

Supplementary Data:

Comparative mitochondrial genomes between the genera *Amiota* and *Phortica* (Diptera: Drosophilidae) with evolutionary insights into D-loop sequence variability

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Table S1. Sizes of the *Amiota* and *Phortica* mitogenomes.

Gene	<i>A. dentata</i>	<i>A. femorata</i>	<i>A. nagatai</i>	<i>A. setosa</i>	<i>A. spinifemorata</i>	<i>A. yifengi</i>	<i>P. (A.) longipenis</i>	<i>P. (A.) tanabei</i>	<i>P. (P.) huazhii</i>	<i>P. (P.) pseudogigas</i>	<i>P. (P.) variegata</i>	<i>P. (S.) hani</i>
<i>trnI</i> (Ile)	64	65	65	65	65	67	65	66	65	65	65	65
<i>trnQ</i> (Gln)	69	69	69	69	69	69	69	69	69	69	69	69
<i>trnM</i> (Met)	69	69	69	69	69	69	69	69	69	69	69	69
<i>ND2</i>	1,026	1,023	1,026	1,026	1,026	1,023	1,026	1,026	1,026	1,026	1,026	1,026
<i>trnW</i> (Trp)	68	68	68	68	68	68	67	67	68	68	68	67
<i>trnC</i> (Cys)	63	63	64	63	63	62	62	62	63	63	63	62
<i>trnY</i> (Tyr)	65	66	67	66	65	65	68	66	66	65	66	66
<i>COX1</i>	1,539	1,539	1,539	1,539	1,539	1,539	1,539	1,539	1,539	1,539	1,539	1,539
<i>trnL1</i> (Leu) (UUR)	66	66	66	66	66	66	66	66	66	66	66	66
<i>COX2</i>	681	681	681	681	681	681	685	685	685	685	685	685
<i>trnK</i> (Lys)	71	71	71	71	71	71	71	71	71	71	71	71
<i>trnD</i> (Asp)	70	70	67	70	66	70	67	67	66	67	67	66
<i>ATP8</i>	162	162	162	162	162	162	162	162	162	162	162	162
<i>ATP6</i>	678	678	678	678	678	678	678	678	678	678	678	678
<i>COX3</i>	789	789	789	789	789	789	789	789	789	789	789	789
<i>trnG</i> (Gly)	64	64	66	65	65	64	64	65	65	64	65	64
<i>ND3</i>	354	354	354	352	354	354	354	354	354	354	354	354
<i>trnA</i> (Ala)	65	67	65	66	65	65	66	65	65	65	65	65
<i>trnR</i> (Arg)	64	64	63	63	63	63	64	63	63	63	63	63
<i>trnN</i> (Asn)	69	65	65	66	65	65	66	67	65	65	65	65
<i>trnS2</i> (Ser) (AGN)	66	68	67	66	68	68	67	67	67	65	67	67
<i>trnE</i> (Glu)	67	68	67	66	67	67	67	67	66	66	66	66
<i>trnF</i> (Phe)	66	66	66	68	66	66	66	66	66	67	67	66
<i>ND5</i>	1,717	1,720	1,720	1,717	1,720	1,720	1,722	1,722	1,720	1,720	1,720	1,720
<i>trnH</i> (His)	65	65	66	66	66	66	66	65	66	65	65	65
<i>ND4</i>	1,339	1,339	1,339	1,339	1,339	1,339	1,339	1,339	1,339	1,339	1,339	1,341
<i>ND4L</i>	291	291	291	291	291	291	291	291	291	291	291	291
<i>trnT</i> (Thr)	64	65	64	65	65	65	65	65	65	65	65	65
<i>trnP</i> (Pro)	67	66	67	66	66	66	66	66	68	67	66	66
<i>ND6</i>	525	525	525	525	525	525	525	525	525	525	525	525
<i>CYTb</i>	1,137	1,137	1,137	1,137	1,137	1,137	1,137	1,137	1,137	1,137	1,137	1,137
<i>trnS1</i> (Ser) (UCN)	67	67	67	68	67	67	66	67	67	67	67	67
<i>ND1</i>	937	937	937	916	937	937	937	937	937	937	937	937
<i>trnL2</i> (Leu) (CUN)	65	66	65	67	65	67	63	64	63	64	64	64
lrRNA	1,329	1,327	1,330	1,322	1,338	1,328	1,323	1,318	1,320	1,322	1,320	1,317
<i>trnV</i> (Val)	72	72	72	72	72	72	72	72	72	72	72	72
srRNA	787	784	789	785	787	783	785	784	788	787	788	787
D-loop region	1,912	1,672	1,554	1,995	1,319	1,515	1,355	1,084	1,182	1,158	1,134	1,118

Table S2. Intergenic nucleotides (IGNs) of the *Amiota* and *Phortica* mitogenomes.

Gene	<i>A. dentata</i>	<i>A. femorata</i>	<i>A. nagatai</i>	<i>A. setosa</i>	<i>A. spinifemorata</i>	<i>A. yifengi</i>	<i>P. (A.) longipenis</i>	<i>P. (A.) tanabei</i>	<i>P. (P.) huazhii</i>	<i>P. (P.) pseudogigas</i>	<i>P. (P.) variegata</i>	<i>P. (S.) hani</i>
<i>trnI</i> (Ile)	0	7	0	1	1	0	100	14	15	15	15	13
<i>trnQ</i> (Gln)	−1	−1	5	−1	−1	−1	−1	−1	−1	−1	−1	−1
<i>trnM</i> (Met)	0	0	0	0	0	0	0	0	0	0	0	0
<i>ND2</i>	0	0	0	0	0	0	0	0	0	0	0	0
<i>trnW</i> (Trp)	6	6	38	6	6	6	6	6	6	6	6	6
<i>trnC</i> (Cys)	2	2	47	0	2	2	1	4	2	2	2	2
<i>trnY</i> (Tyr)	0	0	0	0	0	0	0	0	0	0	0	0
<i>COX1</i>	3	3	3	3	3	3	3	3	3	3	3	3
<i>trnL1</i> (Leu) (UUR)	2	3	6	3	4	3	2	5	2	6	2	2
<i>COX2</i>	4	7	5	6	6	6	3	3	3	3	3	3
<i>trnK</i> (Lys)	1	−1	0	−1	0	2	3	0	2	−1	0	0
<i>trnD</i> (Asp)	0	0	0	0	1	0	0	0	0	0	0	0
<i>ATP8</i>	5	5	5	5	5	5	5	5	5	5	5	5
<i>ATP6</i>	−1	−1	−1	−1	−1	−1	−1	5	9	12	6	11
<i>COX3</i>	8	8	11	8	8	8	9	9	9	9	9	9
<i>trnG</i> (Gly)	0	0	0	0	0	0	0	0	0	0	0	0
<i>ND3</i>	0	0	3	0	0	0	1	2	0	0	0	0
<i>trnA</i> (Ala)	2	8	49	2	2	3	−1	−1	−1	−1	−1	−1
<i>trnR</i> (Arg)	0	3	32	2	1	1	7	9	7	2	2	3
<i>trnN</i> (Asn)	1	0	0	1	0	0	0	0	0	1	0	0
<i>trnS2</i> (Ser) (AGN)	1	0	1	1	0	0	0	0	0	1	0	0
<i>trnE</i> (Glu)	18	18	18	18	18	18	18	18	19	18	18	18
<i>trnF</i> (Phe)	0	0	0	0	0	0	19	9	0	0	0	0
<i>ND5</i>	15	15	15	15	15	15	15	15	15	15	15	15
<i>trnH</i> (His)	0	0	0	0	0	0	0	0	0	0	0	−1
<i>ND4</i>	4	2	6	1	3	4	−1	−1	−1	−1	0	−1
<i>ND4L</i>	2	2	2	2	2	2	2	2	2	2	2	2
<i>trnT</i> (Thr)	0	0	0	0	0	0	0	0	0	0	0	0
<i>trnP</i> (Pro)	2	3	3	2	2	2	2	2	2	2	2	2
<i>ND6</i>	−1	−1	6	−1	−1	−1	−1	−1	−1	−1	−1	−1
<i>CYTb</i>	0	0	−1	0	0	0	0	4	0	0	0	6
<i>trnS1</i> (Ser) (UCN)	15	15	15	15	15	15	18	18	18	18	18	10
<i>ND1</i>	10	10	10	31	10	10	10	10	10	10	10	10
<i>trnL2</i> (Leu) (CUN)	0	0	0	0	0	0	0	0	0	0	0	0
lrRNA	0	0	0	0	0	0	0	0	0	0	0	0
<i>trnV</i> (Val)	0	0	0	0	0	0	0	0	0	0	0	0
srRNA	0	0	0	0	0	0	0	0	0	0	0	0
D-loop region	0	0	0	0	0	0	0	0	0	0	0	0

Table S3. Relative synonymous codon usage (RSCU) values of the protein-coding genes (PCGs) in the *Amiota* and *Phortica* mitogenomes.

Amino acid	Codon	<i>A. dentata</i>	<i>A. femorata</i>	<i>A. nagatai</i>	<i>A. setosa</i>	<i>A. spinifemorata</i>	<i>A. yifengi</i>	<i>P. (A.) longipenis</i>	<i>P. (A.) tanabei</i>	<i>P. (P.) huazhii</i>	<i>P. (P.) pseudogigas</i>	<i>P. (P.) variegata</i>	<i>P. (S.) hani</i>
Ala	GCA	1.13	1.53	1.61	1.46	1.19	1.27	1.48	1.30	1.25	1.30	1.06	1.16
	GCU	2.44	2.40	2.34	2.17	2.53	2.47	2.29	2.47	2.45	2.38	2.58	2.61
	GCG	0.05	0.05	0.00	0.10	0.10	0.03	0.02	0.05	0.07	0.07	0.04	0.05
	GCC	0.38	0.02	0.05	0.27	0.17	0.23	0.21	0.18	0.23	0.25	0.31	0.18
Arg	CGA	2.51	2.85	2.58	2.69	2.85	2.71	2.78	2.98	2.71	2.71	2.78	2.78
	CGU	1.22	0.81	1.36	1.24	0.95	0.95	1.08	0.95	0.95	1.15	1.02	1.08
	CGG	0.14	0.27	0.07	0.07	0.20	0.14	0.14	0.07	0.34	0.14	0.20	0.14
	CGC	0.14	0.07	0.00	0.00	0.00	0.20	0.00	0.00	0.00	0.00	0.00	0.00
Asn	AAU	1.97	1.90	1.88	1.90	1.88	1.89	1.84	1.94	1.71	1.82	1.81	1.85
	AAC	0.10	0.10	0.13	0.10	0.12	0.11	0.16	0.06	0.29	0.18	0.19	0.15
Asp	GAU	1.77	1.84	1.78	1.85	1.81	1.81	1.70	1.82	1.42	1.55	1.55	1.76
	GAC	0.23	0.16	0.22	0.15	0.19	0.19	0.30	0.18	0.58	0.45	0.45	0.24
Cys	UGU	1.95	2.00	2.00	1.95	1.94	1.95	1.90	1.90	1.95	2.00	1.90	1.74
	UGC	0.05	0.00	0.00	0.05	0.06	0.05	0.10	0.10	0.05	0.00	0.10	0.26
Gln	CAA	1.83	1.97	1.94	1.81	1.94	1.88	1.97	1.89	1.86	1.86	1.94	1.86
	CAG	0.17	0.03	0.06	0.19	0.06	0.12	0.03	0.11	0.14	0.14	0.06	0.14
Glu	GAA	1.88	1.85	1.90	1.84	1.90	1.95	1.87	1.97	1.84	1.82	1.89	1.95
	GAG	0.12	0.15	0.10	0.16	0.10	0.05	0.13	0.03	0.16	0.18	0.11	0.05
	GGA	2.66	2.67	2.64	2.42	2.52	2.70	2.72	2.76	2.70	2.73	2.61	2.67
Gly	GGU	0.83	1.00	1.10	1.19	1.10	0.97	1.00	1.04	0.68	0.94	0.97	1.03
	GGG	0.44	0.29	0.20	0.29	0.29	0.22	0.24	0.19	0.57	0.29	0.38	0.28
	GGC	0.07	0.04	0.05	0.09	0.09	0.11	0.04	0.02	0.06	0.04	0.04	0.02
His	CAU	1.48	1.71	1.82	1.50	1.76	1.70	1.61	1.79	1.37	1.45	1.47	1.63
	CAC	0.52	0.29	0.18	0.50	0.24	0.30	0.39	0.21	0.63	0.55	0.53	0.37
Ile	AUU	1.95	1.95	1.97	1.90	1.92	1.91	1.96	1.94	1.84	1.85	1.89	1.95
	AUC	0.05	0.05	0.03	0.10	0.08	0.09	0.04	0.06	0.16	0.15	0.11	0.05
Leu1	UUA	5.02	5.21	5.32	4.94	5.19	5.33	5.08	5.20	4.75	4.77	4.83	5.09
	UUG	0.40	0.25	0.15	0.31	0.27	0.23	0.27	0.29	0.36	0.40	0.26	0.19
	CUA	0.27	0.22	0.19	0.45	0.22	0.20	0.22	0.16	0.39	0.26	0.40	0.25
Leu2	CUU	0.29	0.30	0.33	0.25	0.28	0.22	0.42	0.32	0.48	0.53	0.47	0.43
	CUG	0.00	0.01	0.01	0.01	0.01	0.02	0.00	0.03	0.02	0.01	0.02	0.02
	CUC	0.02	0.00	0.00	0.04	0.03	0.01	0.00	0.00	0.00	0.03	0.02	0.02
Lys	AAA	1.88	1.86	1.78	1.75	1.89	1.83	1.89	1.87	1.61	1.60	1.73	1.57
	AAG	0.12	0.14	0.22	0.25	0.11	0.17	0.11	0.13	0.39	0.40	0.27	0.43
Met	AUA	1.79	1.89	1.84	1.84	1.81	1.85	1.85	1.84	1.84	1.76	1.77	1.81
	AUG	0.21	0.11	0.16	0.16	0.19	0.15	0.15	0.16	0.16	0.24	0.23	0.19
Phe	UUU	1.92	1.89	1.94	1.90	1.95	1.92	1.88	1.91	1.82	1.88	1.82	1.83
	UUC	0.08	0.11	0.06	0.10	0.05	0.08	0.12	0.09	0.18	0.12	0.18	0.17
Pro	CCA	1.15	1.13	1.48	1.10	0.95	1.27	0.71	0.86	1.13	0.89	1.04	0.85
	CCU	2.51	2.69	2.49	2.41	2.74	2.45	3.01	2.80	2.50	2.75	2.66	2.78
	CCG	0.09	0.03	0.00	0.00	0.12	0.00	0.00	0.09	0.15	0.12	0.06	0.09
	CCC	0.25	0.15	0.03	0.49	0.18	0.28	0.28	0.25	0.21	0.24	0.24	0.27

Ser1	UCA	2.57	2.12	2.35	2.04	2.37	2.37	2.00	2.12	2.20	2.48	2.28	2.26
	UCU	2.83	3.30	3.10	3.20	3.00	2.99	3.20	3.13	2.85	2.79	2.96	3.04
	UCG	0.09	0.02	0.05	0.09	0.07	0.12	0.07	0.07	0.23	0.14	0.07	0.12
	UCC	0.09	0.09	0.05	0.26	0.16	0.22	0.05	0.02	0.12	0.07	0.09	0.02
Ser2	AGA	1.64	1.53	1.65	1.56	1.58	1.60	1.51	1.48	1.45	1.48	1.53	1.41
	AGU	0.63	0.88	0.75	0.76	0.77	0.65	1.13	1.08	0.98	0.93	1.04	1.15
	AGG	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
	AGC	0.14	0.05	0.05	0.09	0.05	0.05	0.05	0.09	0.16	0.12	0.02	0.00
Thr	ACA	1.95	1.97	2.02	1.58	1.96	1.72	1.72	1.58	1.74	1.70	1.76	1.86
	ACU	1.77	1.94	1.93	2.09	1.94	2.15	2.17	2.20	2.07	2.06	2.04	1.97
	ACG	0.02	0.04	0.02	0.09	0.00	0.09	0.04	0.07	0.04	0.15	0.07	0.02
	ACC	0.26	0.04	0.02	0.24	0.09	0.04	0.07	0.15	0.17	0.09	0.13	0.15
Trp	UGA	1.92	1.96	1.96	1.88	1.86	1.92	1.94	1.96	1.96	1.96	1.98	1.94
	UGG	0.08	0.04	0.04	0.12	0.14	0.08	0.06	0.04	0.04	0.04	0.02	0.06
Tyr	UAU	1.85	1.89	1.95	1.87	1.83	1.81	1.87	1.84	1.64	1.66	1.63	1.72
	UAC	0.15	0.11	0.05	0.13	0.17	0.19	0.13	0.16	0.36	0.34	0.37	0.28
Val	GUA	1.57	1.71	1.76	2.01	1.79	1.47	1.66	1.73	1.94	1.99	1.74	2.01
	GUU	2.24	2.13	2.17	1.82	2.07	2.31	2.10	2.01	1.72	1.88	2.11	1.87
	GUG	0.17	0.11	0.02	0.09	0.07	0.14	0.17	0.20	0.20	0.09	0.12	0.12
	GUC	0.02	0.05	0.04	0.07	0.07	0.07	0.06	0.07	0.14	0.04	0.04	0.00

Table S4. Codons per thousand codon (CDspT) values of the PCGs in the *Amiota* and *Phortica* mitogenomes.

Amino acid	<i>A. dentata</i>	<i>A. femorata</i>	<i>A. nagatai</i>	<i>A. setosa</i>	<i>A. spinifemorata</i>	<i>A. yifengi</i>	<i>P. (A.) longipenis</i>	<i>P. (A.) tanabei</i>	<i>P. (P.) huazhii</i>	<i>P. (P.) pseudogigas</i>	<i>P. (P.) variegata</i>	<i>P. (S.) hani</i>
Ala	42.85	43.65	43.37	43.74	43.37	41.50	45.23	47.12	46.58	47.12	47.93	46.58
Arg	15.90	15.90	15.89	15.66	15.89	15.90	15.89	15.89	15.89	15.89	15.89	15.89
Asn	56.59	56.05	56.03	56.70	58.73	56.32	54.93	53.85	53.58	53.85	53.58	53.85
Asp	16.44	17.25	16.97	18.09	16.97	16.98	17.77	17.50	17.77	17.77	17.77	17.77
Cys	10.78	10.24	10.51	10.53	9.16	10.78	10.77	10.77	11.04	11.04	11.31	10.50
Glu	22.64	21.83	22.36	20.52	22.09	22.64	20.46	20.73	20.19	20.46	20.19	20.19
Gly	58.74	59.01	59.54	58.86	59.00	57.94	58.16	58.16	58.70	58.43	58.97	58.43
His	19.67	20.75	20.47	20.52	19.94	19.94	20.46	20.46	20.46	20.46	20.46	20.46
Ile	103.48	100.51	101.56	102.32	101.56	106.17	98.55	99.89	95.58	93.97	94.24	96.93
Leu1	148.48	150.63	150.32	144.71	150.05	151.71	147.82	152.40	142.16	143.24	142.16	147.82
Leu2	15.63	14.82	14.55	20.52	14.82	12.13	17.77	14.27	24.77	22.89	25.31	20.19
Lys	23.17	23.17	24.78	23.76	23.98	25.33	24.77	24.23	23.69	24.23	23.96	23.96
Met	59.28	61.71	59.27	60.48	60.88	61.17	62.47	58.97	56.27	56.54	55.74	56.54
Phe	94.04	89.73	92.13	91.52	90.79	93.24	88.58	89.39	89.12	89.12	89.12	89.93
Pro	34.76	35.30	35.02	35.37	35.02	34.76	34.73	35.00	35.27	35.27	35.27	35.27
Ser1	64.40	64.13	61.69	63.71	64.92	64.13	60.85	61.12	62.20	61.93	61.93	62.20
Ser2	27.76	28.56	27.21	27.54	27.75	25.87	30.69	30.43	29.89	28.54	29.62	29.35
Thr	46.35	48.23	46.88	45.90	46.07	48.23	48.20	49.00	50.35	50.08	49.54	49.27
Trp	26.95	26.41	26.40	27.00	26.94	26.68	26.66	26.66	26.93	26.66	26.93	26.66
Tyr	47.97	45.54	46.88	46.98	46.61	45.27	46.58	45.77	46.31	45.77	45.50	46.85
Val	45.27	47.16	49.57	46.17	46.34	44.73	49.81	49.27	53.85	57.35	55.20	51.97

Table S5. Nucleotide compositions and skewness levels of the *Amiota* and *Phortica* mitogenomes.

Regions/genes	Species	Size (bp)	Nucleotides composition (%)				AT-skew	GC-skew
			A	T	G	C		
Whole mitogenome (J-strands)	<i>A. dentata</i>	16,725	40.7	39.2	8.1	12.0	0.019	-0.194
	<i>A. femorata</i>	16,499	40.0	39.9	8.6	11.4	0.001	-0.140
	<i>A. nagatai</i>	16,571	40.2	40.3	8.4	11.2	-0.001	-0.143
	<i>A. setosa</i>	16,803	40.7	38.8	8.1	12.4	0.024	-0.210
	<i>A. spinifemorata</i>	16,143	40.2	39.4	8.7	11.7	0.010	-0.147
	<i>A. yifengi</i>	16,329	40.4	39.7	8.3	11.7	0.009	-0.170
	<i>P. (A.) longipenis</i>	16,290	40.1	39.4	8.4	12.1	0.009	-0.180
	<i>P. (A.) tanabei</i>	15,933	39.9	39.2	8.8	12.0	0.009	-0.154
	<i>P. (P.) huazhii</i>	16,016	39.1	38.1	9.1	13.6	0.013	-0.198
	<i>P. (P.) pseudogigas</i>	15,990	39.1	38.4	9.5	12.9	0.009	-0.152
	<i>P. (P.) variegata</i>	15,958	39.3	38.5	9.2	13.0	0.010	-0.171
	<i>P. (S.) hani</i>	15,937	39.4	39.0	9.1	12.5	0.005	-0.157
PCGs	<i>A. dentata</i>	11,175	32.3	44.9	12.0	10.9	-0.163	0.048
	<i>A. femorata</i>	11,175	32.8	44.9	11.7	10.6	-0.156	0.049
	<i>A. nagatai</i>	11,178	32.9	45.2	11.6	10.2	-0.157	0.064
	<i>A. setosa</i>	11,152	32.2	44.6	11.9	11.3	-0.161	0.026
	<i>A. spinifemorata</i>	11,178	32.6	44.9	11.8	10.7	-0.159	0.049
	<i>A. yifengi</i>	11,175	32.7	45.0	11.5	10.7	-0.158	0.036
	<i>P. (A.) longipenis</i>	11,184	32.4	44.9	11.9	10.8	-0.162	0.048
	<i>P. (A.) tanabei</i>	11,184	32.3	45.1	12.0	10.7	-0.165	0.057
	<i>P. (P.) huazhii</i>	11,182	31.8	43.4	12.7	12.2	-0.154	0.020
	<i>P. (P.) pseudogigas</i>	11,182	31.7	43.9	12.6	11.7	-0.161	0.037
	<i>P. (P.) variegata</i>	11,182	31.7	44.0	12.4	11.9	-0.162	0.021
	<i>P. (S.) hani</i>	11,184	32.0	44.6	12.1	11.3	-0.164	0.034
PCGs (1st codon positions)	<i>A. dentata</i>	3,727	31.6	39.5	18.5	10.4	-0.111	0.280
	<i>A. femorata</i>	3,727	31.7	38.9	18.8	10.6	-0.102	0.279
	<i>A. nagatai</i>	3,728	31.5	39.0	19.1	10.4	-0.106	0.295
	<i>A. setosa</i>	3,720	31.6	38.7	18.7	11.1	-0.101	0.255
	<i>A. spinifemorata</i>	3,728	31.8	39.1	18.7	10.4	-0.103	0.285
	<i>A. yifengi</i>	3,727	32.2	39.4	18.3	10.1	-0.101	0.289
	<i>P. (A.) longipenis</i>	3,730	31.8	38.3	19.1	10.7	-0.093	0.282
	<i>P. (A.) tanabei</i>	3,730	31.5	38.8	19.2	10.4	-0.104	0.297
	<i>P. (P.) huazhii</i>	3,730	30.8	38.0	19.7	11.5	-0.105	0.263
	<i>P. (P.) pseudogigas</i>	3,730	30.6	38.0	20.1	11.3	-0.108	0.280
	<i>P. (P.) variegata</i>	3,730	30.6	37.9	19.9	11.6	-0.107	0.263
	<i>P. (S.) hani</i>	3,730	30.9	38.6	19.4	11.1	-0.111	0.272
PCGs (2nd codon positions)	<i>A. dentata</i>	3,724	20.8	46.5	14.0	18.8	-0.382	-0.146
	<i>A. femorata</i>	3,724	20.6	46.3	14.0	19.1	-0.384	-0.154
	<i>A. nagatai</i>	3,725	20.9	46.6	13.9	18.6	-0.381	-0.145
	<i>A. setosa</i>	3,716	20.8	46.4	13.9	18.8	-0.381	-0.150
	<i>A. spinifemorata</i>	3,725	21.0	46.3	13.8	18.9	-0.376	-0.156
	<i>A. yifengi</i>	3,724	20.8	46.8	13.7	18.8	-0.385	-0.157
	<i>P. (A.) longipenis</i>	3,727	20.6	46.4	14.2	18.8	-0.385	-0.139
	<i>P. (A.) tanabei</i>	3,727	20.4	46.3	14.1	19.2	-0.388	-0.153
	<i>P. (P.) huazhii</i>	3,726	20.4	46.1	14.2	19.4	-0.386	-0.155
	<i>P. (P.) pseudogigas</i>	3,726	20.4	46.2	14.0	19.4	-0.387	-0.162
	<i>P. (P.) variegata</i>	3,726	20.3	46.1	14.2	19.4	-0.389	-0.155
	<i>P. (S.) hani</i>	3,727	20.5	46.2	14.0	19.3	-0.385	-0.159
PCGs (3rd codon positions)	<i>A. dentata</i>	3,724	44.5	48.6	3.5	3.4	-0.044	0.014
	<i>A. femorata</i>	3,724	45.9	49.5	2.4	2.2	-0.038	0.043
	<i>A. nagatai</i>	3,725	46.4	50.1	1.8	1.6	-0.038	0.059
	<i>A. setosa</i>	3,716	44.2	48.7	3.1	4.0	-0.048	-0.127
	<i>A. spinifemorata</i>	3,725	45.0	49.4	2.8	2.8	-0.047	0.000
	<i>A. yifengi</i>	3,724	45.3	49.0	2.5	3.2	-0.039	-0.123
	<i>P. (A.) longipenis</i>	3,727	44.8	49.9	2.4	3.0	-0.054	-0.111
	<i>P. (A.) tanabei</i>	3,727	44.9	50.1	2.5	2.5	-0.055	0.000
	<i>P. (P.) huazhii</i>	3,726	44.2	46.1	4.1	5.6	-0.021	-0.155
	<i>P. (P.) pseudogigas</i>	3,726	44.0	47.6	3.9	4.5	-0.039	-0.071
	<i>P. (P.) variegata</i>	3,726	44.2	48.0	3.1	4.7	-0.041	-0.205
	<i>P. (S.) hani</i>	3,727	44.6	49.0	2.9	3.5	-0.047	-0.094

tRNAs	<i>A. dentata</i>	1,444	38.7	39.4	12.5	9.3	-0.009	0.147
	<i>A. femorata</i>	1,448	39.0	39.0	12.6	9.4	0.000	0.145
	<i>A. nagatai</i>	1,444	38.4	39.8	12.7	9.1	-0.018	0.165
	<i>A. setosa</i>	1,449	38.7	39.9	12.2	9.2	-0.015	0.140
	<i>A. spinifemorata</i>	1,440	38.0	39.7	13.1	9.2	-0.022	0.175
	<i>A. yifengi</i>	1,446	38.9	39.4	12.6	9.1	-0.006	0.161
	<i>P. (A.) longipenis</i>	1,440	38.8	39.3	12.2	9.7	-0.006	0.114
	<i>P. (A.) tanabei</i>	1,440	38.2	39.2	12.7	9.9	-0.013	0.124
	<i>P. (P.) huazhii</i>	1,439	38.2	38.2	13.4	10.2	0.000	0.136
	<i>P. (P.) pseudogigas</i>	1,436	38.0	39.0	13.2	9.8	-0.013	0.148
	<i>P. (P.) variegata</i>	1,439	37.7	38.6	13.5	10.2	-0.012	0.139
	<i>P. (S.) hani</i>	1,434	38.4	38.9	12.8	9.8	-0.006	0.133
rRNAs	<i>A. dentata</i>	2,116	41.3	41.0	11.7	6.0	0.004	0.322
	<i>A. femorata</i>	2,111	41.2	40.8	11.6	6.4	0.005	0.289
	<i>A. nagatai</i>	2,119	41.0	41.2	11.8	6.1	-0.002	0.318
	<i>A. setosa</i>	2,107	40.4	41.0	12.3	6.3	-0.007	0.323
	<i>A. spinifemorata</i>	2,125	41.4	40.9	11.5	6.2	0.006	0.299
	<i>A. yifengi</i>	2,111	41.4	41.1	11.5	6.1	0.004	0.307
	<i>P. (A.) longipenis</i>	2,108	40.3	42.3	11.3	6.1	-0.024	0.299
	<i>P. (A.) tanabei</i>	2,102	40.9	41.4	11.4	6.3	-0.006	0.288
	<i>P. (P.) huazhii</i>	2,108	40.0	40.7	12.7	6.6	-0.009	0.316
	<i>P. (P.) pseudogigas</i>	2,109	40.0	41.0	12.3	6.7	-0.012	0.295
	<i>P. (P.) variegata</i>	2,108	40.1	41.1	12.2	6.6	-0.012	0.298
	<i>P. (S.) hani</i>	2,104	40.7	40.7	12.1	6.6	0.000	0.294
D-loop region	<i>A. dentata</i>	1,912	51.9	41.9	1.5	4.7	0.107	-0.516
	<i>A. femorata</i>	1,672	50.3	43.7	1.8	4.2	0.070	-0.400
	<i>A. nagatai</i>	1,554	49.4	44.6	1.7	4.3	0.051	-0.433
	<i>A. setosa</i>	1,995	50.2	42.8	1.7	5.4	0.080	-0.521
	<i>A. spinifemorata</i>	1,319	51.8	42.1	2.8	3.3	0.103	-0.082
	<i>A. yifengi</i>	1,515	50.8	43.0	2.3	3.8	0.083	-0.246
	<i>P. (A.) longipenis</i>	1,355	48.7	43.5	3.0	4.7	0.056	-0.221
	<i>P. (A.) tanabei</i>	1,084	50.6	42.3	2.4	4.7	0.089	-0.324
	<i>P. (P.) huazhii</i>	1,182	47.5	43.3	3.2	6.0	0.046	-0.304
	<i>P. (P.) pseudogigas</i>	1,158	47.5	42.7	3.8	6.0	0.053	-0.224
	<i>P. (P.) variegata</i>	1,134	50.2	42.1	2.8	4.9	0.088	-0.273
	<i>P. (S.) hani</i>	1,118	47.9	44.1	2.9	5.2	0.041	-0.284

Table S6. Nonsynonymous substitutions per nonsynonymous site (Ka), synonymous substitutions per synonymous site (Ks), and Ka/Ks (ω) values (mean \pm standard deviation, SD) of the 13 PCGs in the *Amiota* and *Phortica* mitogenomes.

PCG	<i>Amiota</i>			<i>Phortica</i>		
	Ka	Ks	ω	Ka	Ks	ω
<i>ND2</i>	0.07310 \pm 0.02511	0.31484 \pm 0.03813	0.22911 \pm 0.05994	0.04121 \pm 0.01843	0.44908 \pm 0.07819	0.09497 \pm 0.04429
<i>COX1</i>	0.02240 \pm 0.00569	0.46136 \pm 0.07231	0.04936 \pm 0.01396	0.01354 \pm 0.00581	0.47929 \pm 0.07440	0.02781 \pm 0.01033
<i>COX2</i>	0.03733 \pm 0.01383	0.35690 \pm 0.05723	0.10890 \pm 0.05272	0.01989 \pm 0.00804	0.41700 \pm 0.08408	0.04769 \pm 0.01928
<i>ATP8</i>	0.08515 \pm 0.01683	0.27083 \pm 0.09634	0.36450 \pm 0.16606	0.04191 \pm 0.01528	0.25053 \pm 0.09556	0.18193 \pm 0.08914
<i>ATP6</i>	0.04048 \pm 0.01084	0.46746 \pm 0.10290	0.09053 \pm 0.02977	0.02583 \pm 0.01104	0.43904 \pm 0.04247	0.05854 \pm 0.02380
<i>COX3</i>	0.03276 \pm 0.01007	0.40396 \pm 0.08413	0.08493 \pm 0.03326	0.01443 \pm 0.00478	0.47062 \pm 0.08853	0.03112 \pm 0.01149
<i>ND3</i>	0.05183 \pm 0.00867	0.37636 \pm 0.09204	0.14624 \pm 0.04529	0.04426 \pm 0.01964	0.50563 \pm 0.08984	0.08602 \pm 0.03596
<i>ND5</i>	0.05822 \pm 0.01502	0.35825 \pm 0.03984	0.16226 \pm 0.03723	0.03616 \pm 0.01356	0.42760 \pm 0.04295	0.08462 \pm 0.03043
<i>ND4</i>	0.06171 \pm 0.01725	0.34988 \pm 0.03464	0.17897 \pm 0.05528	0.03612 \pm 0.01563	0.43492 \pm 0.05970	0.08151 \pm 0.03088
<i>ND4L</i>	0.03065 \pm 0.01447	0.24184 \pm 0.06298	0.13640 \pm 0.07431	0.01354 \pm 0.00661	0.39400 \pm 0.06108	0.03534 \pm 0.01869
<i>ND6</i>	0.07784 \pm 0.02091	0.32163 \pm 0.04968	0.24282 \pm 0.05819	0.05730 \pm 0.02188	0.47782 \pm 0.08720	0.12112 \pm 0.04654
<i>CYTb</i>	0.03774 \pm 0.00735	0.38616 \pm 0.08462	0.10049 \pm 0.02328	0.02564 \pm 0.00831	0.56119 \pm 0.08176	0.04574 \pm 0.01396
<i>ND1</i>	0.03304 \pm 0.00579	0.35991 \pm 0.05560	0.09392 \pm 0.02120	0.01493 \pm 0.00685	0.38131 \pm 0.04933	0.03908 \pm 0.01728

Table S7. Partitioning schemes and data subsets evaluated for the Bayesian inference (BI) and Maximum likelihood (ML) analysis by PartitionFinder. For the data set based on the nucleotides of the 13 PCGs and two rRNAs, best-fit selected substitution models for the PCGs (by codon positions) and rRNAs (by genes) are shown; for the data set of the amino acids based on the 13 PCGs, best-fit selected substitution models for the PCGs (by genes) are shown.

Subset	13 PCGs + two rRNAs (nucleotides)		13 PCGs (amino acids)	
	Partitioning scheme	Best model	Partitioning scheme	Partitioning scheme
1	<i>ATP8</i> 1st, <i>ND2</i> 1st, <i>ND6</i> 1st, <i>ND3</i> 1st	TIM+G	<i>ATP8</i> , <i>ND2</i>	MTART+G+F
2	<i>ATP8</i> 2nd, <i>ND2</i> 2nd	TRN+G	<i>COX1</i> , <i>COX3</i>	MTMAM+I+G+F
3	<i>COX1</i> 3rd, <i>ND2</i> 3rd	TIM+G	<i>COX2</i> , <i>CYTB</i>	MTMAM+I+G+F
4	<i>COX1</i> 1st	TRN+I+G	<i>ATP6</i> , <i>ND1</i>	MTART+I+G
5	<i>COX1</i> 2nd	F81+I+G	<i>ND6</i> , <i>ND3</i>	MTMAM+G+F
6	<i>COX3</i> 1st, <i>ATP6</i> 1st, <i>COX2</i> 1st, <i>CYTB</i> 1st	GTR+G	<i>ND4L</i> , <i>ND5</i> , <i>ND4</i>	MTART+I+G+F
7	<i>COX2</i> 2nd	F81+G		
8	<i>COX2</i> 3rd, <i>COX3</i> 3rd, <i>CYTB</i> 3rd	TIM+G		
9	<i>ATP8</i> 3rd, <i>ND6</i> 3rd, <i>ND3</i> 3rd	TRN+G		
10	<i>ND1</i> 2nd, <i>ATP6</i> 2nd, <i>CYTB</i> 2nd	TVM+I+G		
11	<i>ATP6</i> 3rd	TRN+G		
12	<i>COX3</i> 2nd	TVM+G		
13	<i>ND3</i> 2nd, <i>ND6</i> 2nd	GTR+G		
14	<i>ND4</i> 1st, <i>ND5</i> 1st	GTR+I+G		
15	<i>ND4</i> 2nd, <i>ND5</i> 2nd	GTR+I+G		
16	<i>ND5</i> 3rd, <i>ND4</i> 3rd	TIM+I+G		
17	<i>ND4L</i> 1st, <i>ND1</i> 1st	TIM+G		
18	<i>ND4L</i> 2nd	TRN		
19	<i>ND1</i> 3rd, <i>ND4L</i> 3rd	K81UF+G		
20	srRNA, lrRNA	GTR+I+G		