**S4 Table. Substitution models applied to the respective data matrices of the present phylogenetic analyses (Figs 2 and 3).**

|  |  |
| --- | --- |
|  | Phylogenetic method |
| Data matrix/Figure No. | BI | ML | NJ |
| concatenated SSU and LSU rDNA, *atp*B and *psa*B (first, second codons only) from 29 OTUs/Fig 2 | partitioned intoSSU rDNA (GTR+I+G),LSU rDNA (GTR+I+G),*atp*B (SYM+I+G), and *psa*B (GTR+I+G)1 | partitioned intoSSU rDNA (K2P+I),LSU rDNA (GTR+G4),*atp*B (TIM2e+I), and *psa*B (TNe+I)2 | TrN+I+G3 |
| *rbc*L from 34 OTUs/Fig 3 | partitioned intofirst codons (GTR+I+G),second codons (JC+G), and third codons (GTR+I+G)1 | partitioned intofirst codons (TIM+G4),second codons (JC+I), and third codons (TPM3u+G4)2 | GTR+I+G3 |

Each substation model was selected by hierarchical likelihood ratio test using MrModeltest 2.3 [1] for Bayesian inference (BI) or Modeltest 3.7 [2] for neighbor-joining (NJ) analysis, or selected by the Bayesian information criterion using IQ-TREE v. 1.4.3 [3] for maximum likelihood (ML) analysis.

 Abbreviations: *atp*B, ATP synthase beta subunit gene; LSU rDNA, the large subunit of ribosomal DNA; OTUs, operational taxonomic units; *psa*B, P700 chlorophyll *a* apoprotein A2 gene; *rbc*L, the large subunit of the RuBisCO gene; SSU rDNA, the small subunit of ribosomal DNA.

**References**

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