

Correction

Microbiology

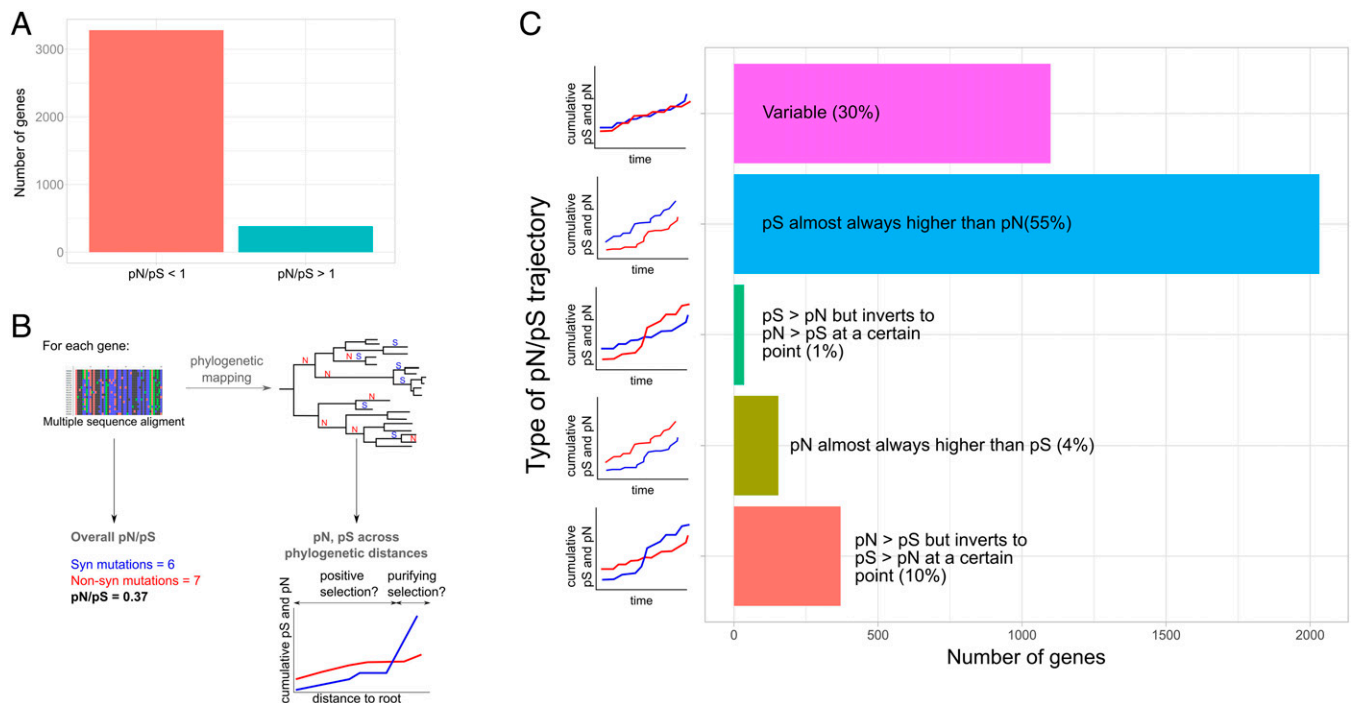
Correction for “Gene evolutionary trajectories in *Mycobacterium tuberculosis* reveal temporal signs of selection,” by Álvaro Chiner-Oms, Mariana G. López, Miguel Moreno-Molina, Victoria Furió, and Inaki Comas, which published April 22, 2022; 10.1073/pnas.2113600119 (*Proc. Natl. Acad. Sci. U.S.A.* **119**, e2113600119).

The authors note that Fig. 1 appeared incorrectly. The corrected figure and its legend appear below. The online version has been corrected.

The authors note that on page 9, right column, second full paragraph, line 1, “Mean pN/pS across time for each gene and for the complete genome were calculated as  $mean\ pN/pS = \frac{\sum_{t=4}^n x_t}{n-4}$ , with  $x$  being the cumulative pN/pS value at each of the sampled  $t$  points.” should instead appear as “Mean pN/pS across time for each gene and for the complete genome were calculated as  $mean\ pN/pS = \frac{\sum_{t=4}^n x_t}{n-3}$ , with  $x$  being the cumulative pN/pS value at each of the sampled  $t$  points.” The online version has been corrected.

The authors note that on page 10, left column, third full paragraph, line 9, “Parameters were estimated using Markov chain Monte Carlo (MCMC) Bayesian inference with  $1 \times 10^7$ -step-long chains with the exception of the larger datasets (L2, L3, L4.1.2, L4.3.4, L4.10), for which longer chains were run ( $1 \times 10^8$ ) and the tree topology was fixed.” should instead appear as “Parameters were estimated using Markov chain Monte Carlo (MCMC) Bayesian inference with  $1 \times 10^7$ -step-long chains with the exception of the larger datasets (L2, L3, L4.1.2, L4.3.4, L4.10), for which longer chains were run ( $1 \times 10^8$ ) and the tree topology was fixed.” The online version has been corrected.

The authors note that the Acknowledgments section should be corrected. The new Acknowledgments section should read: “This project received funding from the European



**Fig. 1.** Gene-by-Genes calculation of pN/pS over phylogenetic time. (A) Bar plot showing the number of genes currently displaying a pN/pS > 1 and a pN/pS < 1. (B) From the alignment, we inferred the current pN/pS; however, when mapping different mutations onto the phylogeny, we inferred how the pN and pS rates changed over time. (C) Five categories grouping studied genes according to their trajectories.

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Research Grant HR21-00415 (TB-TARGET). This research work was also funded by the European Commission–NextGenerationEU (Regulation EU 2020/2094), through CSIC's Global Health Platform (PTI Salud Global).” The online version has been corrected.

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