

Table S1 CodeML analysis of mitochondrial protein-encoding genes (13 genes) (*Coreamachilis* as the foreground branch)

	Model	np	Ln L	Model compared	LRT P-value	Positive sites
Branch model	Two ratio	25	-85287.650122	Model 0 vs. Two ratio Model 2	0.408895446	
	Model 2					
	Model 0	24	-85287.991127			
Branch site model	Model A	27	-83671.873488	Model A vs. Model A null	0.324897750	181 G 0.881, 763 A 0.771, 870 L 0.709, 918 V 0.738, 1000 K 0.969*,1014 K 0.509, 1701 S 0.662, 1819 F 0.578, 2005 L 0.624, 2223 L 0.615, 2278 I 0.570, 2356 L 0.509, 2660 G 0.531, 2662 L 0.610, 2671 E 0.858, 3206 P 0.890, 3305 A 0.671, 3353 V 0.782, 3508 L 0.898, 3592 D 0.508, 3603 N 0.844, 3615 S 0.779, 3618 V 0.562
	Model null	A 26	-83672.358052			Not Allowed
	Model null					
Clade model	CmC	28	-81557.305666	M2a_rel vs CmC	0.000000000	
	M2a_rel	27	-81586.915580			Not Allowed
	M3	28	-81387.375872	M0 vs. M3	0.000000000	
Site model	M0	24	-85287.991127			Not Allowed
	M2a	27	-83679.125055	M1a vs. M2a	1.000000000	
	M1a	25	-83679.125055			Not Allowed
	M8	27	-81490.306203	M7 vs.M8	0.000000000	51 S 0.550, 256 L 0.747, 905 D 0.686, 2123 M 0.775, 2236 N 0.904, 2256 T 0.839, 2390 V 0.621, 2458 G 0.543, 2534 N 0.522, 2930 L 0.523, 3391 L 0.804, 3394 V 0.747, 3397 L 0.509, 3597 L 0.661
	M7	25	-81533.937285			Not Allowed
	M8a	26	-81367.132828	M8a vs.M8	0.000000000	Not Allowed