

**The complete mitochondrial genomes of two skipper genera  
(Lepidoptera: Hesperiiidae) and their associated phylogenetic  
analysis**

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**Supplementary Material S1. Composition and skewness of *Aposticopterus fuliginosus* and *Barca bicolor*.**

**Supplementary Material S2. The secondary structures of tRNA of both two species.**

**Supplementary Material S3. Best-fit partition schemes were selected by PartitionFinder and the corresponding best-fit model were selected by ModelFinder.**

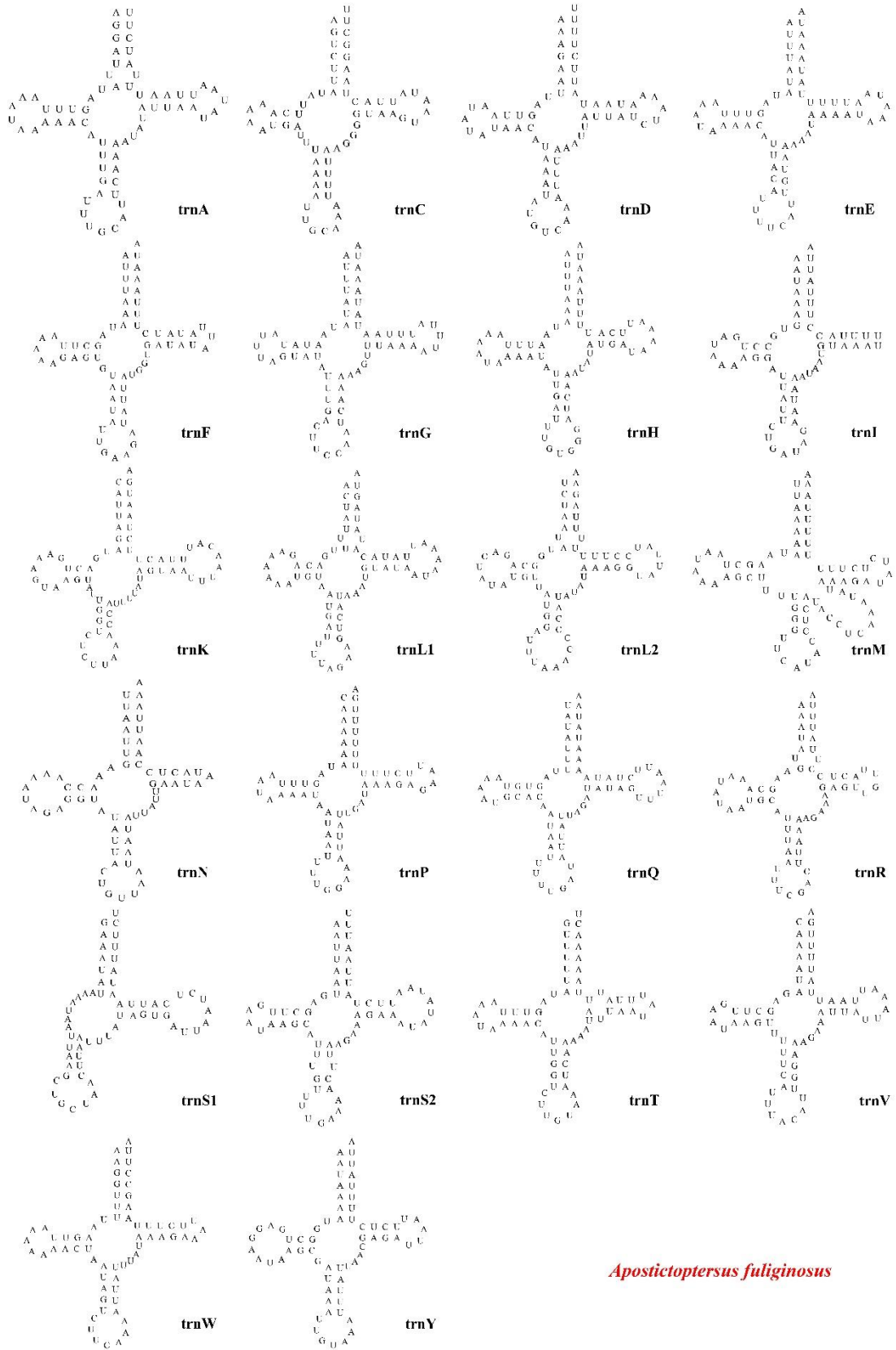
**Supplementary Material S4. The trees based on different datasets and methods.**

**Supplementary Material S5. List of primers used to amplify and sequence two mitochondrial genomes.**

**Supplementary Material S1. Composition and skewness of *Apostictopterus fuliginosus* and *Barca bicolor*.**

		<b>T (bp)</b>	<b>A (bp)</b>	<b>C (bp)</b>	<b>G (bp)</b>	<b>Total Size (bp)</b>	<b>AT skew</b>	<b>GC skew</b>
<i>Apostictopterus fuliginosus</i>	tRNA	609	609	147	110	1475	0	-0.144
	%	41.30	41.00	10.00	8.00			
	rRNA	971	900	217	101	2189	-0.038	-0.365
	%	44.4	41.1	9.9	4.6			
	AT-region	203	182	15	7	407	-0.055	-0.364
	%	49.9	44.7	3.7	1.7			
	PCGs	5088	3736	1169	1201	11194	-0.153	0.013
	%	45.5	33.4	10.4	10.7			
	Whole genome	6259	6188	1822	1148	15417	-0.006	-0.227
%	40.6	40.1	11.8	7.4				
<i>Barca bicolor</i>	tRNA	597	592	158	117	1464	-0.004	-0.15
	%	40.80	40.40	10.80	8.00			
	rRNA	921	926	239	106	2192	0.003	-0.386
	%	42.2	10.9	4.8	42			
	AT-region	284	281	33	16	614	-0.005	-0.347
	%	46.3	45.8	5.4	2.6			
	PCGs	4997	3662	1262	1275	11196	-0.154	0.005
	%	44.6	32.7	11.3	11.4			
	Whole genome	6137	6227	2005	1205	15574	0.007	-0.249
%	39.4	40	12.9	7.7				

Supplementary Material S2. The secondary structures of tRNA of both two species.





**Supplementary Material S3. Best-fit partition schemes were selected by PartitionFinder and the corresponding best-fit model were selected by ModelFinder.**

ATP6\_pos1 = 1-687\3;  
ATP6\_pos2 = 2-687\3;  
ATP6\_pos3 = 3-687\3;  
ATP8\_pos1 = 688-864\3;  
ATP8\_pos2 = 689-864\3;  
ATP8\_pos3 = 690-864\3;  
COI\_pos1 = 865-2415\3;  
COI\_pos2 = 866-2415\3;  
COI\_pos3 = 867-2415\3;  
COII\_pos1 = 2416-3112\3;  
COII\_pos2 = 2417-3112\3;  
COII\_pos3 = 2418-3112\3;  
COIII\_pos1 = 3113-3928\3;  
COIII\_pos2 = 3114-3928\3;  
COIII\_pos3 = 3115-3928\3;  
CYTB\_pos1 = 3929-5095\3;  
CYTB\_pos2 = 3930-5095\3;  
CYTB\_pos3 = 3931-5095\3;  
ND1\_pos1 = 5096-6052\3;  
ND1\_pos2 = 5097-6052\3;  
ND1\_pos3 = 5098-6052\3;  
ND2\_pos1 = 6053-7079\3;  
ND2\_pos2 = 6054-7079\3;  
ND2\_pos3 = 6055-7079\3;  
ND3\_pos1 = 7080-7436\3;  
ND3\_pos2 = 7081-7436\3;  
ND3\_pos3 = 7082-7436\3;  
ND4\_pos1 = 7437-8805\3;  
ND4\_pos2 = 7438-8805\3;  
ND4\_pos3 = 7439-8805\3;  
ND4L\_pos1 = 8806-9135\3;  
ND4L\_pos2 = 8807-9135\3;  
ND4L\_pos3 = 8808-9135\3;  
ND5\_pos1 = 9136-10908\3;  
ND5\_pos2 = 9137-10908\3;  
ND5\_pos3 = 9138-10908\3;  
ND6\_pos1 = 10909-11461\3;  
ND6\_pos2 = 10910-11461\3;  
ND6\_pos3 = 10911-11461\3;  
lrRNA = 11462-12410;  
srRNA = 12411-13001;

tRNA\_Ala =13002-13087;  
tRNA\_Arg= 13088-13171;  
tRNA\_Asn =13172-13245;  
tRNA\_Asp= 13246-13321;  
tRNA\_Cys= 13322-13395;  
tRNA\_Gln= 13396-13464;  
tRNA\_Glu= 13465-13553;  
tRNA\_Gly= 13554-13625;  
tRNA\_His= 13626-13707;  
tRNA\_Ile= 13708-13779;  
tRNA\_Leu1= 13780-13871;  
tRNA\_Leu2= 13872-13940;  
tRNA\_Lys= 13941-14011;  
tRNA\_Met= 14012-14091;  
tRNA\_Phe= 14092-14162;  
tRNA\_Pro= 14163-14233;  
tRNA\_Ser= 14234-14317;  
tRNA\_Ser2= 14318-14402;  
tRNA\_Thr = 14403-14484;  
tRNA\_Trp = 14485-14556;  
tRNA\_Tyr = 14557-14628;  
tRNA\_Val = 14629-14715;

#### PCGD:

##### **Partition:**

charset Subset1 = 2416-3112\2 3929-5095\2 2417-3112\2 1-687\2 7080-7436\2 7081-7436\2  
2-687\2 3930-5095\2 3114-3928\2 3113-3928\2;

charset Subset2 = 689-864\2 688-864\2 10910-11461\2 10909-11461\2;

charset Subset3 = 866-2415\2 865-2415\2;

charset Subset4 = 8807-9135\2 7437-8805\2 7438-8805\2 5096-6052\2 5097-6052\2 9137-  
10908\2 8806-9135\2 9136-10908\2;

charset Subset5 = 6053-7079\2 6054-7079\2;

##### **ML charpartition mymodels =**

GTR+F+I+G4: Subset1,

GTR+F+I+G4: Subset2,

GTR+F+I+G4: Subset3,

GTR+F+I+G4: Subset4,

TIM+F+I+G4: Subset5;

#### PCGC:

##### **Partition:**

charset Subset1 = 10909-11461\3 6053-7079\3 1-687\3 7080-7436\3;

charset Subset2 = 2417-3112\3 3114-3928\3 2-687\3 7081-7436\3 3930-5095\3;

charset Subset3 = 3-687\3 6055-7079\3;  
 charset Subset4 = 688-864\3 689-864\3;  
 charset Subset5 = 690-864\3 10911-11461\3 2418-3112\3 7082-7436\3 867-2415\3 3115-3928\3  
 3931-5095\3;  
 charset Subset6 = 865-2415\3;  
 charset Subset7 = 866-2415\3;  
 charset Subset8 = 2416-3112\3 3113-3928\3 3929-5095\3;  
 charset Subset9 = 7438-8805\3 8806-9135\3 5096-6052\3 9137-10908\3;  
 charset Subset10 = 8807-9135\3 5097-6052\3 9138-10908\3;  
 charset Subset11 = 5098-6052\3 8808-9135\3;  
 charset Subset12 = 10910-11461\3 6054-7079\3;  
 charset Subset13 = 7439-8805\3 7437-8805\3;  
 charset Subset14 = 9136-10908\3;

**ML charpartition mymodels =**

GTR+F+I+G4: Subset1,  
 TVM+F+I+G4: Subset2,  
 TN+F+G4: Subset3,  
 F81+F+I+G4: Subset4,  
 TIM+F+G4: Subset5,  
 TIM2+F+G4: Subset6,  
 F81+F+I+G4: Subset7,  
 GTR+F+I+G4: Subset8,  
 TIM+F+I+G4: Subset9,  
 GTR+F+I+G4: Subset10,  
 TPM2+F+I+G4: Subset11,  
 HKY+F+I+G4: Subset12,  
 GTR+F+I+G4: Subset13,  
 TPM2u+F+G4: Subset14;

**PCGR:**

**Partition:**

charset Subset1 = 2416-3112\2 2417-3112\2 3929-5095\2 1-687\2 7080-7436\2 7081-7436\2  
 2-687\2 3930-5095\2 3114-3928\2 3113-3928\2;  
 charset Subset2 = 689-864\2 688-864\2 10909-11461\2 10910-11461\2;  
 charset Subset3 = 866-2415\2 865-2415\2;  
 charset Subset4 = 8807-9135\2 7437-8805\2 7438-8805\2 5096-6052\2 5097-6052\2 9137-  
 10908\2 8806-9135\2 9136-10908\2;  
 charset Subset5 = 6053-7079\2 6054-7079\2;  
 charset Subset6 = 12411-13001 11462-12410;

**ML charpartition mymodels =**

GTR+F+I+G4: Subset1,  
 GTR+F+I+G4: Subset2,  
 GTR+F+I+G4: Subset3,  
 GTR+F+I+G4: Subset4,



TIM+F+I+G4: Subset5,  
GTR+F+I+G4: Subset6;

PRT:

**Partition:**

charset Subset1 = 14092-14162 13626-13707 10909-11461\3 6053-7079\3 13780-13871 1-687\3 7080-7436\3;

charset Subset2 = 13941-14011 13872-13940 2-687\3 2417-3112\3 3114-3928\3 3930-5095\3;

charset Subset3 = 3-687\3 6055-7079\3;

charset Subset4 = 688-864\3 689-864\3;

charset Subset5 = 690-864\3 10911-11461\3 2418-3112\3 3931-5095\3 867-2415\3 3115-3928\3 7082-7436\3;

charset Subset6 = 865-2415\3;

charset Subset7 = 866-2415\3;

charset Subset8 = 13396-13464 2416-3112\3;

charset Subset9 = 3113-3928\3 3929-5095\3 13322-13395 14485-14556 14012-14091;

charset Subset10 = 7438-8805\3 13708-13779 8806-9135\3 5096-6052\3 9137-10908\3;

charset Subset11 = 8807-9135\3 9138-10908\3 5097-6052\3;

charset Subset12 = 5098-6052\3;

charset Subset13 = 7081-7436\3 10910-11461\3 6054-7079\3;

charset Subset14 = 7439-8805\3 7437-8805\3;

charset Subset15 = 9136-10908\3 8808-9135\3;

charset Subset16 = 14163-14233 14557-14628 14629-14715 12411-13001 11462-12410 13246-13321 13465-13553 13088-13171 13172-13245 13554-13625 14318-14402 14234-14317 13002-13087 14403-14484;

**ML charpartition mymodels =**

GTR+F+I+G4: Subset1,

TVM+F+I+G4: Subset2,

TN+F+G4: Subset3,

F81+F+I+G4: Subset4,

TIM+F+G4: Subset5,

TIM2+F+G4: Subset6,

F81+F+I+G4: Subset7,

TN+F+I+G4: Subset8,

GTR+F+I+G4: Subset9,

TIM+F+I+G4: Subset10,

GTR+F+I+G4: Subset11,

TIM2+F+G4: Subset12,

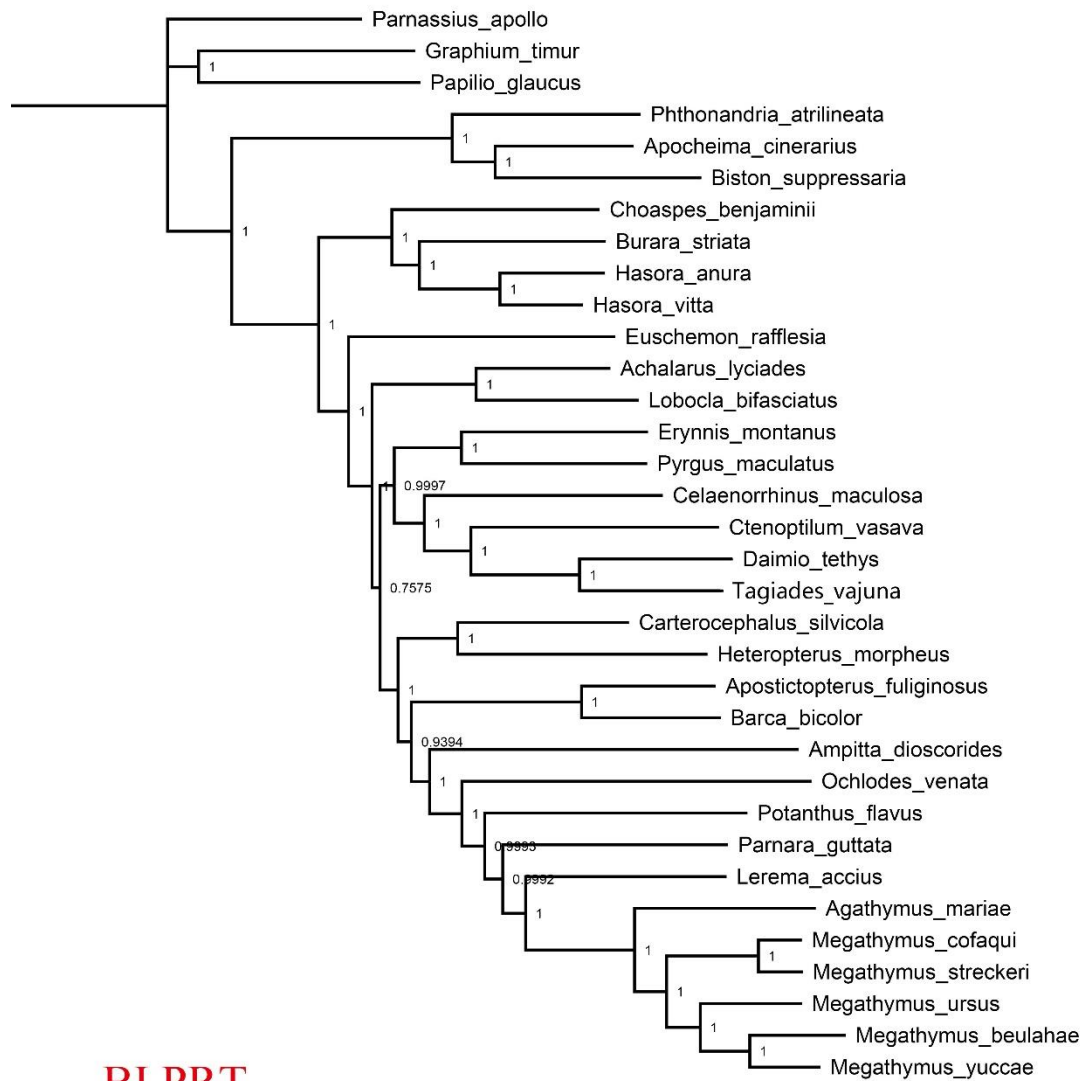
HKY+F+I+G4: Subset13,

GTR+F+I+G4: Subset14,

TIM+F+I+G4: Subset15,

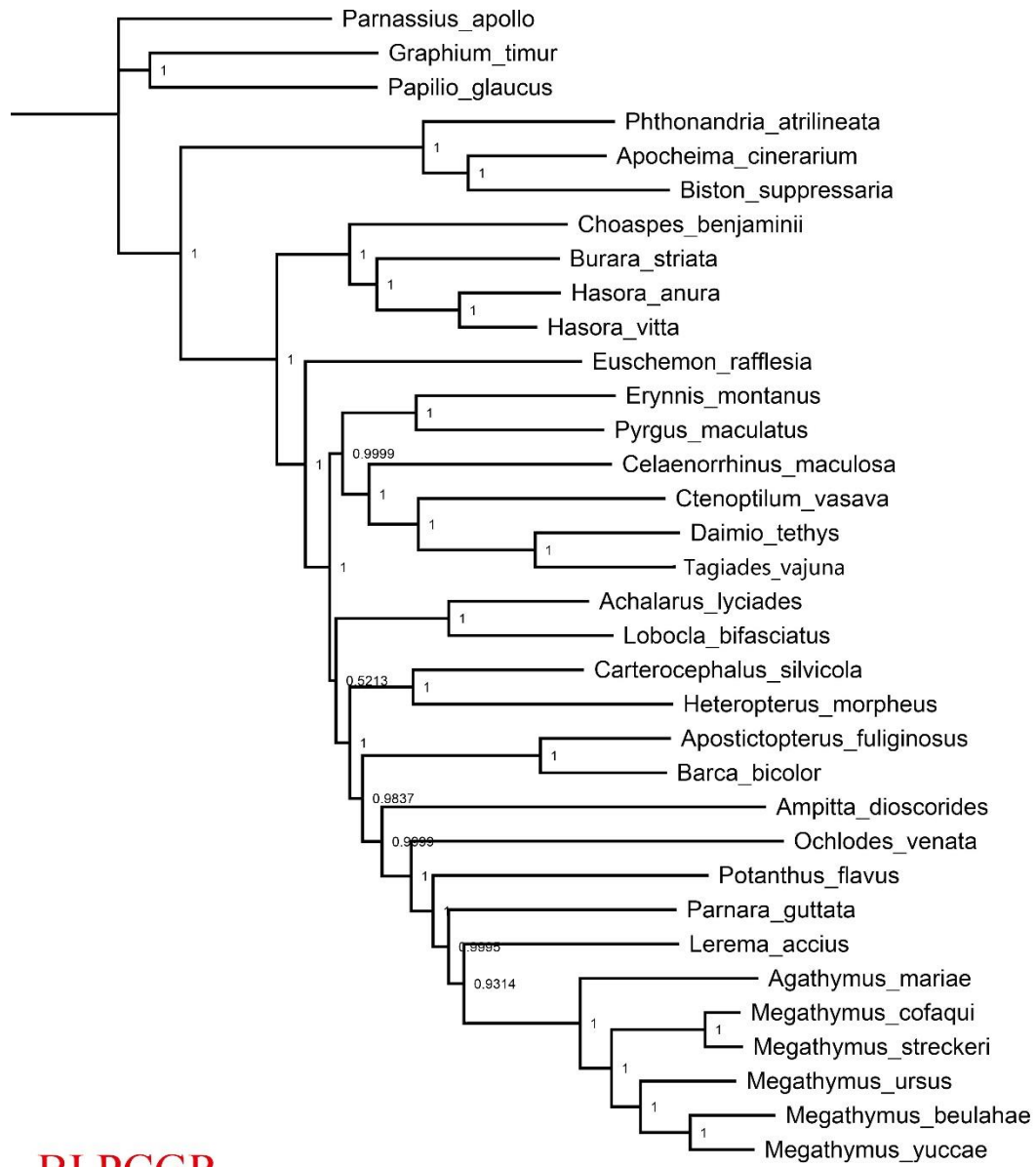
GTR+F+I+G4: Subset16;

**Supplementary Material S4. The trees based on different datasets and methods.**



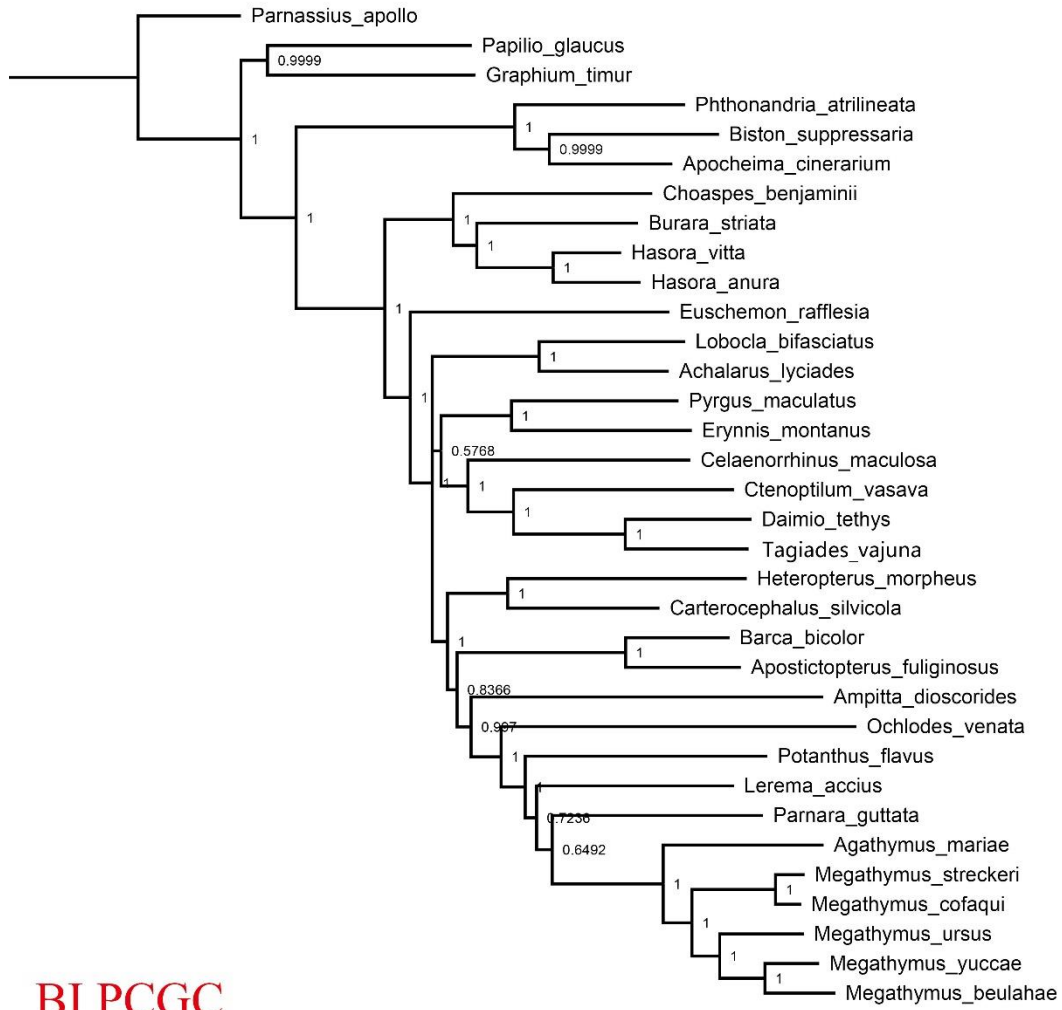
**BI PRT**

0.04

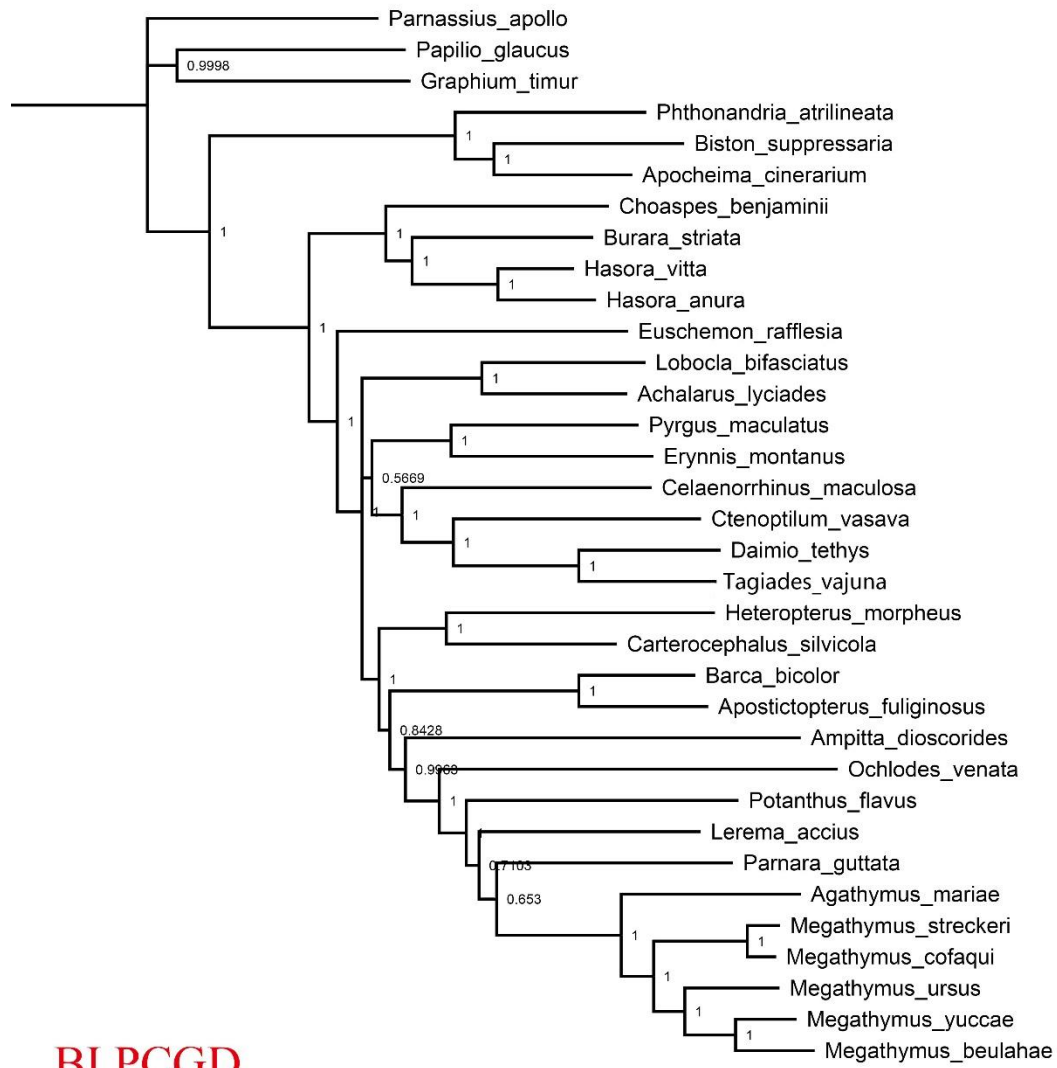


BI PCGR

0.07

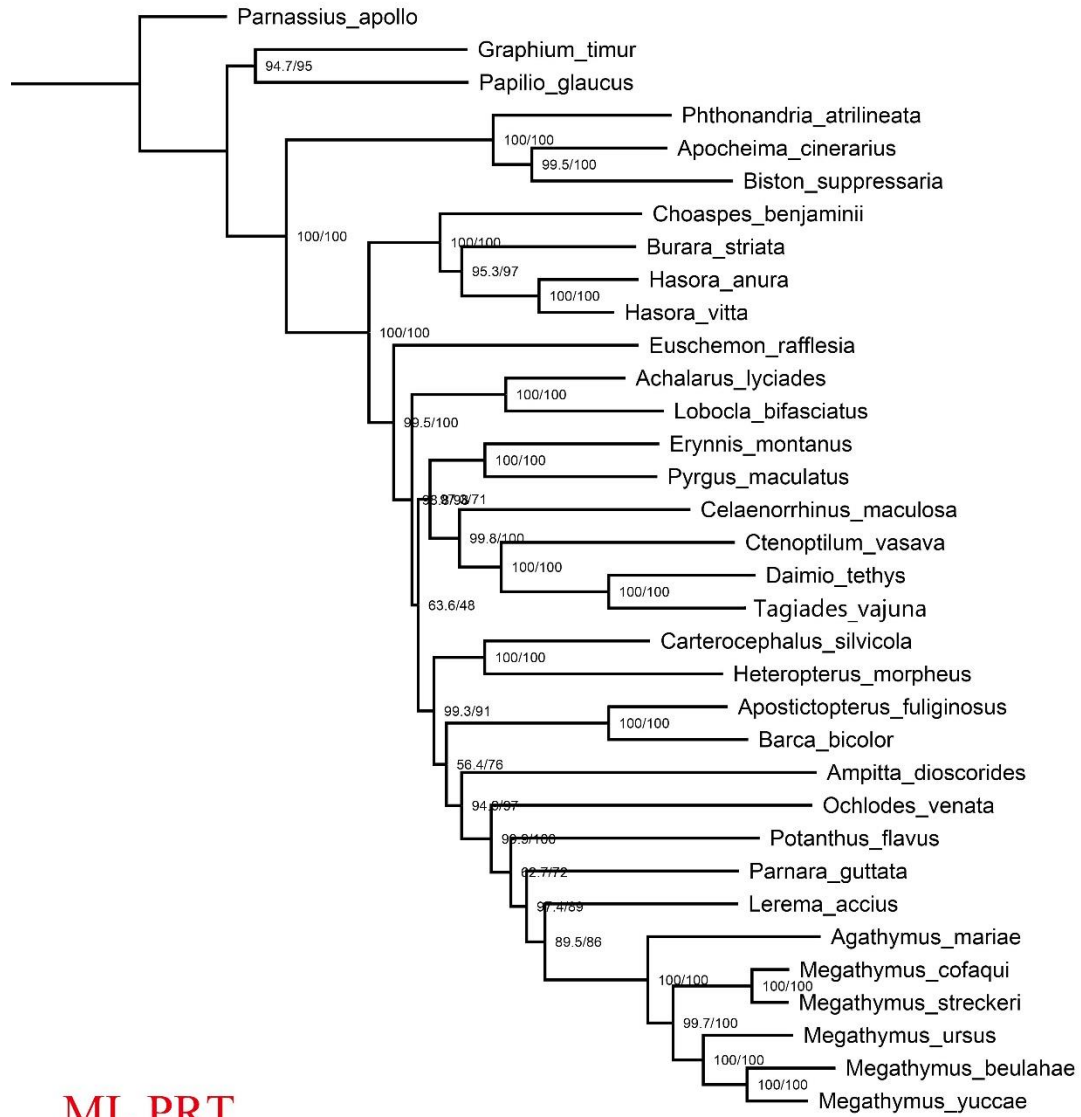


BI PCGC



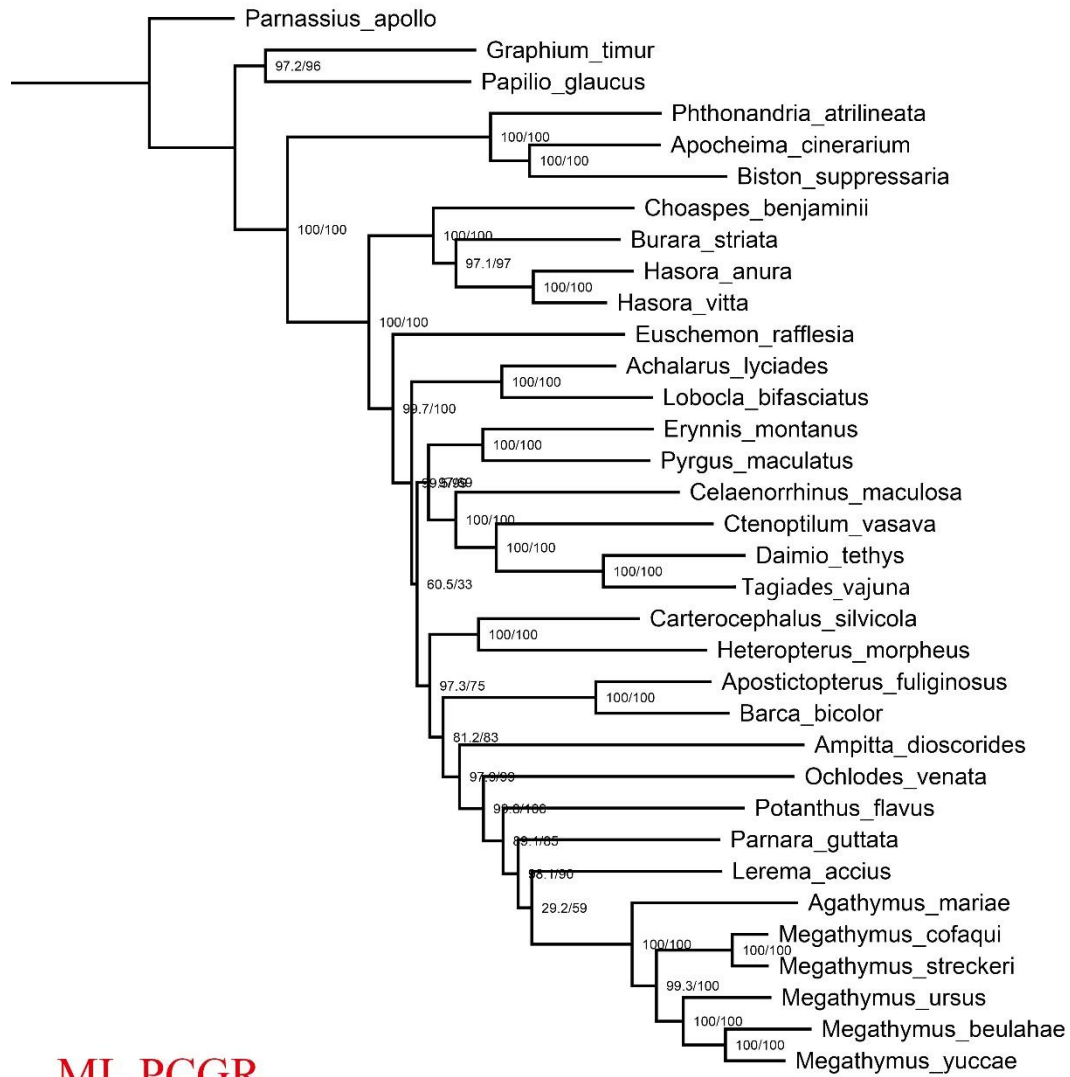
BI PCGD

0.2



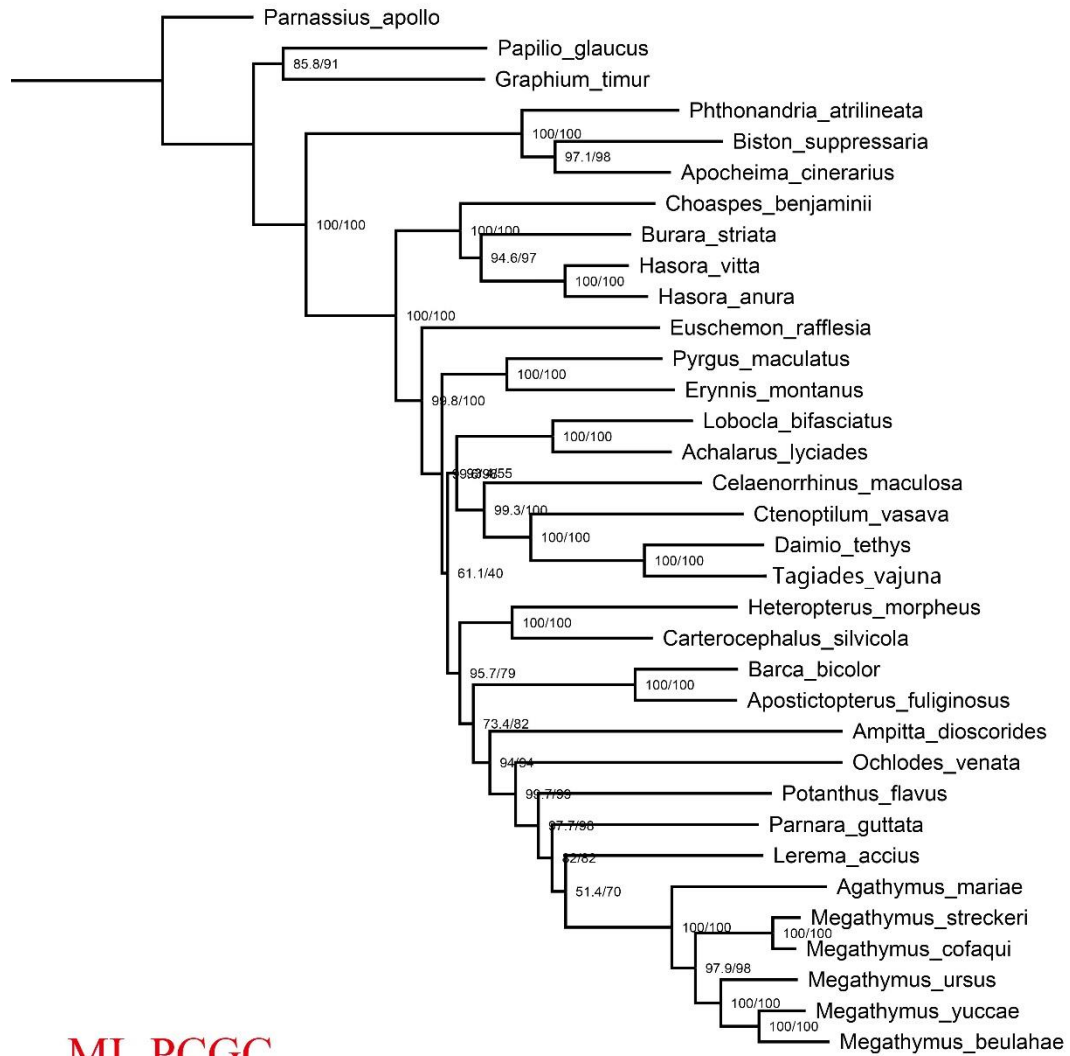
ML PRT

0.05



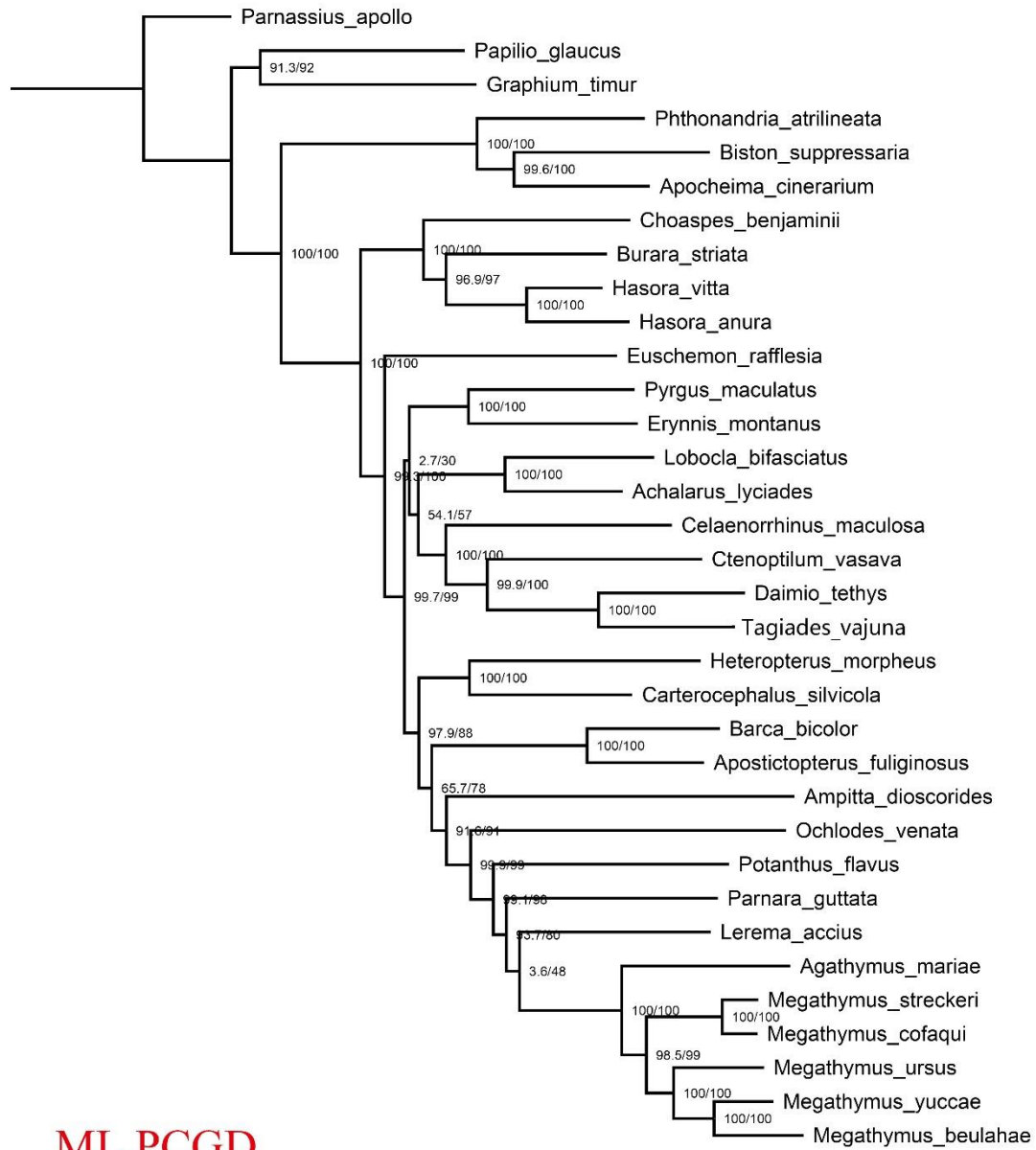
ML PCGR

0.05



ML PCGC





ML PCGD

0.08

**Supplementary Material S5. List of primers used to amplify and sequence two mitochondrial genomes.**

Fragment name	Gene	Direction <sup>a</sup>	Sequence (5'-3')
SF1	<i>tRNA<sup>Met</sup></i>	F	AAGCTTTTGGGYTCATACC
	<i>ND2</i>	R	CAWCCTAAATTATTAATWGAWGA
SF2*	<i>ND2</i>	F	TCTTCWATAATAATRAAAATAGG
	<i>tRNA<sup>Tyr</sup></i>	R	GCGATAAATTGTAAATTTAT
SF3	<i>tRNA<sup>Trp</sup></i>	F	AATCTTCAAAATTATTATAAAG
	<i>COI</i>	R	CTTCAGGATGACCAAAAAATC
SF4	<i>COI</i>	F	GGTATTTTCATCAATTTTAGG
	<i>COI</i>	R	GTCGAGGTATTCCTGCTA
SF5	<i>COI</i>	F	ACWGTAGGAGGATTAACAGG
	<i>COII</i>	R	GTTCAAATTAATTCAATTATTTG
SF6	<i>COII</i>	F	TAGAAATGGCAACWTGATC
	<i>tRNA<sup>Lys</sup></i>	R	CTTGCTTTTCAGTCATCTAAT
SF7	<i>COII</i>	F	CAGGTCGWTTAAATCAAAC
	<i>ATP6</i>	R	GTTCCCTGDGGAATTATATG
SF8	<i>ATP6</i>	F	TTATTTTCAATTTTGTATCC
	<i>COIII</i>	R	CTCGTCATCATTGATATAT
SF9	<i>COIII</i>	F	GTWGATTATAGHCCWTGACC
	<i>tRNA<sup>Gly</sup></i>	R	GATTGGAAGTCAAATATACT
SF10*	<i>COIII</i>	F	AGCTTATGAATATTAYGAAGC
	<i>tRNA<sup>Asn</sup></i>	R	CAATTTTATCATTAACAGTGA
SF11	<i>ND3</i>	F	TAGAAATTGCATTAATTTTHCC
	<i>ND5</i>	R	CCTTATATAATTTATTACC
SF12	<i>ND5</i>	F	AWAHTTCTCTTCAACCYAWATC
	<i>ND5</i>	R	GCTTTATCWACTTTAAGWCA
SF13	<i>ND5</i>	F	TCYTTWGAATAAAAAYCCAG
	<i>ND5</i>	R	GATGGDTTAGGDTTAGTTTCTT
SF14	<i>ND5</i>	F	AAAAAATATAATTTCAWCTHCC
	<i>ND4</i>	R	CATTGATTWCCTTTAAATAT
SF15	<i>tRNA<sup>His</sup></i>	F	ATATTTTTGAYHCCACAAATC
	<i>ND4</i>	R	CAGGTTCAATAATTTTAGC
SF16	<i>ND4</i>	F	TTATAATACCHCCAATWAC
	<i>ND4</i>	R	GGTTTAATTTTATTAAGAATTTG
SF17	<i>ND4</i>	F	ATATTAAGTAGGAATTAAWC
	<i>tRNA<sup>Pro</sup></i>	R	TAATTTTGGAGATTATWGAT
SF18*	<i>ND4L</i>	F	CCTAAAGCACCTCACAWAC

	<i>ND6</i>	R	GTAATTTTACWACWGMWAYTA
SF19	<i>ND6</i> <i>Cytb</i>	F R	TNTCAAGAATTGCHTCWAATG GATATTTGTCCYCAAGGTA
SF20	<i>Cytb</i> <i>Cytb</i>	F R	TATHTHCATATTGGACGAGG CCTTGDATTTTTTTATTAADGT
SF21	<i>Cytb</i> <i>ND1</i>	F R	ACHCCHRTTCATATTCAACC GCTGAAACTAATCGAACTC
SF22*	<i>ND1</i> <i>lrRNA</i>	F R	ACCGRGGWARMGTMCTCG CTGAGTTCAAACCGGTGTRA
SF23	<i>tRNA<sup>Leu</sup></i> <i>lrRNA</i>	F R	GAHTTCTAAAAYCATTAC GACTGTACAAAGGTAGCATAAT
SF24	<i>lrRNA</i> <i>lrRNA</i>	F R	CATCMAATCTTTCATACAAG GTATCTTGTGTATCAGAG
SF25	<i>lrRNA</i> <i>tRNA<sup>Val</sup></i>	F R	ATTATGCTACCTTTGTACAGTC GTATTTCAATTACATTGAAAAGA
SF26	<i>lrRNA</i> <i>srRNA</i>	F R	CTCTGATACACAAGATAC CCAGCAGTTGCGGTAAAC
SF27*	<i>srRNA</i> <i>tRNA<sup>Ile</sup></i>	F R	AATAGGTGATCTAATCCTAG CTATCAGAATAATCCTTWW

<sup>a</sup>F and R, forward and reverse direction of transcription.

\*Primers are newly designed in this study.