Table S2. Partitioning schemes and nucleotide substitution models applied in the four algorithms for phylogenetic reconstruction.

Partition	MrBayes	Beast	TreeFinder	RAxML
12S rRNA 16S rRNA	mixed+I+Γ	TrN+I+Γ	TN+Γ	GTR+Γ
1 codon position of COI	mixed+I	TrNef+I	TN+Γ	
2 codon position of COI	mixed	HKY	HKY {Ts=0.3, Tv=0.1}	GTR+Γ
3 codon position of COI	mixed+Γ	TrN+Γ	J1+Γ	GTR+Γ