Summary of 15 phylogenomic datasets examined in this study.

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| Study ID | Dataset | Taxon  Level | No.  Taxa | No  Loci | Sampling Method | Data  Type | Study Reference |
| Bee | Animal: Bees | Genus | 190 | 753 | UCE | DNA | Blaimer et al. Evolution, 2018 1 |
| Bird | Animal: Birds | Class | 200 | 259 | AHE | DNA | Prum et al. Nature, 2015 2 |
| Butterfly | Animal: Butterflies | Order | 207 | 352 | AHE | DNA | Espeland et al. Current Biology, 2018 3 |
| Lizard | Animal: Lizards | Genus | 29 | 1361 | Exon-Capture | DNA | Blom et al. Syst Biol, 2017 4 |
| Marine-fish | Animal: Marine fishes | Superorder | 120 | 1001 | UCE | DNA | Alfaro et al. 2018, Nat. Ecol. Evol. 5 |
| Rodent | Animal: Rodents | Family | 37 | 1245 | Exon-Capture | DNA | Roycroft et al. Syst Biol, 2019 6 |
| Cardueae | Plant: Cardueae | Family | 85 | 570 | UCE | DNA | Herrando-Moraira et al. Mol Phyloge Evol, 20187 |
| Caryophyllales | Plant: Caryophyllales | Order | 95 | 1122 | Transcriptome | AA | Yang et al. Mol Biol Evol, 2015 8 |
| Green-Plants | Plant: Green plants | Phylum | 1178 | 410 | Transcriptome | AA | 1KP Initiative 2019, Nature 9 |
| Jaltomata | Plant: Jaltomata | Genus | 15 | 6431 | Transcriptome | DNA | Wu et al. Mol Ecol, 2018 10 |
| Protea | Plant: Protea | Genus | 65 | 498 | AHE | DNA | Mitchell et al. American Journal of Botany, 2017 11 |
| Aspergillaceae | Fungi: Aspergillaceae | Order | 93 | 1668 | Genome | DNA | Steenwyk et al. mBio, 2019 12 |
| Saccharomycotina-Cell | Fungi: Budding yeasts | Subphylum | 343 | 2408 | Genome | AA | Shen et al. 2018, Cell 13 |
| Hanseniaspora | Fungi: Hanseniaspora | Family | 29 | 1033 | Genome | AA | Steenwyk et al. PloS Biol, 2019 14 |
| Rhizoplaca | Fungi: Rhizoplaca | Genus | 31 | 303 | Genome | DNA | Leavitt et al., Sci Rep, 2016 15 |

UCE: Ultraconserved Element, AHE: Anchored Hybrid Enriched, DNA: deoxyribonucleic acid, AA: amino acid.

**References**

1. Blaimer, B. B., Mawdsley, J. R. & Brady, S. G. Multiple origins of sexual dichromatism and aposematism within large carpenter bees. *Evolution (N. Y).* **72**, 1874–1889 (2018).

2. Prum, R. O. *et al.* A comprehensive phylogeny of birds (Aves) using targeted next-generation DNA sequencing. *Nature* **526**, 569–573 (2015).

3. Espeland, M. *et al.* A Comprehensive and Dated Phylogenomic Analysis of Butterflies. *Curr. Biol.* **28**, 770-778.e5 (2018).

4. Blom, M. P. K., Bragg, J. G., Potter, S. & Moritz, C. Accounting for uncertainty in gene tree estimation: Summary-coalescent species tree inference in a challenging radiation of Australian lizards. *Syst. Biol.* **66**, 352–366 (2017).

5. Alfaro, M. E. *et al.* Explosive diversification of marine fishes at the Cretaceous–Palaeogene boundary. *Nat. Ecol. Evol.* **2**, 688–696 (2018).

6. Roycroft, E. J., Moussalli, A. & Rowe, K. C. Phylogenomics Uncovers Confidence and Conflict in the Rapid Radiation of Australo-Papuan Rodents. *Syst. Biol.* **0**, 1–14 (2019).

7. Herrando-Moraira, S. *et al.* Exploring data processing strategies in NGS target enrichment to disentangle radiations in the tribe Cardueae (Compositae). *Mol. Phylogenet. Evol.* **128**, 69–87 (2018).

8. Yang, Y. *et al.* Dissecting molecular evolution in the highly diverse plant clade caryophyllales using transcriptome sequencing. *Mol. Biol. Evol.* **32**, 2001–2014 (2015).

9. One Thousand Plant Transcriptomes Initiative. One thousand plant transcriptomes and the phylogenomics of green plants. *Nature* **574**, 679–685 (2019).

10. Wu, M., Kostyun, J. L., Hahn, M. W. & Moyle, L. C. Dissecting the basis of novel trait evolution in a radiation with widespread phylogenetic discordance. *Mol. Ecol.* **27**, 3301–3316 (2018).

11. Mitchell, N., Lewis, P. O., Lemmon, E. M., Lemmon, A. R. & Holsinger, K. E. Anchored phylogenomics improves the resolution of evolutionary relationships in the rapid radiation of *protea* L. *Am. J. Bot.* **104**, 102–115 (2017).

12. Steenwyk, J. L., Shen, X.-X., Lind, A. L., Goldman, G. H. & Rokas, A. A Robust Phylogenomic Time Tree for Biotechnologically and Medically Important Fungi in the Genera *Aspergillus* and *Penicillium*. *MBio* **10**, 1–25 (2019).

13. Shen, X.-X. *et al.* Tempo and Mode of Genome Evolution in the Budding Yeast Subphylum. *Cell* **175**, 1533–1545 (2018).

14. Steenwyk, J. L. *et al.* Extensive loss of cell-cycle and DNA repair genes in an ancient lineage of bipolar budding yeasts. *PLOS Biol.* **17**, e3000255 (2019).

15. Leavitt, S. D. *et al.* Resolving evolutionary relationships in lichen-forming fungi using diverse phylogenomic datasets and analytical approaches. *Sci. Rep.* **6**, 22262 (2016).