Supplementary Materials: The Complete Mitochondrial Genome of *Mindarus keteleerifoliae* (Insecta: Hemiptera: Aphididae) and Comparison with Other Aphididae Insects

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Table S1. Nucleotide composition of the *Mindarus keteleerifoliae* mitogenome.

Composition	A%	G%	C%	T%	A + T%	AT-Skew	GC-Skew	Length (bp)
Whole genome	44.6	6.0	9.6	39.9	84.5	0.056	−0.233	15,199
Protein-coding genes	35.9	7.7	8.4	47.9	83.4	−0.143	−0.041	10,946
First codon	40.8	5.7	5.9	48.0	88.4	−0.078	−0.021	3649
Second codon	38.2	8.9	8.9	44.0	82.2	−0.070	−0.002	3649
Third codon	28.8	8.6	10.4	52.0	81.0	−0.289	−0.094	3648
Protein-coding genes-J	38.6	6.7	10.3	44.4	83.0	−0.070	−0.209	6739
First codon	46.3	4.3	6.6	43.0	89.1	0.040	−0.208	2247
Second codon	40.0	9.3	11.7	39.0	79.0	0.014	−0.114	2246
Third codon	29.4	6.5	12.6	52.0	80.9	−0.274	−0.315	2246
Protein-coding genes-N	31.7	9.4	5.4	53.6	85.2	−0.257	0.269	4207
First codon	35.4	8.3	4.3	52.0	87.4	−0.191	0.311	1403
Second codon	27.9	11.9	6.9	53.0	81.2	−0.313	0.265	1402
Third codon	31.8	7.9	4.9	55	87.2	−0.270	0.233	1402
tRNA genes	45.0	6.2	7.9	40.9	85.9	0.048	−0.120	1478
tRNA genes-J	45.5	7.2	7.3	40.0	85.4	0.065	−0.007	941
tRNA genes-N	44.1	4.5	8.9	42.5	86.6	0.019	−0.333	537
rrnL gene	46.1	4.6	9.9	39.5	85.6	0.077	−0.366	1266
rrnS gene	42.4	5.5	10.2	42.0	84.4	0.005	−0.299	765
Control region	47.5	4.9	6.1	41.5	88.9	0.067	−0.105	687

Table S2. Codon usage in the mitogenome of *Mindarus keteleerifoliae.*

AA	Codon	Number	RSCU	AA	Codon	Number	RSCU
Phe（F)	**UUU**	**471**	**1.93**	Tyr(Y)	**UAU**	**156**	**1.91**
	UUC	17	0.07		UAC	7	0.09
Leu（L2)	**UUA**	**468**	**5.21**	His(H)	**CAU**	**49**	**1.81**
	UUG	24	0.27		CAC	5	0.19
Leu（L1)	CUU	16	0.18	Gln(Q)	**CAA**	**45**	**1.91**
	CUC	2	0.02		CAG	2	0.09
	CUA	**28**	**0.31**	Asn(N)	**AAU**	**283**	**1.9**
	CUG	1	0.01		AAC	15	0.1
Ile（I)	**AUU**	**460**	**1.87**	Lys(K)	**AAA**	**150**	**1.9**
	AUC	32	0.13		AAG	8	0.1
Met（M)	**AUA**	**322**	**1.91**	Asp(D)	**GAU**	**43**	**1.69**
	AUG	15	0.09		GAC	8	0.31
Val（V)	**GUU**	**39**	**2.17**	Glu(E)	**GAA**	**65**	**1.91**
	GUC	2	0.11		GAG	3	0.09
	GUA	30	1.67	Cys(C)	**UGU**	**25**	**1.72**
	GUG	1	0.06		UGC	4	0.28
Ser（S2)	UCU	86	2.32	Trp(W)	**UGA**	**76**	**1.79**
	UCC	12	0.32		UGG	9	0.21
	UCA	**107**	**2.88**	Arg(R)	CGU	12	1.23
	UCG	1	0.03		CGC	0	0
Pro（P)	**CCU**	**51**	**1.76**		**CGA**	**26**	**2.67**
	CCC	12	0.41		CGG	1	0.1
	CCA	**51**	**1.76**	Ser(S1)	AGU	29	0.78
	CCG	2	0.07		AGC	4	0.11
Thr（T)	ACU	45	1.7		**AGA**	**57**	**1.54**
	ACC	2	0.08		AGG	1	0.03
	ACA	**59**	**2.23**	Gly(G)	GGU	39	1.17
	ACG	0	0.00		GGC	0	0
Ala（A)	**GCU**	**38**	**2.34**		**GGA**	**82**	**2.47**
	GCC	2	0.12		GGG	12	0.36
	GCA	25	1.54	stop	UAA	0	0.00
	GCG	0	0.00		UAG	0	0.00

A total of 3637 codons from *Mindarus keteleerifoliae* were analyzed, excluding the stop codons. AA, amino acid; RSCU, Relative synonymous codon usage. Boldface represents each amino acid with the highest frequency codon and underlined letters refer to the codon that matches the tRNA anticodon.

Table S3. Primers used in this study.

No. Fragment	Mainly Locus	Primer ID	Nucleotide Sequence (5′-3′)	Reference
1	Co I & Co II	Lep F	ATTCAACCAATCATAAAGATATTGG	Foottit *et al.*, 2008 [47]
		A3772	GAGACCATTACTTGCTTTCAGTCATCT	Normark *et al.*, 1996 [48]
2	Co II & Co III	CO2Af (mtDNA)	AATCAYAGWTTTATRCCWATTCA	Ortiz-Rivas *et al.*, 2010 [49]
		CO3WWRD (mtDNA)	TCWCGAATWACATCWCGTCATCA	
3	Co II & Co III	Co2f	TAGATGACTGAAAAGCAAAG	Independent design
		Co3r	GTAATCCATGAAATCCTGTT	
4	Co III & ND3	CO3WWRDre	TGATGACGWGATGTWATTCGWGA	Independent design
		nad3r	GATAGTTAGCAGCTTCTTTT	
5	ND3 & ND5	nd31	TGAATGTGGATTTGATCCATT	Independent design
		nd51	CCTTTTTCTTCTTGGTTWCCT	
6	ND5 & ND4	N5-J7572	AAAGGGAATTTGAGCTCTTTTWGT	Simon *et al.*, 2006 [50]
		nad4R	TCATGTTGAAGCTCCAATT	Independent design
7	ND4L & CytB	N4-J8641x	CCAGAAGAACATAAACCATG CCA	Simon *et al.*, 2006 [50], modified
		CB-N10608	AGTARTGAWCCAAARTTTCA	
8	CytB & ND1 & 16S & 12S	CB1	TATGTACTACCATGAGGACAAATATC	Simon *et al.*, 1994 [51]
		12sai	AAACTAGGATTAGATACCCTATTAT	
9	12S & control region & ND2	12saire	ATAATAGGGTATCTAATCCTAGTTT	Simon *et al.*, 1994 [51]
		ND2R②	TAGGTGGTAAACCTATAATT	Independent design
10	ND2& COI	ND2/CO IF	CTCCACATGAATATTATTTGC	Independent design
		ND2/CO IR	TTCCTGATCAAATACCAAATA	