

Appendix 2. — Selected evolutionary models for the different partitioned data sets, best scores and tree length. Modelfinder (IQtree) using the BIC criterion. Bayesian inference under mixed models and unlinked rates.

Alignments	Modelfinder (IQtree)			Bayesian Inference (MrBayes 3.2)
	IQ-TREE Web Server		IQ-TREE Terminal	
<i>RbcL</i> dataset 1239bp 182 sequences GY+F+R7		Merging partitions	Merging partitions	
codon 1	TIME+R4	part1+part2 TIM3e+R3		Unlinked parameters across partitions. Mixed models for each partition. Ratemultiplier= Dirichlet(1.00,1.00,1.00); Topologies equally probable a priori, and Branch lengths= Unconstrained:Gamma Dir(1.0,0.1000,1.0,1.0). Were similar for the codon positions.
codon 2	TNe+R3	part1+part3 GTR+F+R5		
codon 3	TIM2+F+R6	part2+part3 TIM+F+R5		
Best partition		part1+part2+ part3 GTR+F+R5	TIM+F+R4	
Optimal log-likelihood	-25310.603	-26672.625	-26462.317	-27944.90 (run1) -27968.84 (run2)
Total tree length	8.2873	5.299	5.307	
Log-likelihood of consensus tree	-2783.275	-26675.128	-26462.549	
COI-5P 618bp 84 sequences GTR +F+I+G4		Merging partitions		
codon 1	GTR+F+I+G4	part1+part2 GTR+F+I+G4	HKY	
codon 2	TIM+F+I+G4	part1+part3 TIM2+F+I+G4	HKY	
codon 3	TN+F+I+G4	part3+part3 TIM+F+I+G4	GTR	
		part1+part2+par t3 GTR+F+I+G4		
Best partition		GTR+F+I+G4: part1 part2,		

		TN+F+I+G4: part3;	
Optimal log-likelihood	-13116.633	-12499.389	-13268.67 (run1) -13276.06 (run2)
Total tree length	12241	29.086	
Log-likelihood Consensus Tree	-12092.794	-12488.161	
LSU 954bp 85 sequences			
	TIM3e+I+G4		NST=mixed rates=invgamma
Optimal log-likelihood	-7202.045		-7256.96 (run1) -7261.71 (run2)
Total tree length	2.768		
Log-likelihood of consensus tree	-7202.049		
<i>rbcL</i> LSU COI-5P combined data set 71 sequences 2487bp			
<i>rbcL</i> codon1	TIM+F+R3	gtrsubmodel{3}[1 21221] refering to HKY model.	
<i>rbcL</i> codon2	TNe+F+I+G4		
<i>rbcL</i> codon3	TIM3+F+I+G4		
LSU	SYM+R3		
COI-5P codon1	SYM+I+G4		
COI-5P codon2	TIM3+F+I+G4		
COI-5P codon3	TIM2+F+I+G4		
Optimal log-likelihood	-23560.397		-23958.45 (run1) -23968.57 (run2)
Total tree length	12.527		
Log-likelihood of consensus tree	-23565.295		