

Plastid phylogenomics resolves ambiguous relationships within the orchid family and provides a solid timeframe for biogeography and macroevolution

Maria Alejandra Serna-Sánchez^{1,2+}, Oscar A. Pérez-Escobar^{3*+}, Diego Bogarín^{4,5+}, María Fernanda Torres⁶, Astrid Catalina Alvarez-Yela⁷, Juliana E. Arcila¹, Climbie F. Hall⁸, Fabio Pinheiro⁹, Steven Dodsworth¹⁰, Mark W. Chase³, Alexandre Antonelli^{3,6,11}, Tatiana Arias^{1,7,12*}

¹ Laboratorio de Biología Comparativa. Corporación para Investigaciones Biológicas (CIB), Cra. 72 A No. 78 B 141, Medellín, Colombia.

² Biodiversity, Evolution and Conservation. EAFIT University, Cra. 49, No. 7 sur 50, Medellín, Colombia.

³ Royal Botanic Gardens, Kew, TW9 3AE, London, UK.

⁴ Jardín Botánico Lankester, Universidad de Costa Rica, P. O. Box 302-7050, Cartago, Costa Rica.

⁵ Naturalis Biodiversity Center, Endless Forms group, P.O. Box 9517, 2300 RA Leiden, The Netherlands; Herbario UCH, Universidad Autónoma de Chiriquí, David, Panamá.

⁶ Gothenburg Global Biodiversity Centre, Department of Biological and Environmental Sciences, University of Gothenburg, 405 30 Gothenburg, Sweden.

⁷ Centro de Bioinformática y Biología Computacional (BIOS). Ecoparque Los Yarumos Edificio BIOS, Manizales, Colombia.

⁸ Universidade Federal de Mato Grosso do Sul, Tres Lagos, Mato Grosso, Brazil.

⁹ Universidade Estadual de Campinas, Instituto de Biologia, Departamento de Biologia Vegetal, 13083-862, Campinas-SP, Brazil

¹⁰ School of Life Sciences, University of Bedfordshire, University Square, Luton, LU1 3JU, UK.

¹¹ Department of Plant Sciences, University of Oxford, South Parks Road, OX1 3RB Oxford, United Kingdom

¹² Tecnológico de Antioquia, Calle 78B NO. 72A - 220 Medellín- Colombia

* Corresponding Authors: T.A. (tatiana.arias48@tdea.edu.co) & O.A.P.E. (o.perez-escobar@kew.org)

+These authors contributed equally to the study.

ONLINE SUPPLEMENTARY MATERIAL:

Including Supplementary Tables S1-S5

Including Supplementary Figures S1-S4

Supplementary tables

Table S1. Absolute age estimations derived from a strict clock and a Birth-Death tree model applied to a dataset of 264 terminals and 78-coding-sequence plastid gene concatenated alignment. The table is composed of 16 columns and 529 rows and is freely available at <https://doi.org/10.6084/m9.figshare.14068892>.

Table S2. Absolute age estimations derived from a relaxed clock and a Birth-Death tree model applied to a dataset of 264 terminals and 78-coding-sequence plastid gene concatenated alignment. The table is composed of 16 columns and 529 rows and is freely available at <https://doi.org/10.6084/m9.figshare.14068892>.

Table S3. Per-site maximum and minimum phylogenetic informativeness (PI) values per locus, estimated from a dataset of 264 terminals and 78-coding-sequence plastid gene alignments. The table is composed of 80 columns and five rows and is freely available at <https://doi.org/10.6084/m9.figshare.14068892>.

Table S4. Net maximum and minimum phylogenetic informativeness (PI) values per locus, estimated from a dataset of 264 terminals and 78-coding-sequence plastid gene alignments. The table is composed of 80 columns and five rows and is freely available at <https://doi.org/10.6084/m9.figshare.14068892>.

Table S5. Species names and voucher information for material sampled in this study. Newly sequenced taxa are highlighted in light blue. The table is composed of 266 columns and seven rows and is freely available at <https://doi.org/10.6084/m9.figshare.14068892>.

Supplementary figures

Figure S1. Detailed maximum likelihood tree of the orchid family inferred from 78 plastid genes. LBP <100 are shown at nodes, with LBP <85 highlighted in red together with their corresponding subtending branches.

Figure S2. Chronogram of the orchid family as inferred from a strict molecular clock and a birth-death model. LBP at nodes <85 are highlighted in red together with their corresponding subtending branches. Blue bars at nodes denote 95% high density probability (HDP) absolute age intervals.

Figure S3. Chronogram of the orchid family as inferred from a relaxed molecular clock and a birth-death model. LBP at nodes <85 are highlighted in red together with their corresponding subtending branches. Blue bars at nodes denote 95% high density probability (HDP) absolute age intervals.

Figure S4. Phylogenetic informativeness (PI) of 78 plastid gene alignments used in this study to infer orchid relationships. A) Chronogram of Orchidaceae as inferred by PATH8 from the ML tree derived from RAxML; B) Per-site PI; C) Net PI.







