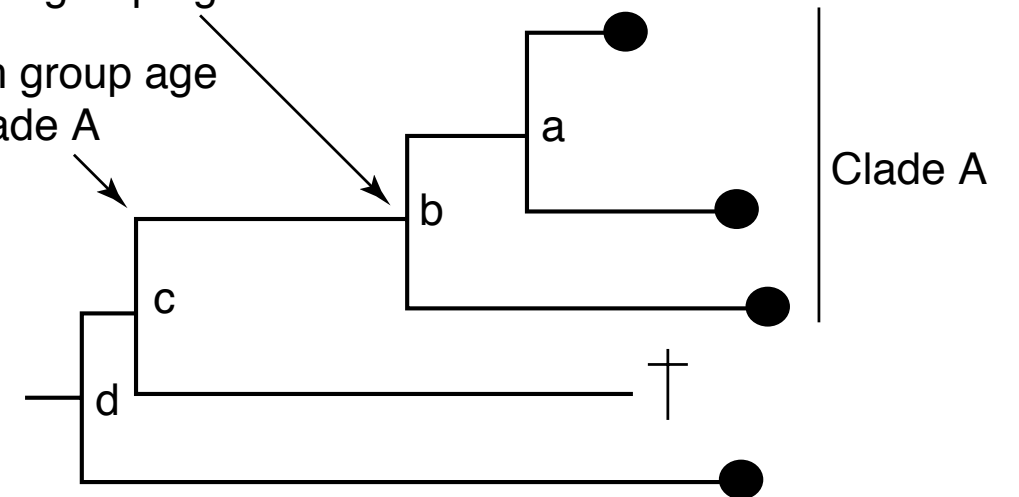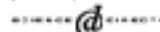
Relaxed molecular clocks for dating historical plant dispersal events

Susanne S. Renner

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