TABLE S1 | Partitioning strategy and best-fit nucleotide substitution models for each genetic partition used in this study. Selected under the Akaike Information Criterion (AIC) for Bayesian inference and maximum-likelihood phylogenetic analyses. pos1, pos2, and pos3 correspond to the first, second, and third codon positions, respectively.

Analysis	Subset	Best Model	Partitions
BI	1	K80+I+G	COI_pos1
	2	HKY+I	COI_pos2
	3	GTR+G	COI_pos3, cyt *b*_pos3
	4	GTR+I+G	cyt *b*_pos1
	5	HKY+G	cyt *b*_pos2
ML	1	TIM2+F+I+ R2	COI_pos1, cyt *b*_pos1
	2	HKY+F+I	COI_pos2, cyt *b*_pos2
	3	GTR+F+R3	COI_pos3, cyt *b*_pos3