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Author/s:

Rispe, C;Legeai, F;Nabity, PD;Fernández, R;Arora, AK;Baa-Puyoulet, P;Banfill, CR;Bao, L;Barberà, M;Bouallègue, M;Bretaudeau, A;Brisson, JA;Calevro, F;Capy, P;Catrice, O;Chertemps, T;Couture, C;Delière, L;Douglas, AE;Dufault-Thompson, K;Escuer, P;Feng, H;Forneck, A;Gabaldón, T;Guigó, R;Hilliou, F;Hinojosa-Alvarez, S;Hsiao, YM;Hudaverdian, S;Jacquin-Joly, E;James, EB;Johnston, S;Joubard, B;Le Goff, G;Le Trionnaire, G;Librado, P;Liu, S;Lombaert, E;Lu, HL;Maibèche, M;Makni, M;Marcet-Houben, M;Martínez-Torres, D;Meslin, C;Montagné, N;Moran, NA;Papura, D;Parisot, N;Rahbé, Y;Lopes, MR;Ripoll-Cladellas, A;Robin, S;Roques, C;Roux, P;Rozas, J;Sánchez-Gracia, A;Sánchez-Herrero, JF;Santesmasses, D;Scatoni, I;Serre, RF;Tang, M;Tian, W;Umina, PA;Van Munster, M;Vincent-Monégat, C;Wemmer, J;Wilson, ACC;Zhang, Y;Zhao, C;Zhao, J;Zhao, S;Zhou, X;Delmotte, F;Tagu, D

Title:

Erratum: The genome sequence of the grape phylloxera provides insights into the evolution, adaptation, and invasion routes of an iconic pest (BMC Biology (2020) 18 (90) DOI: 10.1186/s12915-020-00820-5)

Date:

2020-09-11

Citation:

Rispe, C., Legeai, F., Nabity, P. D., Fernández, R., Arora, A. K., Baa-Puyoulet, P., Banfill, C. R., Bao, L., Barberà, M., Bouallègue, M., Bretaudeau, A., Brisson, J. A., Calevro, F., Capy, P., Catrice, O., Chertemps, T., Couture, C., Delière, L., Douglas, A. E. ,... Tagu, D. (2020). Erratum: The genome sequence of the grape phylloxera provides insights into the evolution, adaptation, and invasion routes of an iconic pest (BMC Biology (2020) 18 (90) DOI: 10.1186/s12915-020-00820-5). BMC Biology, 18 (1), <https://doi.org/10.1186/s12915-020-00864-7>.

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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

Claude Rispe^{1*†}, Fabrice Legeai^{2*†}, Paul D. Nabity³, Rosa Fernández^{4,5}, Arinder K. Arora⁶, Patrice Baa-Puyoulet⁷, Celeste R. Banfill⁸, Leticia Bao⁹, Miquel Barberà¹⁰, Maryem Bouallègue¹¹, Anthony Bretaudeau², Jennifer A. Brisson¹², Federica Calevro⁷, Pierre Capy¹³, Olivier Catrice¹⁴, Thomas Chertemps¹⁵, Carole Couture¹⁶, Laurent Delière¹⁶, Angela E. Douglas^{6,17}, Keith Dufault-Thompson¹⁸, Paula Escuer¹⁹, Honglin Feng^{20,21}, Astrid Forneck²², Toni Gabaldón^{4,23,24}, Roderic Guigó^{25,26}, Frédérique Hilliou²⁷, Silvia Hinojosa-Alvarez¹⁹, Yi-min Hsiao^{28,29}, Sylvie Hudaverdian³⁰, Emmanuelle Jacquin-Joly³¹, Edward B. James⁸, Spencer Johnston³², Benjamin Joubard¹⁶, Gaëlle Le Goff³³, Gaël Le Trionnaire³⁰, Pablo Librado³⁴, Shanlin Liu^{35,36,37}, Eric Lombaert³⁸, Hsiao-ling Lu³⁹, Martine Maibèche¹⁵, Mohamed Makni¹¹, Marina Marcet-Houben⁴, David Martínez-Torres⁴⁰, Camille Meslin³¹, Nicolas Montagné⁴¹, Nancy A. Moran⁴², Daciana Papura¹⁶, Nicolas Parisot⁷, Yvan Rahbé⁴³, Mélanie Ribeiro Lopes⁷, Aida Ripoll-Cladellas²⁵, Stéphanie Robin⁴⁴, Céline Roques⁴⁵, Pascale Roux¹⁶, Julio Rozas¹⁹, Alejandro Sánchez-Gracia¹⁹, Jose F. Sánchez-Herrero¹⁹, Didac Santesmasses^{25,46}, Iris Scatoni⁴⁷, Rémy-Félix Serre⁴⁵, Ming Tang³⁷, Wenhua Tian³, Paul A. Umina⁴⁸, Manuella van Munster⁴⁹, Carole Vincent-Monégat⁷, Joshua Wemmer³, Alex C. C. Wilson⁸, Ying Zhang¹⁸, Chaoyang Zhao³, Jing Zhao^{35,36}, Serena Zhao⁴², Xin Zhou³⁷, François Delmotte^{16*†} and Denis Tagu^{30*†}

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>.

* Correspondence: claudio.rispe@inrae.fr; fabrice.legeai@inrae.fr; francois.delmotte@inrae.fr; denis.tagu@inrae.fr

† Claude Rispe and Fabrice Legeai are co-first authors.

‡ François Delmotte and Denis Tagu are co-last authors.

¹BIOEPAR, INRAE, Oniris, Nantes, France

²BIPAA, IGEPP, Agrocampus Ouest, INRAE, Université de Rennes 1, 35650 Le Rheu, France

¹⁶SAVE, INRAE, Bordeaux Sciences Agro, Villenave d’Ornon, France

³⁰IGEPP, Agrocampus Ouest, INRAE, Université de Rennes 1, 35650 Le Rheu, France

Full list of author information is available at the end of the article



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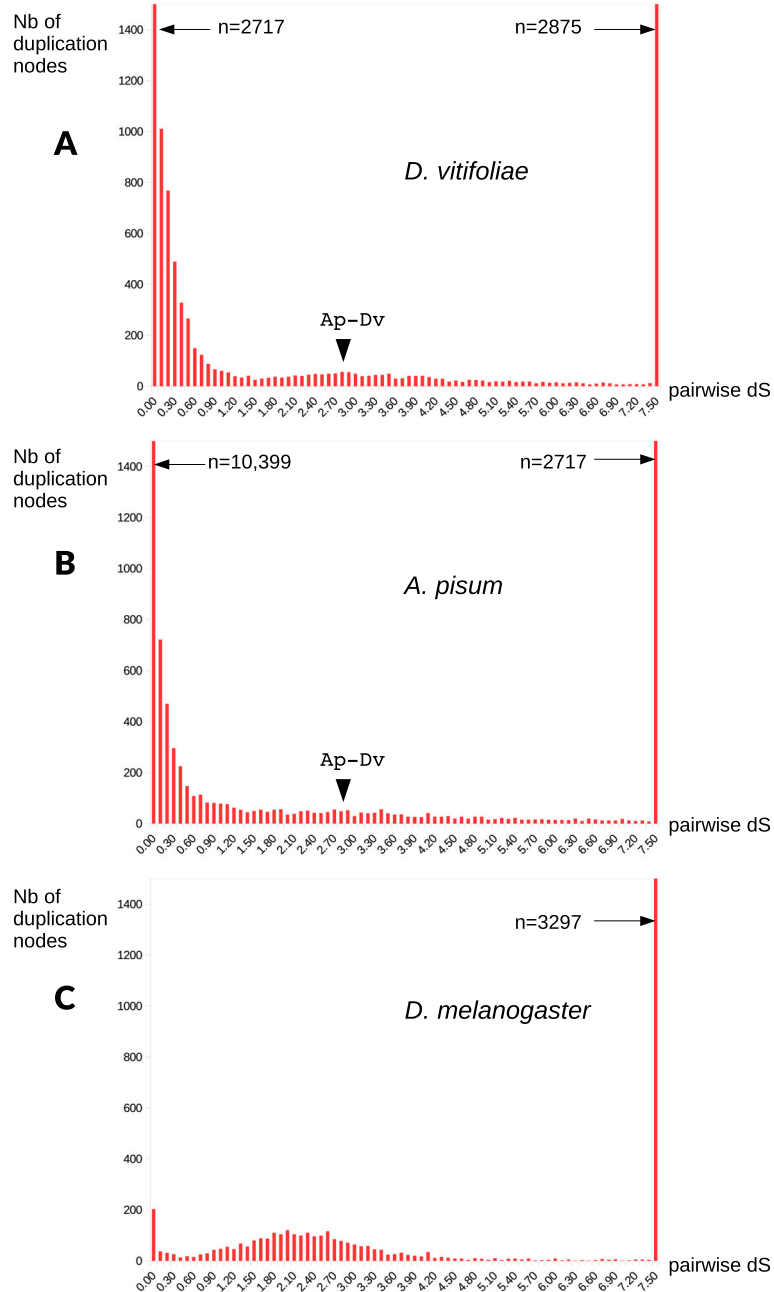


Fig. 4 Distribution of synonymous distances among paralogs for grape vine phylloxera (panel **a**, *D. vitifoliae*), pea aphid (panel **b**, *A. pisum*), and fruit fly (panel **c**, *D. melanogaster*). Paralogs were identified as RBH pairs, with an iterative approach allowing to cover both recent duplications (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

Author details

¹BIOEPAR, INRAE, Oniris, Nantes, France. ²BIPAA, IGEPP, Agrocampus Ouest, INRAE, Université de Rennes 1, 35650 Le Rheu, France. ³Department of Botany and Plant Sciences, University of California, Riverside, USA. ⁴Bioinformatics and Genomics Unit, Centre for Genomic Regulation (CRG), Barcelona Institute of Science and Technology, Dr. Aiguader, 88, 08003 Barcelona, Spain. ⁵Present address: Institute of Evolutionary Biology (CSIC-UPF), Passeig marítim de la Barceloneta 37-49, 08003 Barcelona, Spain. ⁶Department of Entomology, Cornell University, Ithaca, NY 14853, USA. ⁷Univ Lyon, INSA-Lyon, INRAE, BF21, UMR0203, F-69621 Villeurbanne, France. ⁸Department of Biology, University of Miami, Coral Gables, FL 33146, USA. ⁹Facultad de Agronomía, Montevideo, Uruguay. ¹⁰Institut de Biologia Integrativa de Sistemes, Parc Científic Universitat de València, C/ Catedrático José Beltrán n° 2, 46980 Paterna, València, Spain. ¹¹Université de Tunis El Manar, Faculté des Sciences de Tunis, LR01ES05 Biochimie et Biotechnologie, 2092 Tunis, Tunisia. ¹²Department Biol, Univ Rochester, Rochester, NY 14627, USA. ¹³Laboratoire Evolution, Génomes, Comportement, Ecologie CNRS, Univ. Paris-Sud, IRD, Université Paris-Saclay, Gif-sur-Yvette, France. ¹⁴LIPM, Université de Toulouse, INRAE, CNRS, Castanet-Tolosan, France. ¹⁵Sorbonne Université, UPEC, Université Paris 7, INRAE, CNRS, IRD, Institute of Ecology and Environmental Sciences, Paris, France. ¹⁶SAVE, INRAE, Bordeaux Sciences Agro, Villenave d'Ornon, France. ¹⁷Department of Molecular Biology and Genetics, Cornell University, Ithaca, NY 14853, USA. ¹⁸Department of Cell and Molecular Biology, College of the Environment and Life Sciences, University of Rhode Island, Kingston, RI, USA. ¹⁹Departament de Genètica, Microbiologia i Estadística and Institut de Recerca de la Biodiversitat (IRBio), Universitat de Barcelona, 08028 Barcelona, Spain. ²⁰Department of Biology, University of Miami, Coral Gables, USA. ²¹Current affiliation: Boyce Thompson Institute for Plant Research, Cornell University, Ithaca, USA. ²²Universität für Bodenkultur (BOKU), Vienna, Austria. ²³Universitat Pompeu Fabra, 08003 Barcelona, Spain. ²⁴Institució Catalana de Recerca i Estudis Avançats (ICREA), Pg. Lluís Companys 23, 08010 Barcelona, Spain. ²⁵Centre for Genomic Regulation (CRG), The Barcelona Institute of Science and Technology, Barcelona, Spain. ²⁶Universitat Pompeu Fabra (UPF), Barcelona, Spain. ²⁷Université Côte d'Azur, INRAE, CNRS, Institut Sophia Agrobiotech, Sophia-Antipolis, France. ²⁸Institute of Biotechnology and Department of Entomology, College of Bioresources and Agriculture, National Taiwan University, Taipei, Taiwan. ²⁹Present affiliation: Bone and Joint Research Center, Chang Gung Memorial Hospital, Taoyuan, Taiwan. ³⁰GEPP, Agrocampus Ouest, INRAE, Université de Rennes 1, 35650 Le Rheu, France. ³¹INRAE, Institute of Ecology and Environmental Sciences, Versailles, France. ³²Department of Entomology, Texas A&M University, College Station, TX 77843, USA. ³³Université Côte d'Azur, INRAE, CNRS, Institut Sophia Agrobiotech, Sophia-Antipolis, France. ³⁴Laboratoire d'Anthropobiologie Moléculaire et d'Imagerie de Synthèse, CNRS UMR 5288, Université de Toulouse, Université Paul Sabatier, Toulouse, France. ³⁵China National GeneBank-Shenzhen, BGI-Shenzhen, Shenzhen 518083, Guangdong Province, People's Republic of China. ³⁶BGI-Shenzhen, Shenzhen 518083, Guangdong Province, People's Republic of China. ³⁷Department of Entomology, College of Plant Protection, China Agricultural University, Beijing 100193, People's Republic of China. ³⁸Université Côte d'Azur, INRAE, CNRS, ISA, Sophia Antipolis, France. ³⁹Department of Post-Modern Agriculture, MingDao University, Changhua, Taiwan. ⁴⁰Institut de Biologia Integrativa de Sistemes, Parc Científic Universitat de València, C/ Catedrático José Beltrán n° 2, 46980 Paterna, València, Spain. ⁴¹Sorbonne Université, Institute of Ecology and Environmental Sciences, Paris, France. ⁴²Department of Integrative Biology, University of Texas at Austin, Austin, USA. ⁴³Univ Lyon, INRAE, INSA-Lyon, CNRS, UCBL, UMR5240 MAP, F-69622 Villeurbanne, France. ⁴⁴BIPAA IGEPP, Agrocampus Ouest, INRAE, Université de Rennes 1, 35650 Le Rheu, France. ⁴⁵Plateforme Génomique GeT-PlaGe, Centre INRAE de Toulouse Midi-Pyrénées, 24 Chemin de Borde Rouge, Auzeville, CS 52627, 31326 Castanet-Tolosan Cedex, France. ⁴⁶Division of Genetics, Department of Medicine, Brigham and Women's Hospital, Harvard Medical School, Boston,

MA 02115, USA. ⁴⁷Facultad de Agronomía, Montevideo, Uruguay. ⁴⁸School of BioSciences, The University of Melbourne, Parkville, VIC, Australia. ⁴⁹BGPI, Université Montpellier, CIRAD, INRAE, Montpellier SupAgro, Montpellier, France.

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>.