

Chloroplast Phylogenomic Inference of Green Algae Relationships

Linhua Sun¹, Ling Fang¹, Zhenhua Zhang¹, Xin Chang¹, David Penny², Bojian
Zhong^{1,*}

¹Jiangsu Key Laboratory for Biodiversity and Biotechnology, College of Life
Sciences, Nanjing Normal University, Nanjing, China

² Institute of Fundamental Sciences, Massey University, Palmerston North, New
Zealand

*Corresponding author: Email: bjzhong@gmail.com

Table S1. The list of taxon names and z-scores.

Taxon name	Taxonomy	z-score
<i>Acetabularia acetabulum</i>	Ulvophyceae	8.62
<i>Halimeda cylindracea</i>	Ulvophyceae	6.46
<i>Oltmannsiellopsis viridis</i>	Ulvophyceae	5.94
<i>Trentepohlia annulata</i>	Ulvophyceae	5.66
<i>Bryopsis hypnoides</i>	Ulvophyceae	5.15
<i>Codium decortcatum</i>	Ulvophyceae	4.85
<i>Pseudendoclonium akinetum</i>	Ulvophyceae	3.59
<i>Cephaleuros parasiticus</i>	Ulvophyceae	1.89
<i>Hemichloris antarctica</i>	Trebouxiophyceae	17.36
<i>Coccomyxa sp.C-169</i>	Trebouxiophyceae	17.16
<i>Trebouxiophyceae sp.MX-AZ01</i>	Trebouxiophyceae	16.10
<i>Oocystis solitaria</i>	Trebouxiophyceae	8.69
<i>Geminella minor</i>	Trebouxiophyceae	6.94
<i>Gloeotilopsis sterilis</i>	Trebouxiophyceae	6.36
<i>Planctonema lauterbornii</i>	Trebouxiophyceae	5.50
<i>Parachlorella kessleri</i>	Trebouxiophyceae	4.94
<i>Dicloster acuatus</i>	Trebouxiophyceae	4.83
<i>Leptosira terrestris</i>	Trebouxiophyceae	4.02
<i>Marvania geminata</i>	Trebouxiophyceae	3.14
<i>Trebouxia aggregata</i>	Trebouxiophyceae	3.13
<i>Prasiolopsis sp.</i>	Trebouxiophyceae	2.01
<i>Watanabea reniformis</i>	Trebouxiophyceae	1.40
<i>Chlorella variabilis</i>	Trebouxiophyceae	-0.60
<i>Chlorella vulgaris</i>	Trebouxiophyceae	-0.68
<i>Scenedesmus obliquus</i>	Chlorophyceae	6.66
<i>Oedogonium cardiacum</i>	Chlorophyceae	6.43
<i>Stigeoclonium helveticum</i>	Chlorophyceae	5.62
<i>Schizomeris leibleinii</i>	Chlorophyceae	5.29
<i>Dunaliella salina</i>	Chlorophyceae	5.04
<i>Chlamydomonas moewusii</i>	Chlorophyceae	4.87
<i>Chlamydomonas reinhardtii</i>	Chlorophyceae	1.85
<i>Volvox carteri</i>	Chlorophyceae	1.79
<i>Floydiella terrestris</i>	Chlorophyceae	0.68
<i>Tetraselmis spp.</i>	Chlorodendrophyceae	1.15
<i>Marsupiomonas sp. NIES 1824</i>	Pedinophyceae	32.50
<i>Pedinomonas tuberculata</i>	Pedinophyceae	2.64
<i>Pedinomonas minor</i>	Pedinophyceae	1.98
<i>Pedinophyceae sp.YPF-701</i>	Pedinophyceae	1.78
<i>Nephroselmis astigmatica</i>	Prasinophyceae	34.68
<i>Prasinophyceae sp.MBIC 106222</i>	Prasinophyceae	25.32
<i>Micromonas sp.RCC 299</i>	Prasinophyceae	24.92
<i>Ostreococcus tauri</i>	Prasinophyceae	24.75
<i>Nephroselmis olivacea</i>	Prasinophyceae	22.91
<i>Pycnococcus provasolii</i>	Prasinophyceae	20.60
<i>Monomastix sp.OKE-1</i>	Prasinophyceae	5.56
<i>Prasinophyceae sp.CCMP 1205</i>	Prasinophyceae	5.36
<i>Prasinoderma coloniale</i>	Prasinophyceae	3.63
<i>Prasinococcus capsulatus</i>	Prasinophyceae	2.90
<i>Pyramimonas parkeae</i>	Prasinophyceae	2.81
<i>Pterosperma cristatum</i>	Prasinophyceae	2.49
<i>Picocystis salinarum</i>	Prasinophyceae	-1.65
<i>Mesostigma viride</i>	Streptophyta	6.21
<i>Chlorokybus atmophyticus</i>	Streptophyta	4.55

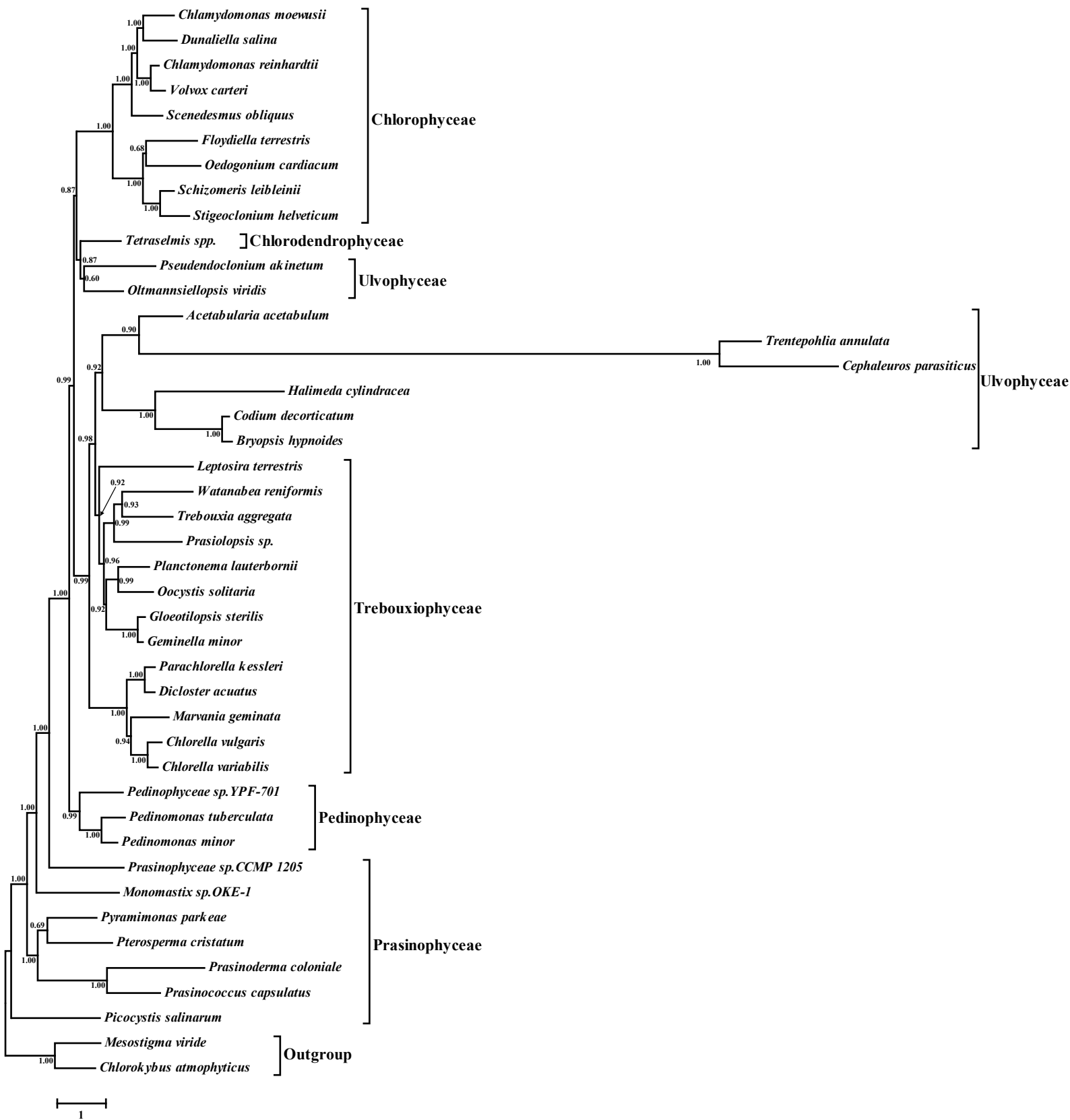


Figure S1. Bayesian phylogenetic tree under the CAT+GTR heterogeneous model based on 30,240 sites with 43 taxa. *Trentepohlia annulata* and *Cephaleuros parasiticus* exhibit extreme long branches. The posterior probability (PP) values are shown on the nodes.

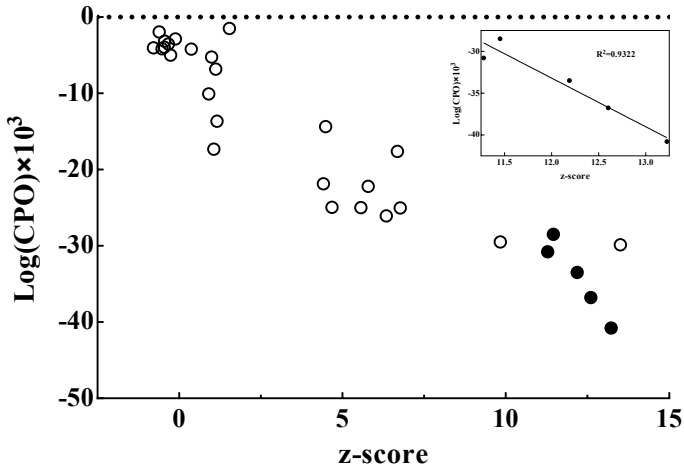


Figure S2. The correlation between the compositional heterogeneity and model fit for a series of subsets, each subset having 1,000 fast-evolving sites. The 5,000 fastest-evolving sites were marked with five solid circles.

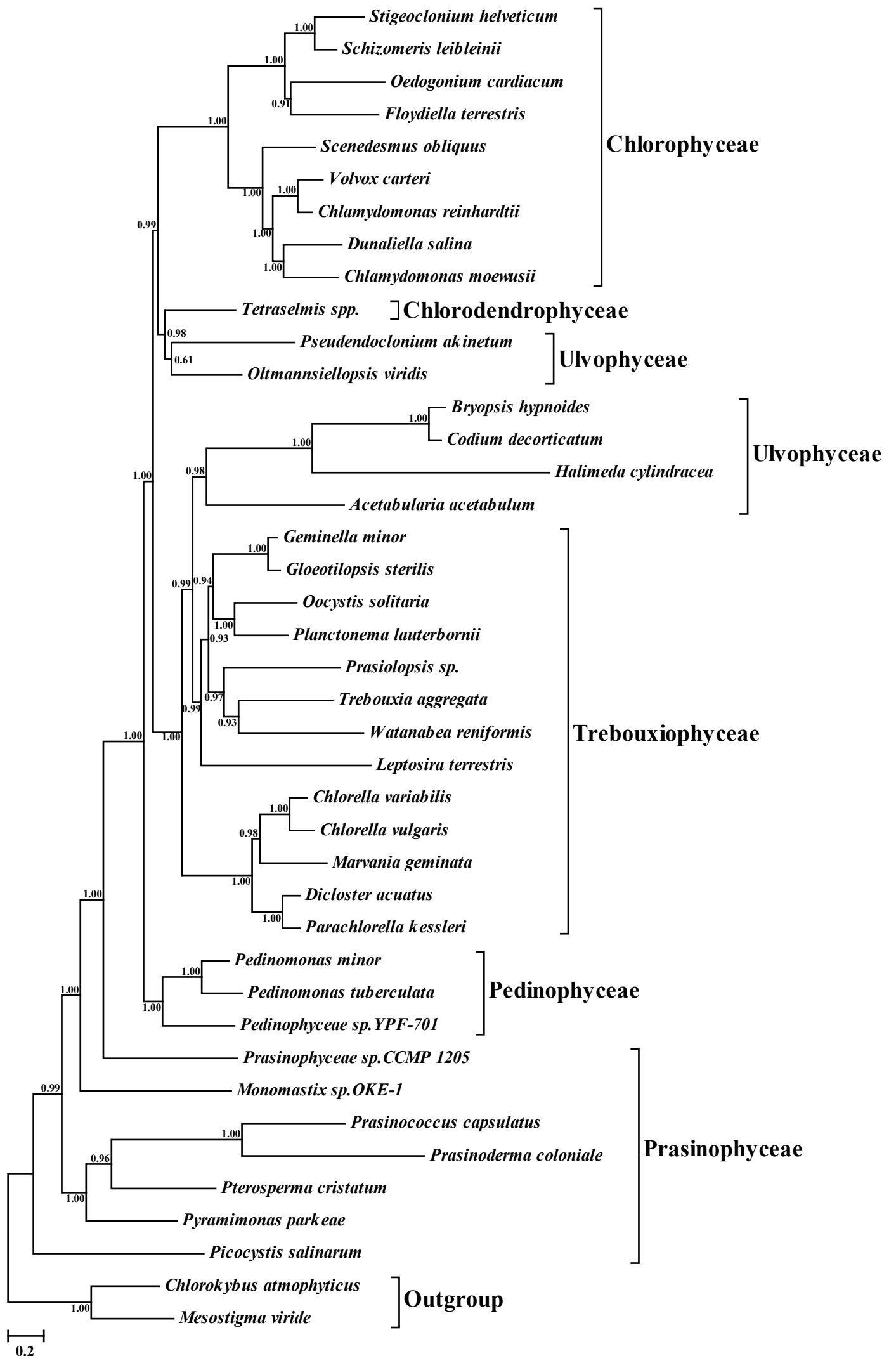


Figure S3. Bayesian phylogenetic tree under the CAT+GTR heterogeneous model based on 29,240 sites with 41 taxa. The posterior probability (PP) values are shown on the nodes.

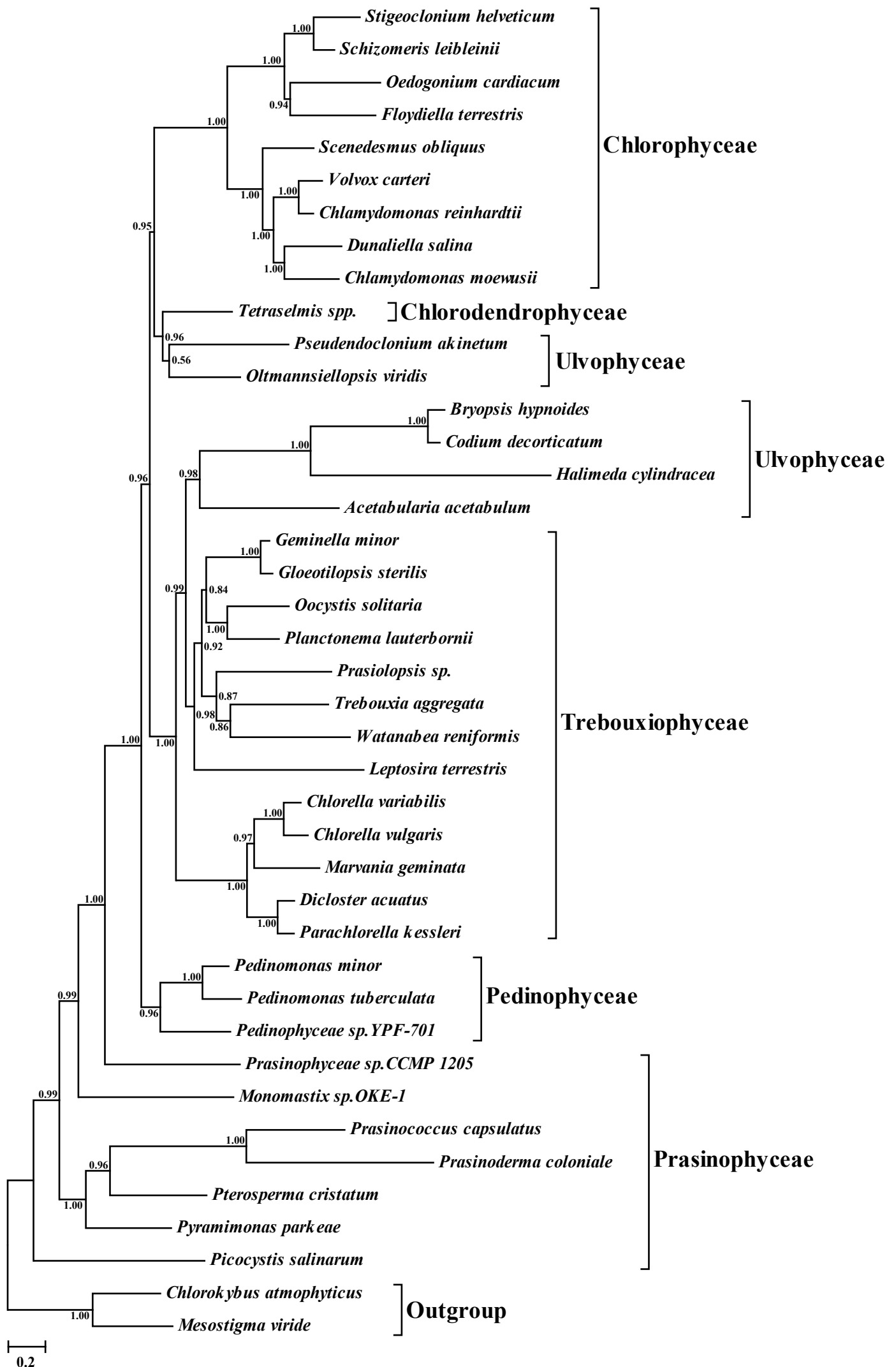


Figure S4. Bayesian phylogenetic tree under the CAT+GTR heterogeneous model based on 28,240 sites with 41 taxa. The posterior probability (PP) values are shown on the nodes.

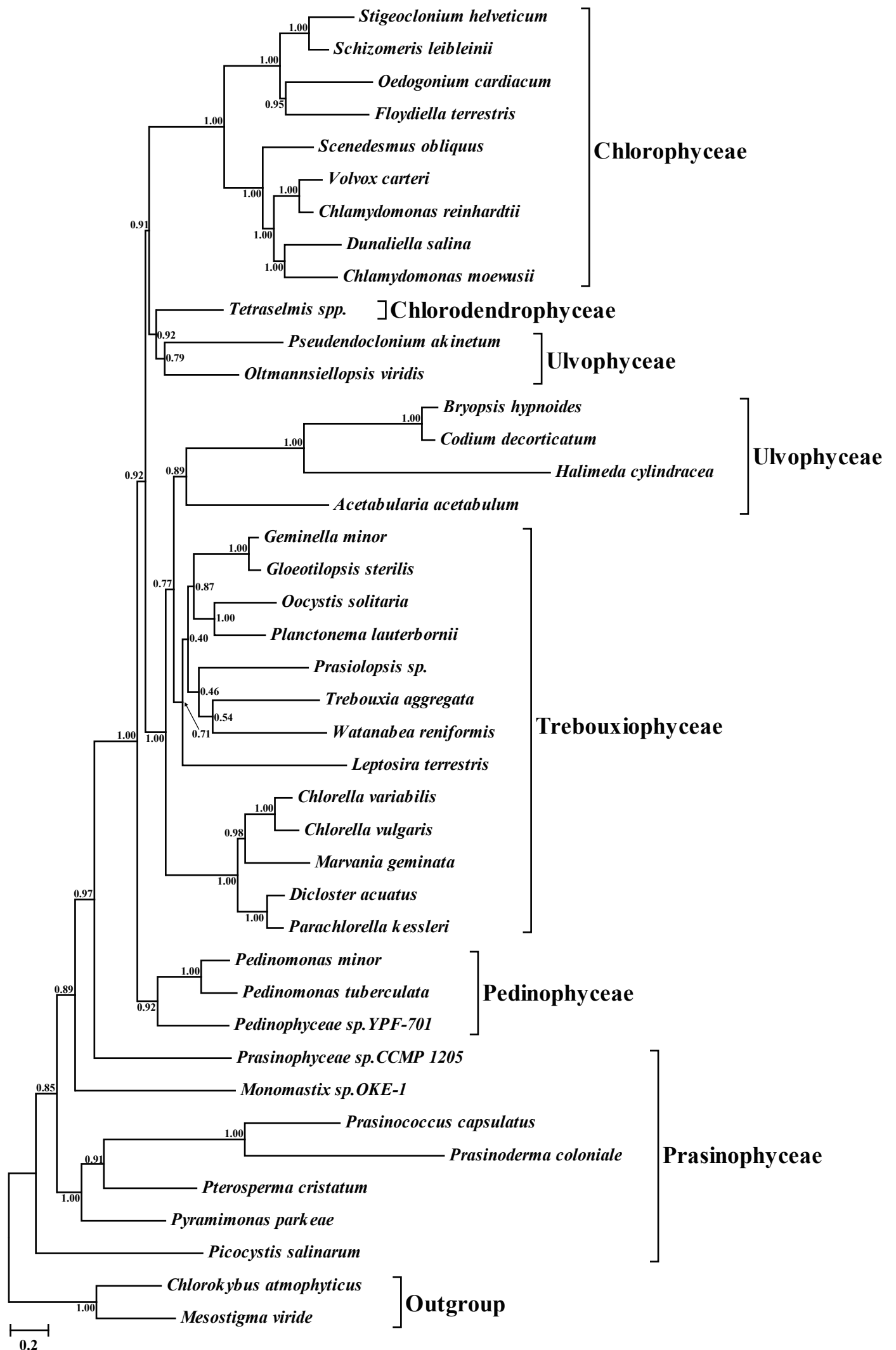


Figure S5. Bayesian phylogenetic tree under the CAT+GTR heterogeneous model based on 27,240 sites with 41 taxa. The posterior probability (PP) values are shown on the nodes.

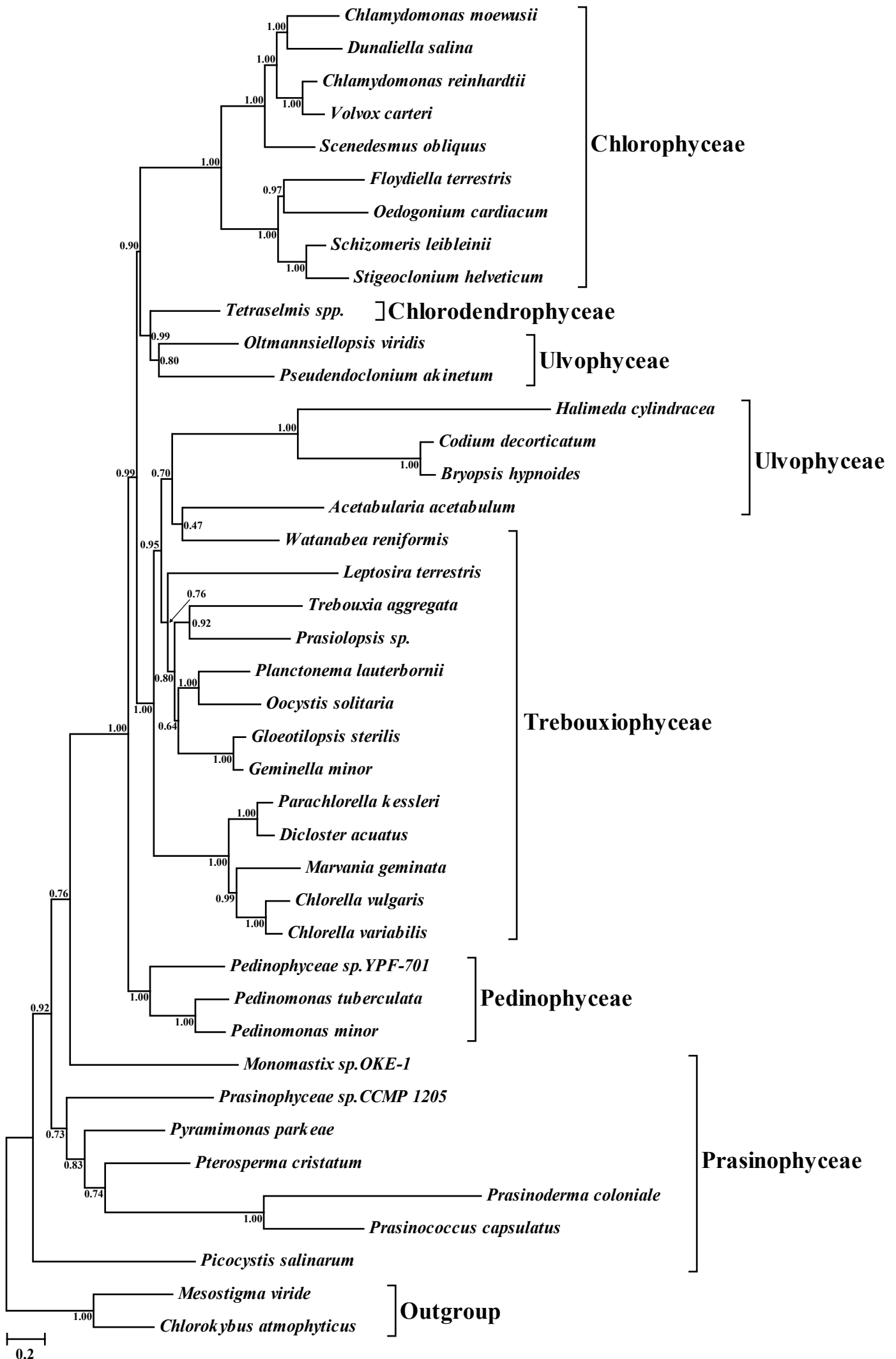


Figure S6. Bayesian phylogenetic tree under the CAT+GTR heterogeneous model based on 26,240 sites with 41 taxa. The posterior probability (PP) values are shown on the nodes.

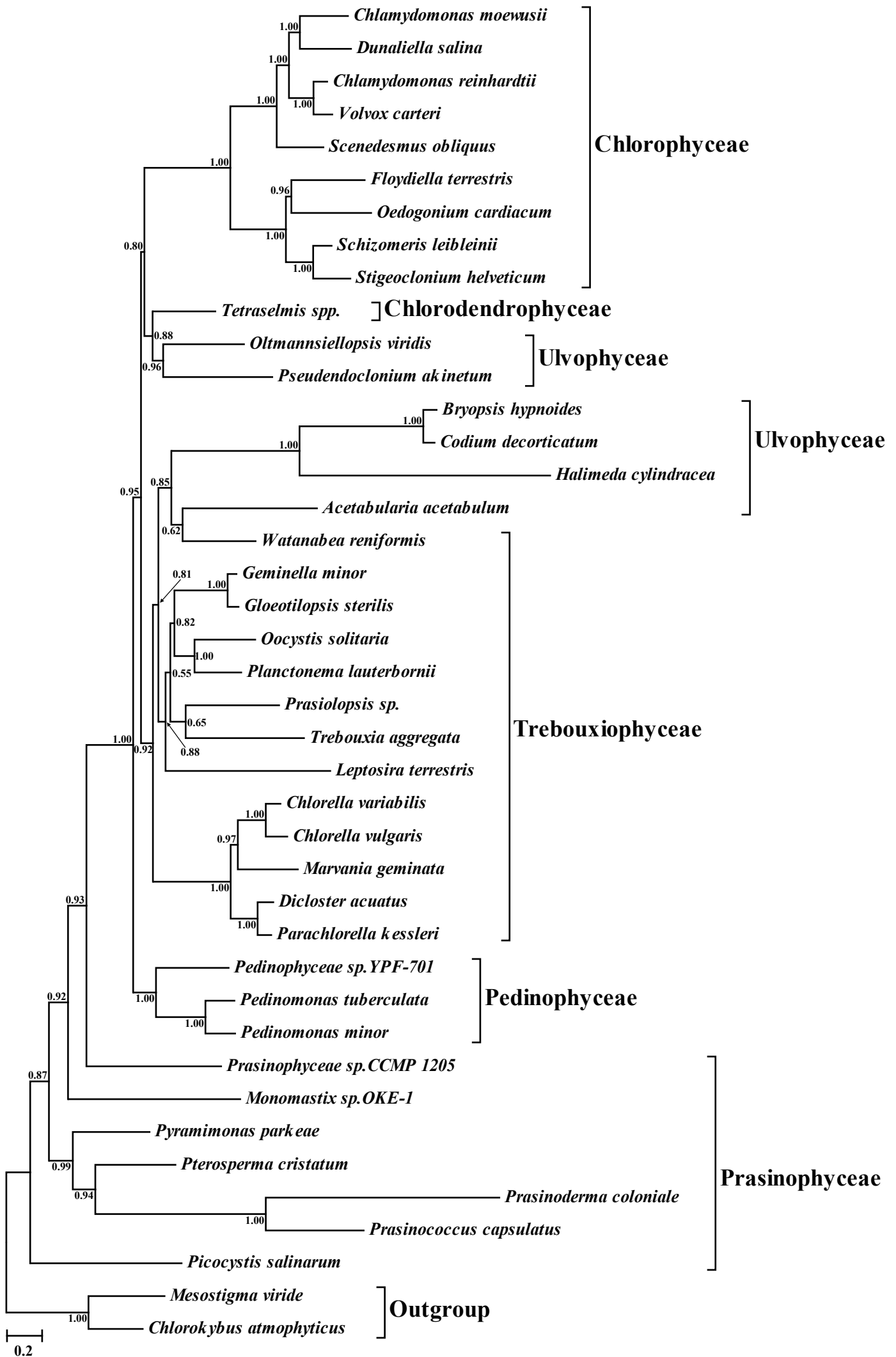


Figure S7. Bayesian phylogenetic tree under the CAT+GTR heterogeneous model based on 25,240 sites with 41 taxa. The posterior probability (PP) values are shown on the nodes.