DOI: 10.1002/ajb2.16049

Corrigendum

In 2021, the special issue of the *American Journal of Botany* "Exploring Angiosperms353: a Universal Toolkit for Flowering Plant Phylogenomics" included several papers that did not fully meet the data availability standards required by the journal. The following articles have been updated, and the revised data availability statements are included here. We apologize for this error.

REFERENCE

Antonelli, A., J. J. Clarkson, K. Kainulainen, O. Maurin, G. E. Brewer, A. P. Davis, N. Epitawalage, et al. 2021. Settling a family feud: a high-level phylogenomic framework for the Gentianales based on 353 nuclear genes and partial plastomes. *American Journal of Botany* 108(7): 1143–1165. https://doi.org/10.1002/ajb2.1697.

Data Availability Statement

All sequences generated for this study are available in the European Nucleotide Archive (ENA) in a custom project area at: https://www.ebi.ac.uk/ena/browser/view/PRJEB35285, and their accession numbers are provided in Appendix S1. The data set is also available via the Kew Tree of Life Explorer (https://treeoflife.kew.org/) using the FTP tab (http://sftp.kew.org/pub/paftol/current_release/). All alignments, Newick tree files, and matrix of genes used in this study can be found at Zenodo: https://doi.org/10.5281/zenodo.6555898.

REFERENCE

Pérez-Escobar, O. A., S. Dodsworth, D. Bogarín, S. Bellot, J. A. Balbuena, R. J. Schley, I. A. Kikuchi, S. K. Morris, et al. 2021. Hundreds of nuclear and plastid loci yield novel insights into orchid relationships. *American Journal of Botany* 108(7): 1166–1180. https://doi.org/10.1002/ajb2.1702.

Data Availability Statement

Raw sequence data generated in this study are accessible via the European Nucleotide Archive (https://www.ebi.ac.uk/ena/browser/home) under project HYPERLINK "http://www.peptideatlas.org/PASS/PRJEB35285" PRJEB35285 and via the Kew Tree of Life Explorer (https://treeoflife.kew.org/). High-resolution figures presented in the supplementary material, together with the raw per-site and net PI values, are freely available at Figshare: https://doi.org/10.6084/m9.figshare.14287538. Multiple DNA sequence alignments of the Angiosperm353 nuclear genes and their corresponding Maximum Likelihood gene trees and the supermatrix phylogeny are accessible via Zenodo: https://zenodo.org/record/6779447#.YrxklnaZOUl.

REFERENCE

Pillon, Y., H. C. F. Hopkins, O. Maurin, N. Epitawalage, J. Bradford, Z. S. Rogers, W. J. Baker, and F. Forest. 2022. Phylogenomics and biogeography of Cunoniaceae (Oxalidales) with complete generic sampling and taxonomic realignments. *American Journal of Botany* 108(7): 1181–1200. https://doi.org/10.1002/ajb2.1688.

Data Availability Statement

All Sequences files (fastq) generated for this study are deposited in the European Nucleotide Archive (ENA accession HYPERLINK "http://www.peptideatlas.org/PASS/PRJEB35285" PRJEB35285; Appendix S1). All alignments, Newick tree files, and matrix of genes used for divergence time estimates can be found at Zenodo: https://doi.org/10.5281/zenodo.6617160.

REFERENCE

Shah, T., J. V. Schneider, G. Zizka, O. Maurin, W. Baker, F. Forest, G. E. Brewer, et al. 2021. Joining forces in Ochnaceae phylogenomics: a tale of two targeted sequencing probe kits. *American Journal of Botany* 108(7): 1201–1216. https://doi.org/10.1002/ajb2.1682.

Data Availability Statement

Raw sequence data for the Ochnaceae-specific probe kit are available from GenBank SRA under the Bioproject number PRJNA602196: http://www.ncbi.nlm.nih.gov/bioproject/602196 (Schneider et al., 2020). Raw sequence data for the universal Angiosperms353 probe kit are available from European Nucleotide Archive under the umbrella project number PRJEB35285:

https://www.ebi.ac.uk/ena/browser/view/PRJEB35285. Voucher information for all samples used are listed in Appendix 1. All the sequence alignments, gene trees and species trees for both probe kits and the combined dataset are available from the Dryad Digital Repository at https://doi.org/10.5061/dryad.2547d7wsz.

REFERENCE

Buerki, S., Callmander, M. W., Acevedo-Rodriguez, P., Lowry, P. P., Munzinger, J., Bailey, P., Maurin, O., Brewer, G. E., Epitawalage, N., Baker, W. J., Forest, F. 2021. An updated infra-familial classification of Sapindaceae based on targeted enrichment data. *American Journal of Botany* 108(7): 1234–1251. https://doi.org/10.1002/ajb2.1693.

Data Availability Statement

The data (a spreadsheet summarizing sampling as well as ASTRAL and RAxML phylogenetic trees in newick format) and R code (scripts to produce Table 1, Fig. 1, and Appendices S2 and S3) underpinning this study are available on GitHub: https://github.com/svenbuerki/Angio353_Sapindaceae. All Sequences files (fastq) generated for this study are deposited in the European Nucleotide Archive (ENA accession PRJEB35285; Appendix S1). All alignments and Newick tree files can be found at Zenodo: https://doi.org/10.5281/zenodo.6616570.

REFERENCE

Clarkson, J. J., A. R. Zuntini, O. Maurin, S. R. Downie, G. M. Plunkett, A. A. Nicolas, J. F. Smith, et al. 2011. A higher-level nuclear phylogenomic study of the carrot family (Apiaceae). *American Journal of Botany* 108(7): 1252–1269. https://doi.org/10.1002/ajb2.1701.

Data Availability Statement

All sequences generated for this study are available in the European Nucleotide Archive (ENA) in a custom project area at: https://www.ebi.ac.uk/ena/browser/view/PRJEB35285 (see Appendix S2 for accession numbers). The dataset is also available via the Kew Tree of Life Explorer (https://treeoflife.kew.org/) using the FTP tab (http://sftp.kew.org/pub/paftol/current_release/). Taxa which had been sequenced previously were mined from the ENA and NCBI (National Center for Biotechnology Information) databases. Recovery statistics were generated using custom scripts available at GitHub: https://github.com/sidonieB/. All alignments, Newick tree files, and gene matrices used in this study can be found at Zenodo: https://doi.org/10.5281/zenodo.6631246.

REFERENCE

Thomas, A. E., J. Igea, H. M. Meudt, D. C. Albach, W. G. Lee, and A. J. Tanentzap. 2021. Using target sequence capture to improve the phylogenetic resolution of a rapid radiation in New Zealand Veronica. *American Journal of Botany* 108(7): 1289–1306. https://doi.org/10.1002/ajb2.1678.

Data Availability Statement

Raw Illumina sequencing reads have been deposited in the NCBI Sequence Read Archive at http://www.ncbi.nlm.nih.gov/bioproject/715342. Alignments and phylogenies used in the analysis are available on Zenodo: https://doi.org/10.5281/zenodo.6639322. All analysis scripts are available at GitHub: https://github.com/annethomas/veronica_phylo.