

Table S5: Overview of markers, datasets, and phylogenetic analyses

| Marker | No. of characters (coded indels)¹ | | No. of parsimony informative characters (%) | | BA Model AIC (million generations) | ML Model AIC |
|------------------------------------|---|-------|--|--------|---|---------------------|
| ptDNA (combined) | 2281 | (81) | 106 | (4.6) | TVM+I+G (1.5) | TVM+F+I+G4 |
| ITS | 715 | (3) | 99 | (13.8) | GTR+I+G (2) | GTR+F+I+G4 |
| ETS | 575 | (7) | 92 | (16.0) | TVM+G (1) | TVM+F+G4 |
| ITS+ETS (combined) | 1290 | (10) | 191 | (14.8) | GTR+I+G (1) | GTR+F+I+G4 |
| 5S-NTS | 275 | (23) | 77 | (28.0) | TVMef+G (2) | TPM2u+F+G4 |
| <i>gsh1</i> | 1182 | (142) | 234 | (19.8) | GTR+I+G (1) | GTR+F+I+G4 |
| <i>gsh1</i> (paralogs/pseudogenes) | 887 | (55) | 93 | (10.5) | TVM+I (2.5) | GTR+F+I+G4 |
| <i>sqs</i> | 1408 | (102) | 291 | (20.7) | TVM+I+G (2) | TVM+F+I+G4 |
| combined dataset | 6085 | (223) | 432 | (7.1) | GTR+I+G (1) | TIM+F+I+G4 |

¹ The number of coded indels is included in the number of characters. BA – Bayesian analysis; ML – Maximum Likelihood; AIC – Akaike Information Criterion