

Supplementary Materials: Comparative Mitogenomic Analysis of Species Representing Six Subfamilies in the Family Tenebrionidae

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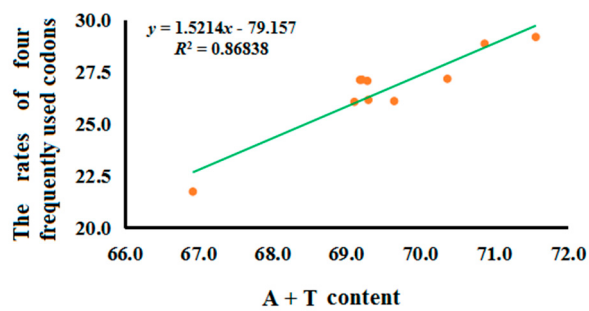


Figure S1. Correlation between the percentage of the four most frequently used codons and A + T content of all protein-coding genes.

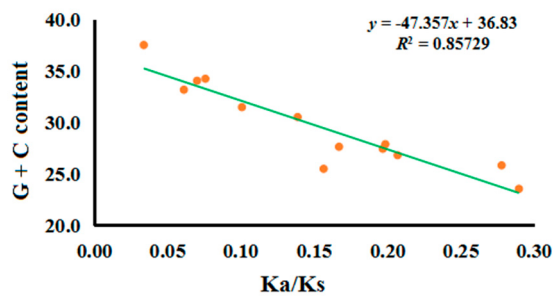


Figure S2. Correlation between ω and G + C content of protein-coding genes.

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          ***** ** *****
Ad -ATACTAATTTTTATTAA
As -ATACTAAATTTTATTAA
Te1 -ATACTAAATTTTATTAA
Te2 -ATACTAAATTTTATTAA
Ul AGTACTAAAATTATTAA
Tr1 -ATACTAAATTTTATTAA
Tr2 -ATACTAAATTTTATTAA
Tr3 -ATACTAAATTTTATTAA
Tr4 -TTACTAAATTTTATTAA
Tr5 -GTACTAAATTTTATTAA
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Figure S3. The sequence of the gap between *trnS^{UCN}* and *ND1* in ten Tenebrionidae mitogenomes. Note: Nucleotides with red color denote the site of nucleotide mutation; * denote the completely conserved site.

	***	*	***	*	****
<i>Ad</i>	AAA - C	TTTTCTA	GTAA		
<i>As</i>	AAATC	TTTTTTTG	ATAA		
<i>Te1</i>	AAATC	TTTTTTT	GTAA		
<i>Te2</i>	AAATC	TTTTTTT	GTAA		
<i>Ul</i>	AAA - C	TTTTCTT	ATAC		
<i>Tr1</i>	AAAAC	TTTATTT	GTAA		
<i>Tr2</i>	AAAAC	TTTATTT	GTAA		
<i>Tr3</i>	AAAAC	TTTATTT	GTAA		
<i>Tr4</i>	AAAAC	TTTTTTT	GTAA		
<i>Tr5</i>	AAAAC	TTTTTTA	GTAA		

Figure S4. T stretch in the minor strand and the abutting flanking regions in ten Tenebrionidae mitogenomes. * denote the completely conserved site.

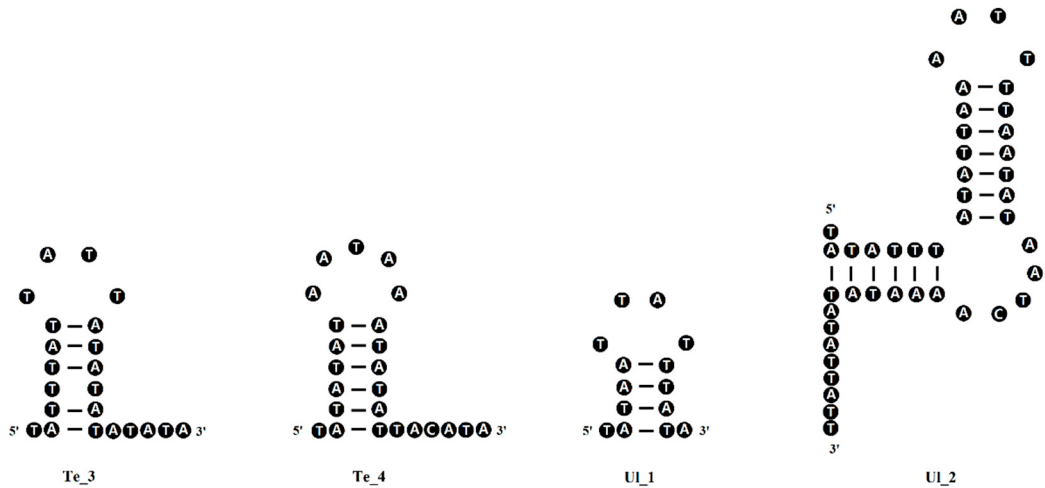


Figure S5. The putative secondary structure of four repeat unit sequences in the AT-rich region. Note: Bars denote Watson-Crick base pairings.

Table S1. The A + T content of different parts in ten Tenebrionidae mitogenomes.

Feature	<i>Ad</i>	<i>As</i>	<i>Te1</i>	<i>Te2</i>	<i>Ul</i>	<i>Tr1</i>	<i>Tr2</i>	<i>Tr3</i>	<i>Tr4</i>	<i>Tr5</i>
Whole mitogenome	72.7	69.7	72.4	72.2	72.1	71.7	71.7	71.8	72.8	73.6
Protein coding genes	70.4	66.9	69.3	69.1	69.6	69.2	69.2	69.3	70.9	71.6
The 1st codon sites	66.1	65.4	64.8	64.9	64.5	64.7	64.7	64.7	65.9	67.0
The 2nd codon sites	67.0	66.3	66.8	66.8	66.5	66.3	66.1	66.3	65.7	66.2
The 3rd codon sites	78.0	69.1	76.3	75.6	78.0	76.5	76.8	76.8	81.0	81.5
rRNA genes	78.0	74.5	78.3	78.4	77.3	76.1	76.2	76.1	77.4	76.9
tRNA genes	76.6	74.3	76.9	77.0	76.9	75.6	75.8	75.8	76.9	77.4
AT-rich region	79.3	80.5	85.4	85.1	83.7	82.5	82.3	82.9	79.5	81.4

Table S2. The AT-skew of different parts in ten Tenebrionidae mitogenomes.

Feature	<i>Ad</i>	<i>As</i>	<i>Te1</i>	<i>Te2</i>	<i>Ul</i>	<i>Tr1</i>	<i>Tr2</i>	<i>Tr3</i>	<i>Tr4</i>	<i>Tr5</i>
Whole mitogenome	0.14	0.20	0.20	0.20	0.14	0.11	0.11	0.11	0.13	0.11
PCG-J	0.03	0.10	0.10	0.09	0.00	−0.01	0.00	0.00	0.01	0.01
PCG1-J	0.13	0.21	0.20	0.20	0.15	0.14	0.14	0.14	0.16	0.14
PCG2-J	−0.36	−0.35	−0.37	−0.37	−0.38	−0.36	−0.36	−0.36	−0.37	−0.35
PCG3-J	0.26	0.44	0.41	0.40	0.21	0.18	0.20	0.19	0.20	0.19
PCG-N	−0.32	−0.38	−0.38	−0.38	−0.36	−0.29	−0.30	−0.30	−0.31	−0.28
PCG1-N	−0.12	−0.18	−0.12	−0.12	−0.19	−0.14	−0.14	−0.14	−0.18	−0.13
PCG2-N	−0.43	−0.44	−0.45	−0.45	−0.48	−0.47	−0.47	−0.47	−0.48	−0.46
PCG3-N	−0.39	−0.52	−0.54	−0.54	−0.41	−0.28	−0.28	−0.28	−0.28	−0.27
rRNA genes	−0.17	−0.19	−0.23	−0.22	−0.17	−0.13	−0.13	−0.13	−0.16	−0.13
tRNA-J	0.07	0.13	0.09	0.09	0.09	0.09	0.09	0.09	0.10	0.08
tRNA-N	−0.06	−0.09	−0.06	−0.06	−0.05	−0.06	−0.06	−0.06	−0.09	−0.06
AT-rich region	0.06	0.11	0.22	0.22	−0.02	0.02	0.02	0.03	0.00	0.02

AT skew = $[A - T]/[A + T]$; PCG1-3 denotes the three codon sites in PCGs; J and N denote the encoded strand, respectively.

Table S3. The GC-skew of different parts in ten Tenebrionidae mitogenomes.

Feature	<i>Ad</i>	<i>As</i>	<i>Te1</i>	<i>Te2</i>	<i>Ul</i>	<i>Tr1</i>	<i>Tr2</i>	<i>Tr3</i>	<i>Tr4</i>	<i>Tr5</i>
Whole mitogenome	−0.22	−0.36	−0.27	−0.27	−0.33	−0.31	−0.31	−0.31	−0.31	−0.27
PCG-J	−0.20	−0.36	−0.27	−0.26	−0.32	−0.29	−0.30	−0.29	−0.28	−0.25
PCG1-J	0.09	−0.03	0.04	0.05	−0.06	−0.02	−0.03	−0.02	−0.01	−0.01
PCG2-J	−0.27	−0.32	−0.29	−0.29	−0.28	−0.28	−0.28	−0.28	−0.27	−0.28
PCG3-J	−0.54	−0.78	−0.69	−0.67	−0.82	−0.69	−0.74	−0.73	−0.77	−0.62
PCG-N	0.24	0.41	0.28	0.28	0.37	0.35	0.36	0.36	0.36	0.32
PCG1-N	0.33	0.45	0.28	0.28	0.41	0.42	0.41	0.41	0.47	0.45
PCG2-N	0.03	0.04	0.04	0.04	0.04	0.08	0.08	0.08	0.08	0.08
PCG3-N	0.45	0.75	0.62	0.60	0.82	0.69	0.73	0.73	0.73	0.57
rRNA genes	0.31	0.39	0.34	0.34	0.40	0.40	0.39	0.39	0.39	0.38
tRNA-J	0.01	−0.05	0.00	0.01	−0.02	−0.04	−0.04	−0.04	−0.03	−0.03
tRNA-N	0.36	0.38	0.41	0.41	0.43	0.42	0.42	0.42	0.42	0.42
AT-rich region	−0.17	−0.36	−0.39	−0.34	−0.22	−0.20	−0.18	−0.19	−0.36	−0.19

GC skew = $[G - C]/[G + C]$; PCG1-3 denotes the three codon sites in PCGs; J and N denote the encoded strand, respectively.

Table S4. The A + T content of each protein coding gene in ten Tenebrionidae mitogenomes.

Feature	<i>Ad</i>	<i>As</i>	<i>Te1</i>	<i>Te2</i>	<i>Ul</i>	<i>Tr1</i>	<i>Tr2</i>	<i>Tr3</i>	<i>Tr4</i>	<i>Tr5</i>
<i>ATP6</i>	70.4	65.6	67.7	68.0	67.7	68.5	68.8	68.6	68.9	71.2
<i>ATP8</i>	75.0	68.6	76.5	76.5	75.2	81.7	81.4	82.1	74.2	73.7
<i>COX1</i>	63.1	61.6	62.0	61.4	64.1	61.3	61.1	61.4	64.8	64.3
<i>COX2</i>	68.4	63.5	66.1	66.7	67.4	66.4	65.9	66.2	68.1	69.7
<i>COX3</i>	66.9	62.8	64.1	64.2	65.3	66.3	66.5	66.8	68.5	68.2
<i>CYTB</i>	66.2	63.1	66.3	66.4	64.9	64.8	65.0	64.7	67.0	69.3
<i>ND1</i>	73.2	70.0	71.4	71.2	71.7	72.5	72.9	72.9	73.0	75.2
<i>ND2</i>	72.1	69.0	73.9	73.8	74.0	72.1	71.5	71.4	71.5	72.2
<i>ND3</i>	69.8	65.2	67.8	68.1	68.7	70.6	70.0	70.6	71.8	72.4
<i>ND4</i>	73.7	69.5	72.1	71.8	72.5	72.3	72.4	72.4	74.5	74.4
<i>ND4L</i>	76.8	70.9	74.7	73.3	72.0	74.4	74.4	74.0	77.2	77.5
<i>ND5</i>	73.9	71.2	72.8	72.5	73.5	72.9	73.0	73.1	74.5	74.8
<i>ND6</i>	75.4	71.8	76.0	75.2	74.6	72.2	72.6	72.8	75.6	76.0

Table S5. The AT-skew of each protein coding gene in ten Tenebrionidae mitogenomes.

Feature	<i>Ad</i>	<i>As</i>	<i>Te1</i>	<i>Te2</i>	<i>Ul</i>	<i>Tr1</i>	<i>Tr2</i>	<i>Tr3</i>	<i>Tr4</i>	<i>Tr5</i>
<i>ATP6</i>	−0.03	0.09	0.07	0.07	−0.04	−0.01	0.00	0.00	−0.02	0.00
<i>ATP8</i>	0.18	0.29	0.25	0.25	0.10	0.10	0.12	0.11	0.10	0.06
<i>COX1</i>	0.01	0.04	0.05	0.05	−0.02	−0.02	−0.02	−0.02	−0.01	0.01
<i>COX2</i>	0.08	0.11	0.11	0.10	0.05	0.12	0.12	0.12	0.06	0.09
<i>COX3</i>	−0.02	0.10	0.06	0.06	−0.03	−0.06	−0.04	−0.04	−0.03	−0.03
<i>CYTB</i>	−0.01	0.11	0.10	0.09	0.00	−0.02	−0.02	−0.02	−0.02	−0.02
<i>ND1</i>	−0.36	−0.41	−0.41	−0.41	−0.41	−0.33	−0.33	−0.33	−0.34	−0.32
<i>ND2</i>	0.09	0.13	0.13	0.13	0.06	0.01	0.03	0.03	0.06	0.03
<i>ND3</i>	−0.05	0.07	0.02	0.01	−0.08	−0.09	−0.08	−0.09	−0.04	−0.06
<i>ND4</i>	−0.35	−0.40	−0.42	−0.42	−0.41	−0.31	−0.31	−0.31	−0.37	−0.31
<i>ND4L</i>	−0.38	−0.42	−0.37	−0.40	−0.36	−0.30	−0.29	−0.29	−0.27	−0.31
<i>ND5</i>	−0.29	−0.37	−0.35	−0.36	−0.32	−0.28	−0.28	−0.28	−0.28	−0.26
<i>ND6</i>	0.08	0.20	0.20	0.20	0.05	−0.04	−0.04	−0.04	0.09	−0.03

$$\text{AT skew} = [A - T]/[A + T].$$

Table S6. The GC-skew of each protein coding gene in ten Tenebrionidae mitogenomes.

Feature	<i>Ad</i>	<i>As</i>	<i>Te1</i>	<i>Te2</i>	<i>Ul</i>	<i>Tr1</i>	<i>Tr2</i>	<i>Tr3</i>	<i>Tr4</i>	<i>Tr5</i>
<i>ATP6</i>	−0.21	−0.37	−0.29	−0.28	−0.37	−0.36	−0.37	−0.37	−0.35	−0.34
<i>ATP8</i>	−0.49	−0.76	−0.56	−0.56	−0.58	−0.43	−0.45	−0.43	−0.56	−0.71
<i>COX1</i>	−0.11	−0.21	−0.16	−0.16	−0.16	−0.19	−0.19	−0.19	−0.13	−0.13
<i>COX2</i>	−0.20	−0.31	−0.26	−0.26	−0.37	−0.33	−0.32	−0.32	−0.28	−0.24
<i>COX3</i>	−0.13	−0.31	−0.23	−0.22	−0.24	−0.13	−0.15	−0.15	−0.20	−0.18
<i>CYTB</i>	−0.22	−0.34	−0.25	−0.24	−0.32	−0.31	−0.32	−0.31	−0.24	−0.23
<i>ND1</i>	0.28	0.39	0.27	0.27	0.37	0.27	0.29	0.28	0.34	0.23
<i>ND2</i>	−0.27	−0.51	−0.41	−0.40	−0.42	−0.37	−0.41	−0.40	−0.44	−0.33
<i>ND3</i>	−0.32	−0.49	−0.33	−0.32	−0.44	−0.39	−0.40	−0.39	−0.45	−0.36
<i>ND4</i>	0.20	0.43	0.28	0.26	0.35	0.36	0.36	0.35	0.36	0.32
<i>ND4L</i>	0.36	0.52	0.31	0.32	0.54	0.40	0.37	0.35	0.57	0.38
<i>ND5</i>	0.24	0.39	0.27	0.29	0.36	0.37	0.38	0.38	0.35	0.34
<i>ND6</i>	−0.34	−0.62	−0.51	−0.48	−0.57	−0.47	−0.50	−0.49	−0.45	−0.46

$$\text{GC skew} = [G - C]/[G + C].$$

Table S7. Initiation codons in each protein coding gene of ten Tenebrionidae mitogenomes.

Species	<i>ATP6</i>	<i>ATP8</i>	<i>COX1</i>	<i>COX2</i>	<i>COX3</i>	<i>CYTB</i>	<i>ND2</i>	<i>ND3</i>	<i>ND6</i>	<i>ND1</i>	<i>ND4</i>	<i>ND4L</i>	<i>ND5</i>
<i>Ad</i>	ATG	ATA	CCG	ATA	ATG	ATG	ATA	TTG	ATC	ATA	ATA	ATG	ATT
<i>As</i>	ATG	ATT	CCG	ATA	ATG	ATG	ATA	ATC	ATA	ATA	ATG	ATG	ATT
<i>Te1</i>	ATG	ATA	CCG	ATA	ATG	ATG	ATC	ATT	ATT	ATA	ATG	ATG	ATT
<i>Te2</i>	ATG	ATA	CCG	ATA	ATG	ATG	ATC	ATT	ATT	ATA	ATG	ATG	ATT
<i>Ul</i>	ATG	ATT	CCG	ATA	ATG	ATG	ATT	ATT	ATC	ATA	ATG	ATG	TTG
<i>Tr1</i>	ATG	ATT	CTG	ATA	ATG	ATG	ATA	ATA	ATC	ATA	ATG	ATG	ATT
<i>Tr2</i>	ATG	ATT	CTG	ATA	ATG	ATG	ATA	ATA	ATC	ATA	ATG	ATG	ATT
<i>Tr3</i>	ATG	ATT	CTG	ATA	ATG	ATG	ATA	ATA	ATC	ATA	ATG	ATG	ATT
<i>Tr4</i>	ATG	ATA	CCG	ATA	ATG	ATG	ATT	ATA	ATA	ATA	ATG	ATG	ATT
<i>Tr5</i>	ATG	ATC	CTG	ATA	ATG	ATG	ATA	ATT	ATT	ATA	ATG	ATG	ATT

Table S8. Termination codons in each protein coding gene of ten Tenebrionidae mitogenomes.

Species	ATP6	ATP8	COX1	COX2	COX3	CYTB	ND2	ND3	ND6	ND1	ND4	ND4L	ND5
<i>Ad</i>	TAA	TAA	T	T	T	TAA	TAA	TAG	TAA	TAG	TAA	TAA	T
<i>As</i>	TAA	TAA	T	T	T	TAA	TAA	TAG	TAA	TAG	TAA	TAA	T
<i>Te1</i>	TAA	TAA	TAA	T	T	TAA	TAA	TAG	TAA	TAG	TA	TAA	T
<i>Te2</i>	TAA	TAA	TAA	T	T	TAA	TAA	TAG	TAA	TAG	TA	TAA	T
<i>Ul</i>	TAA	TAG	T	T	TAA	TAA	TAA	TAG	TAA	TAG	TA	TAA	T
<i>Tr1</i>	TAA	TAG	TAA	TAA	TAA	TAA	TAA	TAG	TAA	TAG	TA	TAA	T
<i>Tr2</i>	TAA	TAG	TAA	T	TAA	TAA	TAA	TAG	TAA	TAG	TA	TAA	T
<i>Tr3</i>	TAA	TAG	TAA	T	TAA	TAA	TAA	TAG	TAA	TAG	TA	TAA	T
<i>Tr4</i>	TAA	TAG	T	T	T	TAA	TAG	TAA	TAA	TAG	TA	TAA	T
<i>Tr5</i>	TAA	TAG	TAA	T	TAA	TAA	TAA	TAA	TAA	TAG	TA	TAA	T

Table S9. The usage rate of four most frequently used codons in ten Tenebrionidae mitogenomes.

Species	UUU(F)	UUA(L)	AUU(I)	AUA(M)	SUM	Total	Rate
<i>Ad</i>	298	310	307	243	1158	4264	27.2%
<i>As</i>	247	221	248	211	927	4267	21.7%
<i>Te1</i>	289	225	328	275	1117	4273	26.1%
<i>Te2</i>	293	229	325	266	1113	4273	26.0%
<i>Ul</i>	299	293	331	189	1112	4263	26.1%
<i>Tr1</i>	295	291	366	204	1156	4265	27.1%
<i>Tr2</i>	293	292	368	204	1157	4267	27.1%
<i>Tr3</i>	297	287	365	205	1154	4265	27.1%
<i>Tr4</i>	295	355	347	234	1231	4267	28.8%
<i>Tr5</i>	289	357	369	230	1245	4268	29.2%

Table S10. The usage rate of codons ended with different nucleotides.

Feature	NNU	NNC	NNA	NNG
PCG	38.0%	14.2%	39.0%	8.8%
PCG-J	27.6%	21.1%	47.7%	3.6%
PCG-N	54.5%	3.2%	25.0%	17.2%

Table S11. The size of 22 tRNA genes and two rRNA genes in ten Tenebrionidae mitogenomes.

Feature	<i>Ad</i>	<i>As</i>	<i>Te1</i>	<i>Te2</i>	<i>Ul</i>	<i>Tr1</i>	<i>Tr2</i>	<i>Tr3</i>	<i>Tr4</i>	<i>Tr5</i>	AVE	STDEV	%INUC
<i>trnI</i>	64	64	64	64	64	63	63	63	63	63	64	0.5	77.3
<i>trnQ</i>	69	69	69	69	69	69	69	69	69	69	69	0.0	53.6
<i>trnM</i>	66	69	68	68	68	68	68	68	68	68	68	0.7	79.7
<i>trnW</i>	64	68	66	66	64	67	67	67	64	67	66	1.5	75.4
<i>trnC</i>	62	61	61	61	65	61	61	61	62	61	62	1.3	57.6
<i>trnY</i>	64	64	66	66	63	65	64	64	65	66	65	1.1	47.1
<i>trnL^{UUR}</i>	65	64	65	65	65	65	65	65	66	68	65	1.1	73.5
<i>trnK</i>	70	71	70	70	70	71	71	71	71	71	71	0.5	73.6
<i>trnD</i>	64	65	65	65	66	66	66	66	66	68	66	1.1	50.0
<i>trnG</i>	62	63	62	62	63	62	62	62	64	65	63	1.1	63.6
<i>trnA</i>	65	67	66	66	66	67	67	67	65	67	66	0.8	69.1
<i>trnR</i>	63	66	64	64	64	63	63	63	68	65	64	1.6	54.4
<i>trnN</i>	66	66	65	65	65	64	64	64	66	65	65	0.8	76.1
<i>trnS^{AGN}</i>	58	60	60	60	60	59	59	59	60	59	59	0.7	76.2
<i>trnE</i>	62	64	62	62	62	64	65	65	63	64	63	1.3	66.2
<i>trnF</i>	64	64	64	64	68	65	65	65	65	67	65	1.4	50.0
<i>trnH</i>	63	64	63	63	65	65	65	65	65	65	64	0.9	51.5
<i>trnT</i>	63	62	63	63	63	63	63	63	63	63	63	0.3	69.8
<i>trnP</i>	64	63	66	66	64	66	66	66	66	67	65	1.3	67.6
<i>trnS^{UCN}</i>	67	67	66	66	68	68	68	68	67	67	67	0.8	66.7
<i>trnL^{CUN}</i>	62	62	65	65	65	64	64	64	66	65	64	1.3	71.2
<i>trnV</i>	69	69	69	69	68	69	69	69	68	69	69	0.4	78.3
16S rRNA	1280	1279	1280	1281	1279	1280	1281	1282	1277	1288	1281	2.9	54.3
12S rRNA	762	747	761	761	764	754	754	754	759	760	758	5.2	57.6

AVE denotes the average size of each RNA; STDEV denotes standard deviation of the RNA size from different Tenebrionidae mitogenomes; %INUC denotes the identical percent of nucleotide in each RNA.

Table S12. The identical percent of nucleotide in each part of the secondary structure of tRNAs in ten Tenebrionidae mitogenomes.

Feature	AA Stem	DHU Arm	AC Arm	TψC Arm	D-loop	AC Loop	Variable Loop	TψC Loop
<i>trnI</i>	93.33%	100.00%	90.00%	75.00%	80.00%	100%	40.00%	0.00%
<i>trnQ</i>	46.67%	87.50%	0.00%	40.00%	80.00%	100%	50.00%	85.71%
<i>trnM</i>	86.67%	100.00%	70.00%	100.00%	66.67%	100%	50.00%	50.00%
<i>trnW</i>	80.00%	100.00%	90.00%	75.00%	37.50%	100%	75.00%	0.00%
<i>trnC</i>	66.67%	75.00%	60.00%	50.00%	25.00%	85.71%	75.00%	25.00%
<i>trnY</i>	40.00%	66.67%	70.00%	62.50%	37.50%	100%	25.00%	0.00%
<i>trnL^{UUR}</i>	93.33%	100.00%	60.00%	100.00%	83.33%	71.43%	50.00%	16.67%
<i>trnK</i>	86.67%	66.67%	100%	60.00%	100%	100%	33.33%	57.14%
<i>trnD</i>	53.33%	87.50%	30.00%	50.00%	40.00%	71.43%	50.00%	20.00%
<i>trnG</i>	33.33%	100.00%	60.00%	100.00%	71.43%	100%	100.00%	50.00%
<i>trnA</i>	93.33%	100.00%	100%	37.50%	50.00%	71.43%	75.00%	0.00%
<i>trnR</i>	53.33%	66.67%	60.00%	66.67%	14.29%	100%	60.00%	0.00%
<i>trnN</i>	93.33%	100.00%	70.00%	100.00%	75.00%	100%	40.00%	0.00%
<i>trnS^{AGN}</i>	100.00%		90.00%	100.00%		100%	25.00%	50.00%
<i>trnE</i>	60.00%	100.00%	80.00%	33.33%	40.00%	85.71%	75.00%	0.00%
<i>trnF</i>	60.00%	87.50%	30.00%	33.33%	33.33%	100%	50.00%	0.00%
<i>trnH</i>	53.33%	75.00%	20.00%	50.00%	60.00%	85.71%	75.00%	0.00%
<i>trnT</i>	73.33%	100.00%	70.00%	33.33%	60.00%	100%	75.00%	0.00%
<i>trnP</i>	73.33%	100.00%	80.00%	25.00%	80.00%	100%	50.00%	0.00%
<i>trnS^{UCN}</i>	93.33%	50.00%	20.00%	75.00%	60.00%	85.71%	50.00%	33.33%
<i>trnL^{CUN}</i>	73.33%	100.00%	50.00%	62.50%	83.33%	100%	75.00%	16.67%
<i>trnV</i>	93.33%	75.00%	100%	70.00%	40.00%	85.71%	25.00%	71.43%
AVE	72.73%	87.50%	63.64%	63.60%	57.97%	92.86%	55.61%	21.63%

Table S13. The identical percent of nucleotide in each helix of the secondary structure of 12S rRNA in ten Tenebrionidae mitogenomes.

Domain	Helix	Total Site	Conserved Site	Percentage of Conserved Site
I	H9	10	9	90.00%
	H17	6	1	16.67%
	H27	18	6	33.33%
	H39	10	4	40.00%
	H47	59	14	23.73%
	H367	31	16	51.61%
	H500	10	1	10.00%
	H511	26	21	80.77%
II	H567	6	1	16.67%
	H577	32	14	43.75%
	H673	39	8	20.51%
	H769	33	20	60.61%
	H885	22	14	63.64%

Table S13. Cont.

Domain	Helix	Total Site	Conserved Site	Percentage of Conserved Site
III	H921	35	34	97.14%
	H939	10	10	100.00%
	H944	25	21	84.00%
	H960	8	7	87.50%
	H984	14	5	35.71%
	H1047	40	31	77.50%
	H1068	12	8	66.67%
	H1074	6	4	66.67%
	H1113	8	0	0.00%
	H1241	4	1	25.00%
	H1303	16	6	37.50%
	H1350	18	6	33.33%
IV	H1399	34	27	79.41%
	H1506	20	16	80.00%

Table S14. The identical percent of nucleotide in each helix of the secondary structure of *16S rRNA* in ten Tenebrionidae mitogenomes.

Domain	Helix	Total Site	Conserved Site	Percentage of Conserved Site
I	H183	6	2	33.33%
	H235	18	12	66.67%
	H461	4	0	0.00%
	H533	6	0	0.00%
	H563	6	6	100.00%
II	H579	12	8	66.67%
	H589	12	5	41.67%
	H671	29	18	62.07%
	H687	31	6	19.35%
	H736	8	6	75.00%
	H777	6	6	100.00%
	H812	12	3	25.00%
	H822	10	6	60.00%
	H837	20	2	10.00%
	H946	20	6	30.00%
	H991	21	4	19.05%
	H1196	21	3	14.29%
	H1507	12	10	83.33%
	H1807	10	3	30.00%
IV	H1648	39	15	38.46%
	H1764	19	9	47.37%
	H1775	6	6	100.00%
	H1792	10	7	70.00%
	H1830	8	6	75.00%
	H1835	20	14	70.00%
	H1906	12	12	100.00%
	H1925	2	2	100.00%
	H1935	12	8	66.67%

Table S14. Cont.

Domain	Helix	Total Site	Conserved Site	Percentage of Conserved Site
V	H2023	10	8	80.00%
	H2043	24	18	75.00%
	H2064	25	24	96.00%
	H2077	50	6	12.00%
	H2246	10	5	50.00%
	H2259	12	6	50.00%
	H2347	16	7	43.75%
	H2395	8	8	100.00%
	H2455	35	28	80.00%
	H2507	27	27	100.00%
	H2520	19	14	73.68%
	H2547	10	7	70.00%
	H2588	15	12	80.00%
VI	H2646	16	6	37.50%
	H2675	8	4	50.00%
	H2735	4	4	100.00%

Table S15. Intergenic gaps and overlaps in ten Tenebrionidae mitogenomes.

Feature	Gene Gaps and Overlaps									
	<i>Ad</i>	<i>As</i>	<i>Te1</i>	<i>Te2</i>	<i>Ul</i>	<i>Tr1</i>	<i>Tr2</i>	<i>Tr3</i>	<i>Tr4</i>	<i>Tr5</i>
Genome size	16449	15828	15785	15784	15434	15881	15883	15876	15813	15925
<i>trnI-trnQ</i>	-3	-3	-3	-3	6	-3	-3	-3	-3	-3
<i>trnQ-trnM</i>	-1	-1	-1	-1	0	-1	-1	-1	-1	-1
<i>trnM-ND2</i>	0	0	-15	-15	6	6	6	6	6	6
<i>ND2-trnW</i>	-2	-2	-2	-2	6	-2	-2	-2	1	-2
<i>trnW-trnC</i>	-1	-1	22	22	12	-1	-1	-1	-1	-1
<i>trnC-trnY</i>	0	0	0	0	10	2	2	2	0	1
<i>trnY-COX1</i>	1	1	1	1	1	7	7	7	1	2
<i>COX1-trnL(UUR)</i>	0	0	-5	-5	0	1	1	1	0	1
<i>trnL(UUR)-COX2</i>	0	0	0	0	0	0	0	0	0	0
<i>COX2-trnK</i>	0	0	0	0	0	1	0	0	0	0
<i>trnK-trnD</i>	-1	-1	-1	-1	-1	33	33	31	48	12
<i>trnD-ATP8</i>	732	0	0	0	0	0	0	0	0	0
<i>ATP8-ATP6</i>	-7	-7	-7	-7	-7	-7	-7	-7	-7	-7
<i>ATP6-COX3</i>	-1	-1	-1	-1	-1	-1	-1	-1	-1	-1
<i>COX3-trnG</i>	0	0	0	0	0	2	2	2	0	0
<i>trnG-ND3</i>	0	0	0	0	0	-7	-7	-7	0	0
<i>ND3-trnA</i>	-2	-2	-2	-2	-2	-2	-2	-2	2	2
<i>trnA-trnR</i>	-1	-1	-1	-1	-1	-1	-1	-1	-1	-1
<i>trnR-trnN</i>	-1	-1	-1	-1	-1	-1	-1	-1	-1	-1
<i>trnN-trnS(AGN)</i>	0	0	0	0	0	0	0	0	0	0
<i>trnS(AGN)-trnE</i>	0	0	1	1	0	0	0	0	0	0
<i>trnE-trnF</i>	-2	-2	-2	-2	-2	-2	-2	-2	-2	-2
<i>trnF-ND5</i>	0	0	0	0	0	0	0	0	0	0
<i>ND5-trnH</i>	0	0	0	0	1	0	0	0	0	0
<i>trnH-ND4</i>	-1	-1	-1	-1	-1	-1	-1	-1	-1	-1
<i>ND4-ND4L</i>	-4	-7	-7	-7	-7	-7	-7	-7	-7	-7
<i>ND4L-trnT</i>	2	2	2	2	2	2	2	2	2	2
<i>trnT-trnP</i>	0	0	0	0	0	0	0	0	0	0
<i>trnP-ND6</i>	2	2	2	2	2	2	2	2	2	2
<i>ND6-CYTB</i>	-1	-1	-1	-1	-1	-1	-1	-1	-1	-1
<i>CYTB-trnS(UCN)</i>	-2	-2	-2	-2	-2	-2	-2	-2	-2	-2
<i>trnS(UCN)-ND1</i>	17	17	17	17	18	17	17	17	17	17
<i>ND1-trnL(CUN)</i>	-3	-3	-3	-3	-3	-3	-3	-3	-6	-3
<i>trnV-12SrRNA</i>	11	2	12	21	4	21	21	2	15	21
AT-rich region	1157	1244	1170	1160	798	1239	1237	1256	1147	1266

Numbers with “-” denote gene overlaps; those without “-” denote gene gaps.