

Erratum: Comparative genomics reveals high prophage diversity and horizontal gene transfer of effectors and phage defence systems in the *Pseudomonas syringae* complex

Dominique Holtappels^{1,*}, George E.J. Rickus², Túlio Morgan³, Rafael R. de Rezende³, Britt Koskella^{2,4} and Poliane Alfenas-Zerbini³

Microbial Genomics 2026;12, doi: 10.1099/mgen.0.001711

In the published version of this article, the legends for Figs 2 and 3 were incorrectly switched. The correct figure legends are provided below. The published article has been updated accordingly.

The Microbiology Society apologises for any inconvenience caused.

Funding information

This research was funded by an NSF and USDA/NIFA Career Award (NSF # 1942881, USDA/NIFA # 1024053). We further acknowledge the Coordenação de Aperfeiçoamento Pessoal de Nível Superior-Brasil (CAPES) PrInt #88887.697048/2022-00, Fundação de Amparo à Pesquisa do Estado de Minas Gerais (FAPEMIG) Fapemig #APQ-00661-18, INCT Plant Pest Interactions #406440/2022-0 and Conselho Nacional de Desenvolvimento Científico e Tecnológico (CNPq #313528/2021-7). B.K. is a Chan-Zuckerberg San Francisco Biohub investigator. DH was supported by NIFA Multistate HATCH funding (#NE2335).

Conflicts of interest

The authors declare that there are no conflicts of interest.

Received 29 May 2026; Published 18 June 2026

Author affiliations: ¹Plant Pathology and Plant-Microbe Biology section, School of Integrative Plant Science, Cornell University, Cornell AgriTech, Geneva, NY, USA; ²Department of Integrative Biology, University of California, Berkeley, CA, USA; ³Departamento de Microbiologia, Instituto de Biotecnologia Aplicada à Agropecuária, Viçosa 36570-900, MG, Brazil; ⁴Chan-Zuckerberg Biohub, San Francisco, CA, USA.

***Correspondence:** Dominique Holtappels, Dh774@cornell.edu

001761 © 2026 The Authors



This is an open-access article distributed under the terms of the Creative Commons Attribution License.

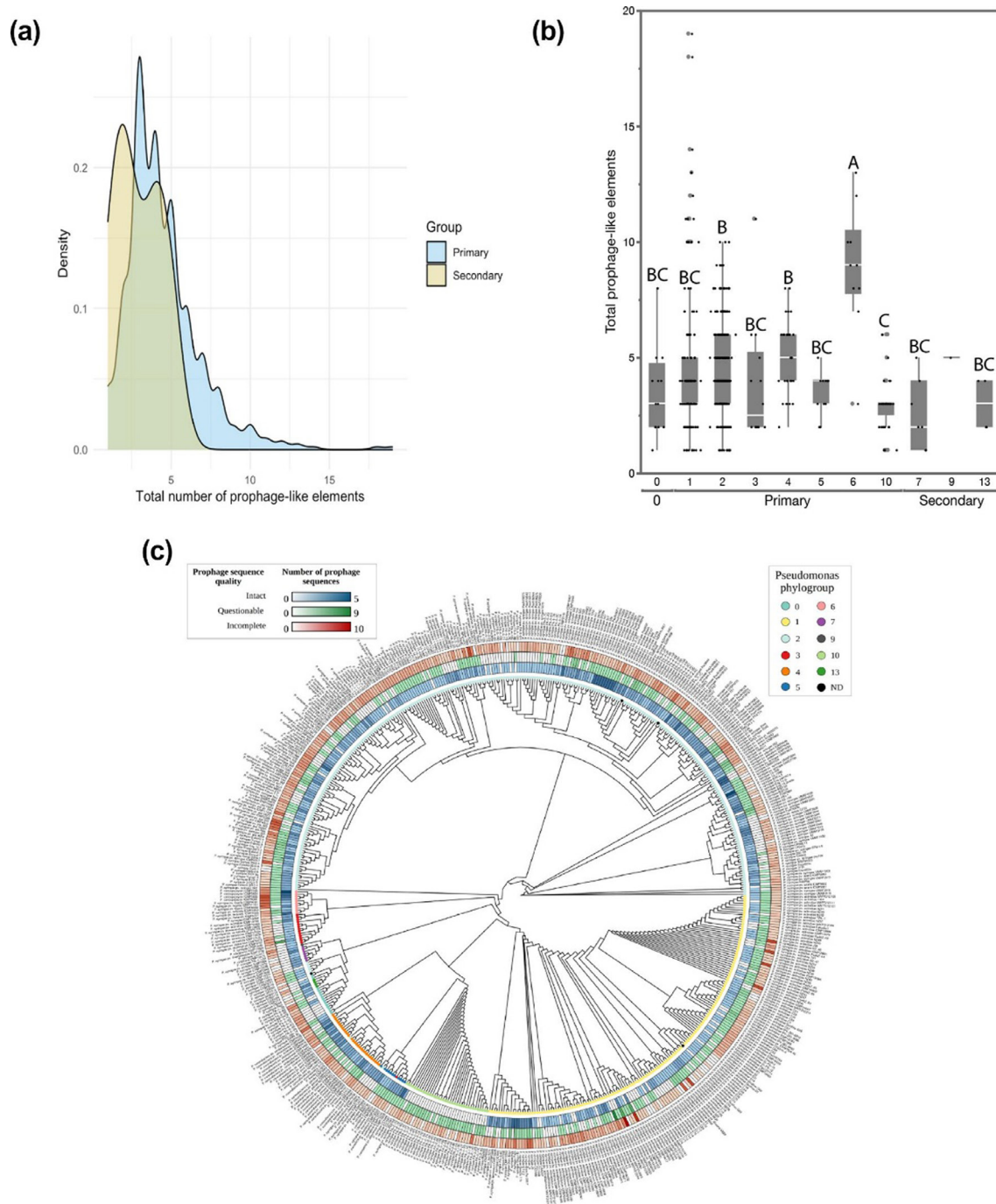


Fig. 2. Number of prophage-like elements encoded in the *P. syringae* species complex. (a) Distribution of primary (blue) and secondary (yellow) phylogroups and the total number of prophage-like elements encoded with significantly more prophage-like elements encoded in the primary phylogroups (Student's t-test, P -value=0.0017). (b) Quantile box plots of the total number of prophage-like elements per individual phylogroup. Based on a Tukey –Kramer test with corrections for multiple comparisons, three groups of significance were identified with phylogroups 6 on average the highest number of prophage-like elements per genome as summarized with connecting letters indicating the groups of significance (A, B, and C). (c) Phylogenetic tree of 587 *Pseudomonas* isolates. The “ggtree” package in the R environment was used for tree visualization ignoring branch lengths. Heatmaps were added as concentric rings at the tree tips, representing the quality and quantity of prophages detected in each *P. syringae* genome by PHASTER.

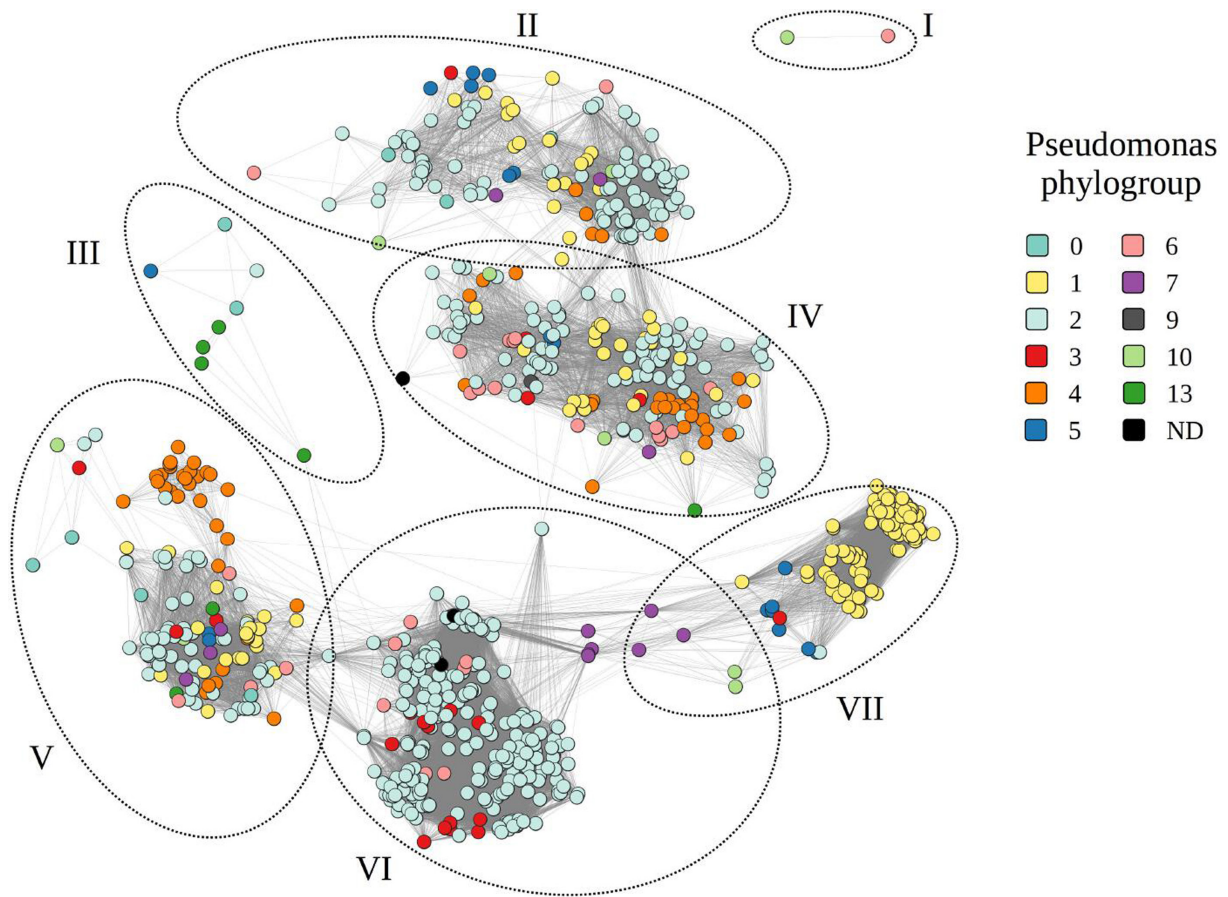


Fig. 3. Gene sharing network between the different prophage genomes annotated in the *P. syringae* species complex. The nodes are colored along the phylogroup (PG0, teal; PG1, yellow; PG2, light blue; PG3, red; PG4, orange; PG5, blue; PG6, pink; PG7, purple; PG9, grey; PG10, light green; PG13, dark green). Every connection represents a similarity to another predicted viral sequence. The different clusters are outlined and numbered (I, II, III, IV, V, VI, VII).