Supplementary material

Table S1. List of taxa used from GenBank database.

Table S2. List of the outgroup taxa used for this study, their localities, voucher information and accession numbers.

Table S3. Sequence length of individual gene regions, combined dataset, parsimoniously informative variable sites, best fit model of sequence evolution in Bayesian phylogenetic and relaxed molecular clock dating analyses.

Fig. S1. Maximum-likelihood of the combined five marker dataset as obtained from RAxML using the GTR▒+▒G▒+▒I model.

Fig. S2. Geographical locations of different clades observed in phylogenetic analysis.