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Title

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Permalink

<https://escholarship.org/uc/item/7v8845rd>

Journal

BMC Biology, 18(1)

ISSN

1478-5854

Authors

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et al.

Publication Date

2020-12-01

DOI

10.1186/s12915-020-00864-7

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Peer reviewed

CORRECTION

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Correction to: The genome sequence of the grape phylloxera provides insights into the evolution, adaptation, and invasion routes of an iconic pest

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Correction to: BMC Biol 18, 90 (2020)

<https://doi.org/10.1186/s12915-020-00820-5>

Following publication of the original article [1], the authors identified an error in Fig. 4. The error was made in the x-axis labels of the three panels, which were noted

as “pairwise dN/dS”. The figure represents distributions of dS, so the labels were corrected as “pairwise dS”. The correct Fig. 4 is given below.

The original article can be found online at <https://doi.org/10.1186/s12915-020-00820-5>.

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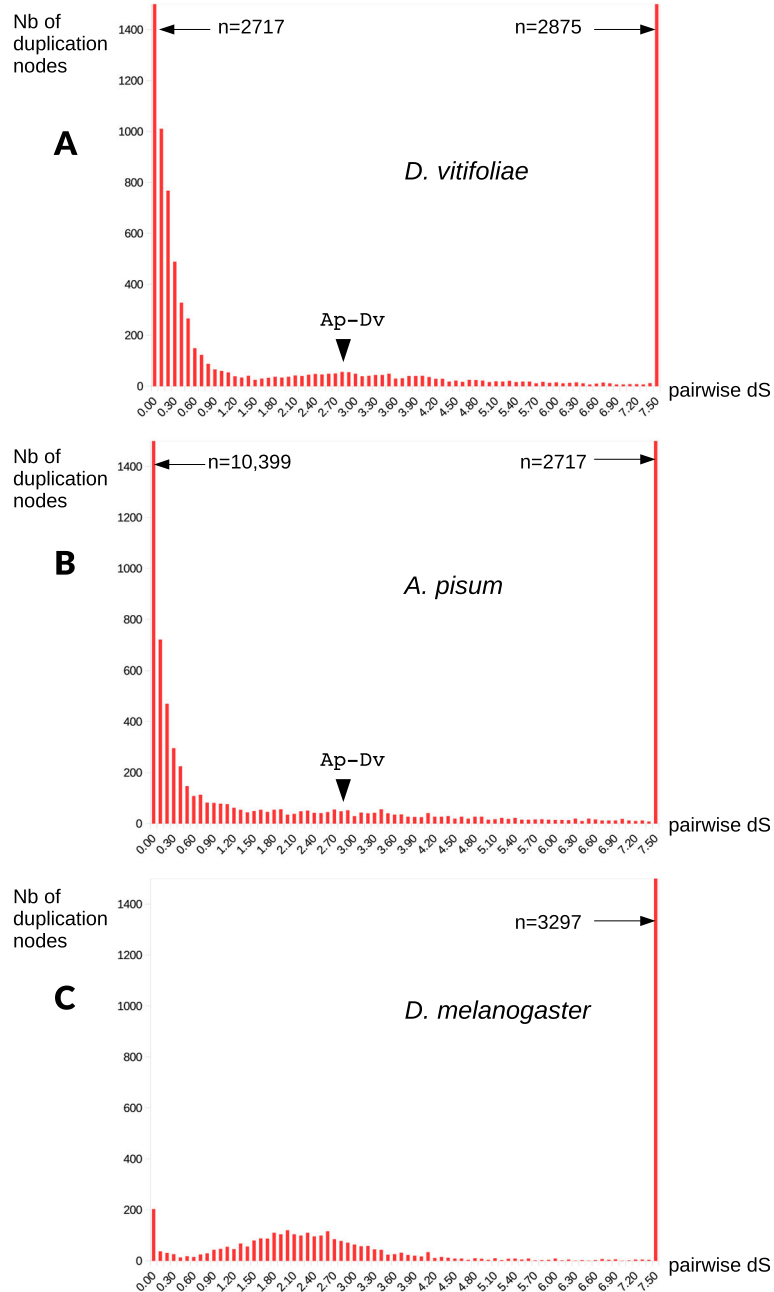


Fig. 4 Distribution of synonymous distances among paralogs for grape vine phylloxera (panel **a**, *D. vitifoliae*), pea aphid (panel **b**, *A. pisum*), and fruit fly (panel **c**, *D. melanogaster*). Paralogs were identified as RBH pairs, with an iterative approach allowing to cover both recent duplications (terminal nodes in gene families) and more ancient duplications (internal nodes). For readability, the y-axis (number of dS classes) is truncated to 1500 (numbers above that threshold are indicated on the figures). For both *A. pisum* and *D. vitifoliae*, an arrowhead indicates the median dS between orthologs (RBH genes between the two species), $dS = 2.83$: this metric, a proxy of the age of separation between the two species allows to distinguish duplications that are more recent (left of the arrow, lower dS values) *or more ancient (right of the arrowhead, higher dS) than the speciation event

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Published online: 11 September 2020

Reference

1. Rispe C, et al. The genome sequence of the grape phylloxera provides insights into the evolution, adaptation, and invasion routes of an iconic pest. *BMC Biol.* 2020;18:90. <https://doi.org/10.1186/s12915-020-00820-5>.