

Supplementary material

Phylogenetic position of the genera *Caryandoides*, *Paratoacris*, *Fer* and *Longchuanacris* (Orthoptera : Acrididae) revealed by complete mitogenome sequences

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Table S1. Collecting data of species with mitogenomes newly sequenced in this study

Species	Voucher number	Collecting data of voucher specimens
Acrididae		
Catantopinae		
<i>Diaboloacantops pinguis</i>	mt1936	Yaoqu Town, Mengla County, Yunnan Province, China; 30 July 2013; Jianhua Huang leg.
<i>Stenocatantops mistshenkoi</i>	mt1808	Meihuashan, Gutian Township, Shanghang County, Fujian Province, China; 9 August 2016; Yang Liu leg.
<i>Stenocatantops splendens</i>	mt1809	Longrui, Longzhou County, Guangxi, China; 23 July 2013; Tao Wei leg.
<i>Xenocatantops brachycerus</i>	mt1810	South gate of Tianmushan, Yuqian Township, Lin'an District, Hangzhou City, Zhejiang Province, China; 25 August 2016; Jianhua Huang leg.
Oxyinae		
<i>Caryandoides hunanica</i>	mt1824	Mangshan, Yizhang County, Hunan Province, China, 23 August 2018, Xiang Zeng leg.
<i>Fer nigripennis</i>	mt1823	Mangshan, Yizhang County, Hunan Province, China, 23 August 2018, Xiang Zeng leg.
<i>Oxytauchira brachyptera</i>	mt1941	Nangongshan (Manbandong, Longlin village, Mengla Town), Mengla County, Yunnan Province, China, 31 July 2013, Jianhua Huang leg.
<i>Oxytauchira flange</i>	mt1942	Nangongshan (Manbandong, Longlin village, Mengla Town), Mengla County, Yunnan Province, China, 31 July 2013, Jianhua Huang leg.
<i>Paratoacris reticulipennis</i>	mt1940	Guposhan, Hezhou, Guangxi, China, 28 July 2013, Guohao Lin leg.

Table S2. Sizes, A+T contents, A-T- and G-C-skews of the nine newly sequenced complete mitogenomes

$$\text{AT-skew} = (A - T)/(A + T) \text{ and } \text{GC-skew} = (G - C)/(G + C)$$

Subfamily	Species	Whole genome				Protein coding genes				Control region			
		Size(bp)	A+T (%)	AT-skew	GC-skew	Size(bp)	A+T (%)	AT-skew	GC-skew	Size(bp)	A+T (%)	AT-skew	GC-skew
Oxyinae	<i>Oxytauchira brachyptera</i>	16402	75.9	0.1779	-0.195	11139	75.2	-0.1250	-0.0242	1514	80.3	0.3051	-0.2424
	<i>Oxytauchira flange</i>	16250	75.6	0.1825	-0.2049	11133	74.8	-0.1257	-0.0159	1480	80.2	0.3367	-0.2929
	<i>Paratoacris reticulipennis</i>	16321	75.2	0.1463	-0.1613	11199	74.3	-0.1440	-0.0195	1493	79.2	0.3232	-0.25
	<i>Fer nigripennis</i>	15669	76.4	0.1545	-0.1949	11163	75.5	-0.1338	-0.0204	873	86	0.1698	-0.3429
	<i>Caryandoides hunanica</i>	15555	76.7	0.1134	-0.133	11154	75.8	-0.1504	0.0000	739	88.4	0.0995	-0.0256
Catantopinae	<i>Diabolocatantops pinguis</i>	16317	72.6	0.1791	-0.1825	11169	71.8	-0.1421	-0.0106	1473	79.4	0.3199	-0.2683
	<i>Stenocatantops splendens</i>	15657	72.8	0.1676	-0.1838	11169	71.5	-0.1413	0.0000	808	88.6	0.1512	-0.2456
	<i>Stenocatantops mistshenkoi</i>	15660	73	0.1644	-0.1822	11154	71.7	-0.1437	0.0035	811	89.1	0.1448	-0.2294
	<i>Xenocatantops brachycerus</i>	15605	73.8	0.1572	-0.1603	11154	72.8	-0.1374	0.0000	757	87.7	0.1425	-0.122

Table S3. Initiation codons of protein coding genes (PCGs) of the nine newly sequenced complete mitogenomes

PCGs	ND2	COX1	COX2	ATP8	APT6	COX3	ND3	ND5	ND4	ND4L	ND6	CYTB	ND1
<i>Oxytauchira brachyptera</i>	ATG	ATC	ATG	ATC	ATG	ATG	ATC	ATT	ATG	ATG	ATG	ATG	ATA
<i>Oxytauchira flange</i>	ATG	ATC	ATG	ATC	ATG	ATG	ATC	ATT	ATG	ATG	ATG	ATG	ATA
<i>Paratoacris reticulipennis</i>	ATG	ATC	ATG	ATC	ATG	ATG	ATC	ATT	ATG	ATG	ATG	ATG	ATT
<i>Fer nigripennis</i>	ATG	ATC	ATG	ATC	ATG	ATG	ATT	ATA	ATG	ATG	ACC	ATG	ATA
<i>Caryandoides hunanica</i>	ATG	ATC	ATG	ATC	ATG	ATG	ATT	ATT	ATG	ATG	ATG	ATG	ATA
<i>Diabolocatantops pinguis</i>	ATG	ATC	ATG	ATC	ATG	ATG	ATT	ATT	ATG	ATG	ATG	ATG	ATA
<i>Stenocatantops splendens</i>	ATG	ATC	ATG	ATC	ATG	ATG	ATT	ATT	ATG	ATG	ATG	ATG	ATA
<i>Stenocatantops mistshenkoi</i>	ATG	ATC	ATG	ATC	ATG	ATG	ATT	ATT	ATG	ATG	ATG	ATG	ATA
<i>Xenocatantops brachycerus</i>	ATG	ACC	ATG	ATC	ATG	ATG	ATT	ATT	ATG	ATG	ATG	ATG	ATA

Table S4. Termination codons of protein coding genes (PCGs) of the nine newly sequenced complete mitogenomes

PCGs	ND2	COX1	COX2	ATP8	APT6	COX3	ND3	ND5	ND4	ND4L	ND6	CYTB	ND1
<i>Oxytauchira brachyptera</i>	TAA	TAA	TAA	TAA	TAA	TAA	TAA	TA	TAG	TAA	TAA	TAA	TAA
<i>Oxytauchira flange</i>	TAA	TAA	TAA	TAA	TAA	TAA	TAA	TA	TAG	TAA	TAA	TAA	TAA
<i>Paratoacris reticulipennis</i>	TAA	TAA	TAA	TAA	TAA	TAA	TAA	TAA	TAG	TAA	TAA	TAA	TAG
<i>Fer nigripennis</i>	TAA	TAA	TAA	TAA	TAA	TAA	TAA	TA	TAA	TAA	TAA	TA	TAA
<i>Caryandoides hunanica</i>	TAA	TAA	TAA	TAA	TAA	TAA	TAA	TA	TAA	TAA	TAA	TAA	TAG
<i>Diabolocatantops pinguis</i>	TAA	TAA	TAA	TAA	TAA	TAA	TAA	TAA	TAG	TAA	TAA	TAA	TAG
<i>Stenocatantops splendens</i>	TAA	TAA	TAA	TAA	TAA	TAA	TAA	TA	TAG	TAA	TAA	TAA	TAG
<i>Stenocatantops mistshenkoi</i>	TAA	TAA	TAA	TAA	TAA	TAA	TAA	TA	TAG	TAA	TAA	TAA	TAG
<i>Xenocatantops brachycerus</i>	TAA	TAA	TAA	TAA	TAA	TAA	TAA	TAA	TAA	TAA	TAA	TAA	TAG

Table S5. Codon usage of protein coding genes (PCGs) of the nine newly sequenced complete mitogenomes

Amino acid		Phe		Leu				Ile			Met		Val	
Codon		UUU	UUC	UUA	UUG	CUU	CUC	CUA	CUG	AUU	AUC	AUA	AUG	GUU
<i>Oxytauchira brachyptera</i>	frequency	305	53	350	56	65	2	48	5	327	45	244	32	98
	RSCU	1.7	0.3	3.99	0.64	0.74	0.02	0.55	0.06	1.76	0.24	1.77	0.23	2.25
<i>Oxytauchira flange</i>	frequency	294	62	324	64	52	7	68	4	366	52	246	40	86
	RSCU	1.65	0.35	3.75	0.74	0.6	0.08	0.79	0.05	1.73	0.27	1.72	0.28	2.02
<i>Paratoacris reticulipennis</i>	frequency	303	46	382	32	65	3	70	2	333	51	212	26	107
	RSCU	1.74	0.26	4.14	0.35	0.7	0.03	0.76	0.02	1.73	0.27	1.78	0.22	2.25
<i>Fer nigripennis</i>	frequency	303	46	382	32	65	3	70	2	333	51	212	26	107
	RSCU	1.74	0.26	4.14	0.35	0.7	0.03	0.76	0.02	1.73	0.27	1.78	0.22	2.25
<i>Caryandoides hunanica</i>	frequency	325	43	396	30	62	2	40	1	357	29	251	15	105
	RSCU	1.77	0.23	4.47	0.34	0.7	0.02	0.45	0.01	1.85	0.15	1.89	0.11	2.36
<i>Diabolocatantops pinguis</i>	frequency	255	81	306	67	74	5	82	9	296	60	194	54	111
	RSCU	1.52	0.48	3.38	0.74	0.82	0.06	0.91	0.1	1.66	0.34	1.56	0.44	2.12
<i>Stenocatantops splendens</i>	frequency	261	75	298	82	70	5	76	7	304	53	205	41	115
	RSCU	1.55	0.45	3.32	0.91	0.78	0.06	0.85	0.08	1.7	0.3	1.67	0.33	2.12
<i>Stenocatantops mistshenkoi</i>	frequency	268	70	297	83	71	4	73	6	306	52	206	41	113
	RSCU	1.59	0.41	3.34	0.93	0.8	0.04	0.82	0.07	1.71	0.29	1.67	0.33	2.08
<i>Xenocatantops brachycerus</i>	frequency	283	51	334	54	72	8	59	3	300	50	229	36	111
	RSCU	1.69	0.31	3.78	0.61	0.82	0.09	0.67	0.03	1.71	0.29	1.73	0.27	2.12
Averages	frequency													
	RSCU	1.66	0.34	3.81	0.62	0.74	0.05	0.73	0.05	1.73	0.27	1.73	0.27	2.17
Amino acid		Val		Ser				Pro			Thr			
Codon		GUC	GUA	GUG	UCU	UCC	UCA	UCG	CCU	CCC	CCA	CCG	ACU	ACC
<i>Oxytauchira brachyptera</i>	frequency	4	67	5	115	5	135	2	56	10	63	4	66	12
	RSCU	0.09	1.54	0.11	2.46	0.11	2.89	0.04	1.68	0.3	1.89	0.12	1.23	0.22
<i>Oxytauchira flange</i>	frequency	5	76	3	114	9	137	3	50	12	68	3	64	10
	RSCU	0.12	1.79	0.07	2.41	0.19	2.9	0.06	1.5	0.36	2.05	0.09	1.35	0.21
<i>Paratoacris reticulipennis</i>	frequency	8	70	5	112	12	131	1	59	7	68	3	68	11

	RSCU	0.17	1.47	0.11	2.36	0.25	2.76	0.02	1.72	0.2	1.99	0.09	1.42	0.23
<i>Fer nigripennis</i>	frequency	3	68	3	123	10	124	3	61	11	57	4	70	9
	RSCU	0.08	1.71	0.08	2.53	0.21	2.55	0.06	1.83	0.33	1.71	0.12	1.46	0.19
<i>Caryandoides hunanica</i>	frequency	4	69	0	118	10	120	4	68	2	65	2	62	10
	RSCU	0.09	1.55	0	2.54	0.22	2.59	0.09	1.99	0.06	1.9	0.06	1.32	0.21
<i>Diabolocatantops pinguis</i>	frequency	3	91	4	113	10	116	5	70	7	59	4	67	12
	RSCU	0.06	1.74	0.08	2.58	0.23	2.64	0.11	2	0.2	1.69	0.11	1.36	0.24
<i>Stenocatantops splendens</i>	frequency	7	84	11	120	10	110	5	61	5	67	7	61	16
	RSCU	0.13	1.55	0.2	2.73	0.23	2.5	0.11	1.74	0.14	1.91	0.2	1.24	0.33
<i>Stenocatantops mistshenkoi</i>	frequency	7	86	11	118	10	112	4	62	4	69	5	61	16
	RSCU	0.13	1.59	0.2	2.7	0.23	2.57	0.09	1.77	0.11	1.97	0.14	1.24	0.32
<i>Xenocatantops brachycerus</i>	frequency	9	82	7	116	13	108	7	65	6	65	3	68	11
	RSCU	0.17	1.57	0.13	2.67	0.3	2.49	0.16	1.87	0.17	1.87	0.09	1.35	0.22
Averages	frequency													
	RSCU	0.12	1.61	0.11	2.55	0.22	2.65	0.08	1.79	0.21	1.89	0.11	1.33	0.24
Amino acid		Thr		Ala				Tyr		End		His		Gln
Codon		ACA	ACG	GCU	GCC	GCA	GCG	UAU	UAC	UAA	UAG	CAU	CAC	CAA
<i>Oxytauchira brachyptera</i>	frequency	132	5	48	7	67	2	160	33	0	0	47	17	59
	RSCU	2.46	0.09	1.55	0.23	2.16	0.06	1.66	0.34	0	0	1.47	0.53	1.87
<i>Oxytauchira flange</i>	frequency	114	1	57	6	65	3	153	24	0	0	51	17	59
	RSCU	2.41	0.02	1.74	0.18	1.98	0.09	1.73	0.27	0	0	1.5	0.5	1.84
<i>Paratoacris reticulipennis</i>	frequency	110	2	79	11	73	1	156	20	0	0	62	11	58
	RSCU	2.3	0.04	1.93	0.27	1.78	0.02	1.77	0.23	0	0	1.7	0.3	1.78
<i>Fer nigripennis</i>	frequency	111	2	59	10	69	1	155	20	0	0	54	11	61
	RSCU	2.31	0.04	1.7	0.29	1.99	0.03	1.77	0.23	0	0	1.66	0.34	1.79
<i>Caryandoides hunanica</i>	frequency	111	5	60	14	76	0	154	18	0	0	61	8	58
	RSCU	2.36	0.11	1.6	0.37	2.03	0	1.79	0.21	0	0	1.77	0.23	1.78
<i>Diabolocatantops pinguis</i>	frequency	115	3	89	12	85	1	141	29	0	0	44	26	58
	RSCU	2.34	0.06	1.9	0.26	1.82	0.02	1.66	0.34	0	0	1.26	0.74	1.73
<i>Stenocatantops splendens</i>	frequency	116	3	77	14	89	3	133	35	0	0	34	36	60

	RSCU	2.37	0.06	1.68	0.31	1.95	0.07	1.58	0.42	0	0	0.97	1.03	1.79
<i>Stenocatantops mistshenkoi</i>	frequency	117	3	78	14	85	4	134	33	0	0	33	37	60
	RSCU	2.38	0.06	1.72	0.31	1.88	0.09	1.6	0.4	0	0	0.94	1.06	1.79
<i>Xenocatantops brachycerus</i>	frequency	119	4	78	11	86	1	140	29	0	0	42	29	59
	RSCU	2.36	0.08	1.77	0.25	1.95	0.02	1.66	0.34	0	0	1.18	0.82	1.76
Averages	frequency													
	RSCU	2.37	0.06	1.73	0.27	1.95	0.04	1.69	0.31	0	0	1.38	0.62	1.79
Amino acid		Gln	Asn		Lys		Asp		Glu		Cys		Trp	
Codon		CAG	AAU	AAC	AAA	AAG	GAU	GAC	GAA	GAG	UGU	UGC	UGA	UGG
<i>Oxytauchira brachyptera</i>	frequency	4	144	37	79	25	57	15	74	10	34	5	92	7
	RSCU	0.13	1.59	0.41	1.52	0.48	1.58	0.42	1.76	0.24	1.74	0.26	1.86	0.14
<i>Oxytauchira flange</i>	frequency	5	148	38	82	17	62	11	65	13	43	4	89	10
	RSCU	0.16	1.59	0.41	1.66	0.34	1.7	0.3	1.67	0.33	1.83	0.17	1.8	0.2
<i>Paratoacris reticulipennis</i>	frequency	7	141	28	70	20	61	15	70	11	34	6	90	11
	RSCU	0.22	1.67	0.33	1.56	0.44	1.61	0.39	1.73	0.27	1.7	0.3	1.78	0.22
<i>Fer nigripennis</i>	frequency	7	140	37	82	14	58	14	69	13	46	3	87	13
	RSCU	0.21	1.58	0.42	1.71	0.29	1.61	0.39	1.68	0.32	1.88	0.12	1.74	0.26
<i>Caryandoides hunanica</i>	frequency	7	146	29	75	15	63	9	74	8	46	1	91	10
	RSCU	0.22	1.67	0.33	1.67	0.33	1.75	0.25	1.8	0.2	1.96	0.04	1.8	0.2
<i>Diabolocatantops pinguis</i>	frequency	9	116	49	49	44	61	18	69	15	38	4	93	7
	RSCU	0.27	1.41	0.59	1.05	0.95	1.54	0.46	1.64	0.36	1.81	0.19	1.86	0.14
<i>Stenocatantops splendens</i>	frequency	7	119	47	60	32	59	20	69	16	38	4	83	17
	RSCU	0.21	1.43	0.57	1.3	0.7	1.49	0.51	1.62	0.38	1.81	0.19	1.66	0.34
<i>Stenocatantops mistshenkoi</i>	frequency	7	119	48	57	36	60	17	69	16	40	2	84	16
	RSCU	0.21	1.43	0.57	1.23	0.77	1.56	0.44	1.62	0.38	1.9	0.1	1.68	0.32
<i>Xenocatantops brachycerus</i>	frequency	8	134	35	71	24	63	16	68	18	38	4	93	8
	RSCU	0.24	1.59	0.41	1.49	0.51	1.59	0.41	1.58	0.42	1.81	0.19	1.84	0.16
Averages	frequency													
	RSCU	0.21	1.55	0.45	1.47	0.53	1.6	0.4	1.68	0.32	1.83	0.17	1.78	0.22
Amino acid		Arg				Ser					Gly			

Codon		CGU	CGC	CGA	CGG	AGU	AGC	AGA	AGG	GGU	GGC	GGA	GGG
<i>Oxytauchira brachyptera</i>	frequency	18	1	32	4	26	3	85	3	87	3	108	9
	RSCU	1.31	0.07	2.33	0.29	0.56	0.06	1.82	0.06	1.68	0.06	2.09	0.17
<i>Oxytauchira flange</i>	frequency	20	1	32	2	20	0	88	7	90	4	114	7
	RSCU	1.45	0.07	2.33	0.15	0.42	0	1.86	0.15	1.67	0.07	2.12	0.13
<i>Paratoacris reticulipennis</i>	frequency	17	3	33	4	27	7	86	4	87	3	116	12
	RSCU	1.19	0.21	2.32	0.28	0.57	0.15	1.81	0.08	1.6	0.06	2.13	0.22
<i>Fer nigripennis</i>	frequency	22	2	28	2	35	1	87	6	84	7	105	9
	RSCU	1.63	0.15	2.07	0.15	0.72	0.02	1.79	0.12	1.64	0.14	2.05	0.18
<i>Caryandoides hunanica</i>	frequency	17	0	39	1	27	1	87	4	93	10	91	19
	RSCU	1.19	0	2.74	0.07	0.58	0.02	1.88	0.09	1.75	0.19	1.71	0.36
<i>Diabolocatantops pinguis</i>	frequency	17	1	37	2	20	7	79	1	105	2	108	14
	RSCU	1.19	0.07	2.6	0.14	0.46	0.16	1.8	0.02	1.83	0.03	1.89	0.24
<i>Stenocatantops splendens</i>	frequency	18	1	34	4	22	3	80	2	104	5	102	21
	RSCU	1.26	0.07	2.39	0.28	0.5	0.07	1.82	0.05	1.79	0.09	1.76	0.36
<i>Stenocatantops mistshenkoi</i>	frequency	17	2	35	3	22	1	81	1	107	4	100	21
	RSCU	1.19	0.14	2.46	0.21	0.5	0.02	1.86	0.02	1.84	0.07	1.72	0.36
<i>Xenocatantops brachycerus</i>	frequency	17	2	36	2	23	4	75	1	101	5	96	28
	RSCU	1.19	0.14	2.53	0.14	0.53	0.09	1.73	0.02	1.76	0.09	1.67	0.49
Averages	frequency												
	RSCU	1.29	0.1	2.42	0.19	0.54	0.07	1.82	0.07	1.73	0.09	1.9	0.28

Table S6. Sizes of tRNAs and rRNAs of the nine newly sequenced mitogenomes

Species	<i>trnI</i> (bp)	<i>trnQ</i> (bp)	<i>trnM</i> (bp)	<i>trnW</i> (bp)	<i>trnC</i> (bp)	<i>trnY</i> (bp)	<i>trnL2</i> (bp)	<i>trnD</i> (bp)	<i>trnK</i> (bp)	<i>trnG</i> (bp)	<i>trnA</i> (bp)	<i>trnR</i> (bp)
<i>mt1941-Oxytauchira brachyptera</i>	65	69	69	66	62	66	65	65	71	65	68	64
<i>mt1942-Oxytauchira flange</i>	64	69	69	66	62	67	66	65	71	66	64	64
<i>mt1940-Paratoacris reticulipennis</i>	65	69	69	68	63	65	66	66	71	66	68	66
<i>mt1823-Fer nigripennis</i>	65	69	69	66	61	68	66	65	71	65	65	64
<i>mt1824-Caryandoides maguas</i>	66	69	69	68	62	66	66	65	70	66	68	63
<i>mt1936-Diabolocatantops pinguis</i>	67	69	69	68	65	67	66	65	71	67	65	67
<i>mt1809-Stenocatantops splendens</i>	66	69	69	68	64	68	66	65	71	67	65	66
<i>mt1808-Stenocatantops mistshenkoi</i>	66	69	69	68	64	68	66	65	71	67	65	66
<i>mt1810-Xenocatantops brachycerus</i>	67	69	69	67	64	67	66	65	71	68	65	65
Range of variation	64–67	69–69	69–69	66–68	61–65	65–68	65–66	65–66	70–71	65–68	64–68	63–67
	<i>trnN</i> (bp)	<i>trnS1</i> (bp)	<i>trnE</i> (bp)	<i>trnF</i> (bp)	<i>trnH</i> (bp)	<i>trnT</i> (bp)	<i>trnP</i> (bp)	<i>trnS2</i> (bp)	<i>trnL1</i> (bp)	<i>trnV</i> (bp)	<i>rnrL</i> (bp)	<i>rnrS</i> (bp)
<i>mt1941-Oxytauchira brachyptera</i>	68	65	67	65	66	70	62	68	65	71	1379	873
<i>mt1942-Oxytauchira flange</i>	68	67	67	65	67	70	62	69	66	72	1378	780
<i>mt1940-Paratoacris reticulipennis</i>	67	67	67	67	66	70	65	70	66	70	1370	782
<i>mt1823-Fer nigripennis</i>	67	66	67	64	66	69	62	67	65	71	1318	788
<i>mt1824-Caryandoides maguas</i>	67	66	67	66	67	70	64	71	65	71	1376	786
<i>mt1936-Diabolocatantops pinguis</i>	69	67	66	67	67	69	65	70	66	71	1374	791
<i>mt1809-Stenocatantops splendens</i>	68	67	66	66	66	69	65	70	66	71	1322	797
<i>mt1808-Stenocatantops mistshenkoi</i>	68	67	66	66	66	69	65	70	66	71	1322	797
<i>mt1810-Xenocatantops brachycerus</i>	68	67	66	67	66	69	65	70	65	71	1318	796
Range of variation	67–69	65–67	66–67	64–67	66–67	69–70	62–65	67–71	65–66	70–71	1318–1379	780–873

Table S7. Total numbers of different types of base mismatches in tRNAs of the nine newly sequenced mitogenomes

Species	A-A	A-G	A-C	G-U	C-U	U-U
<i>Oxytauchira brachyptera</i>	1 (<i>trnD</i>)	1 (<i>trnW</i>)	0	25	0	3 (<i>trnH</i> , <i>trnR</i> , <i>trnV</i>)
<i>Oxytauchira flange</i>	1 (<i>trnD</i>)	1 (<i>trnW</i>)	0	27	0	3 (<i>trnH</i> , <i>trnR</i> , <i>trnL1</i>)
<i>Paratoacris reticulipennis</i>	1 (<i>trnD</i>)	1 (<i>trnW</i>)	0	22	0	1 (<i>trnH</i>)
<i>Fer nigripennis</i>	1 (<i>trnD</i>)	1 (<i>trnW</i>)	1 (<i>trnI</i>)	20	0	3 (<i>trnH</i> , <i>trnE</i> , <i>trnM</i>)
<i>Caryandoides hunanica</i>	1 (<i>trnD</i>)	1 (<i>trnW</i>)	0	20	0	1 (<i>trnH</i>)
<i>Diabolocatantops pinguis</i>	0	1 (<i>trnW</i>)	2 (<i>trnG</i> , <i>trnD</i>)	15	0	2 (<i>trnH</i> , <i>trnQ</i>)
<i>Stenocatantops splendens</i>	1 (<i>trnD</i>)	1 (<i>trnW</i>)	1 (<i>trnG</i>)	23	0	2 (<i>trnH</i> , <i>trnQ</i>)
<i>Stenocatantops mistshenkoi</i>	1 (<i>trnD</i>)	1 (<i>trnW</i>)	1 (<i>trnG</i>)	22	0	2 (<i>trnH</i> , <i>trnQ</i>)
<i>Xenocatantops brachycerus</i>	1 (<i>trnD</i>)	1 (<i>trnW</i>)	1 (<i>trnG</i>)	23	1 (<i>trnQ</i>)	2 (<i>trnH</i> , <i>trnF</i>)

Table S8. Distribution of G–U base mismatches in tRNAs of the nine newly sequenced mitogenome

Transfer RNA	<i>trn I</i>	<i>trn Q</i>	<i>trn M</i>	<i>trn W</i>	<i>trn C</i>	<i>trn Y</i>	<i>trn L2</i>	<i>trn D</i>	<i>trn K</i>	<i>trn G</i>	<i>trn A</i>	<i>trn R</i>	<i>trn N</i>	<i>trn S1</i>	<i>trn E</i>	<i>trn F</i>	<i>trn H</i>	<i>trn T</i>	<i>trn P</i>	<i>trn S2</i>	<i>trn L1</i>	<i>trn V</i>
<i>Oxytauchira brachyptera</i>	0	3	1	0	2	3	0	0	1	2	2	0	0	2	0	2	1	0	2	1	2	1
<i>Oxytauchira flange</i>	1	3	0	0	3	3	0	0	0	1	1	0	1	1	0	2	3	0	3	1	3	1
<i>Paratoacris reticulipennis</i>	0	3	1	1	1	4	0	0	0	2	2	1	0	1	0	3	0	0	2	0	0	1
<i>Fer nigripennis</i>	0	1	0	1	2	1	1	0	0	1	1	0	0	2	0	2	2	0	3	0	0	3
<i>Caryandoides hunanica</i>	0	2	0	0	2	3	0	0	0	2	2	1	0	1	0	3	0	1	1	0	0	2
<i>Diabolocatantops pinguis</i>	0	1	0	0	0	2	0	0	0	1	2	1	0	2	0	3	1	0	1	0	0	1
<i>Stenocatantops splendens</i>	0	1	1	0	2	3	0	0	1	1	2	1	0	2	0	4	1	0	2	0	0	2
<i>Stenocatantops mistshenkoi</i>	0	1	1	0	2	3	0	0	1	1	2	1	0	2	0	4	1	0	2	0	0	1
<i>Xenocatantops brachycerus</i>	1	1	0	0	2	3	0	0	0	2	2	1	0	2	0	2	1	1	3	0	0	2

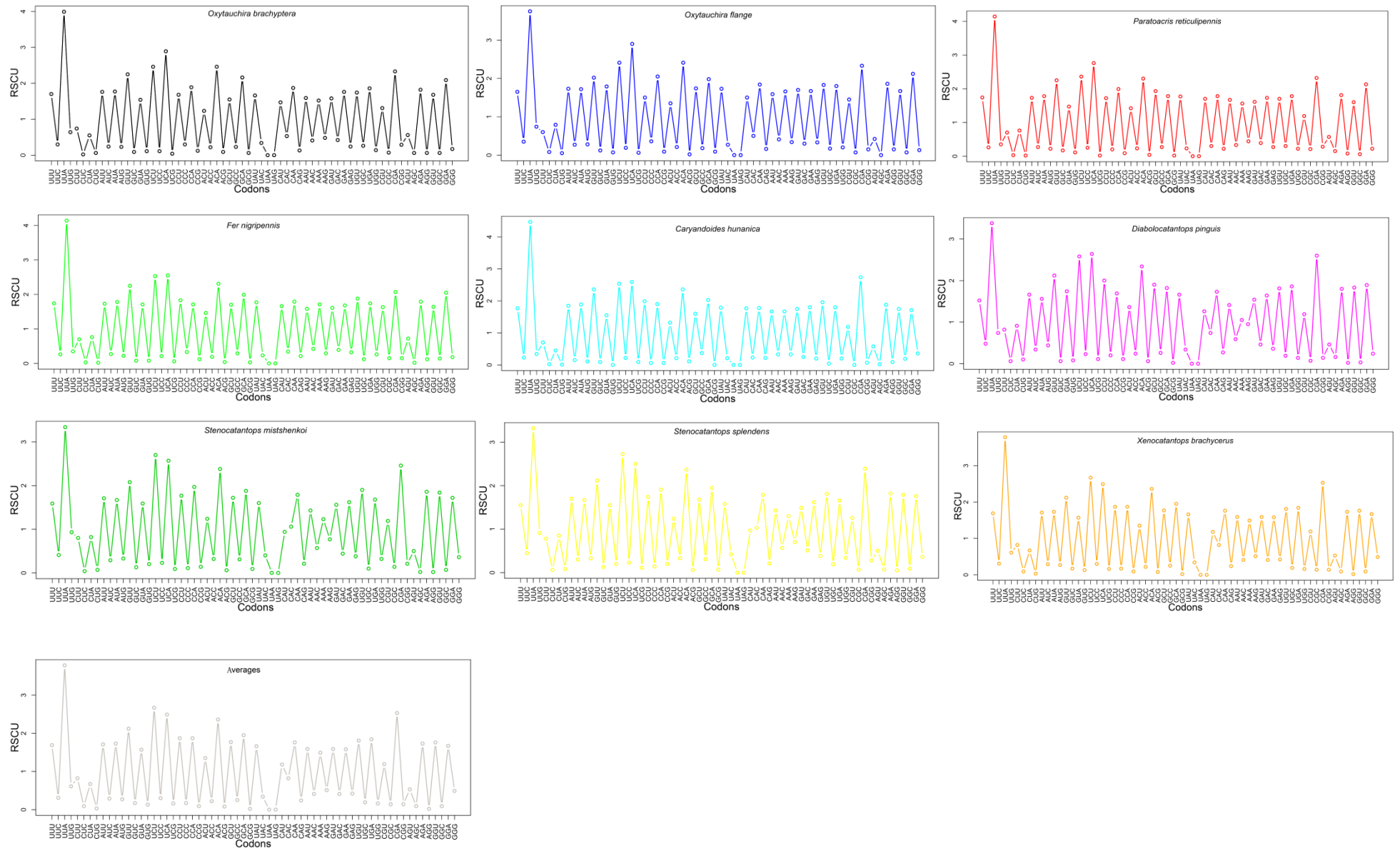


Fig. S1. Codon usage patterns of the nine newly sequenced mitogenomes.

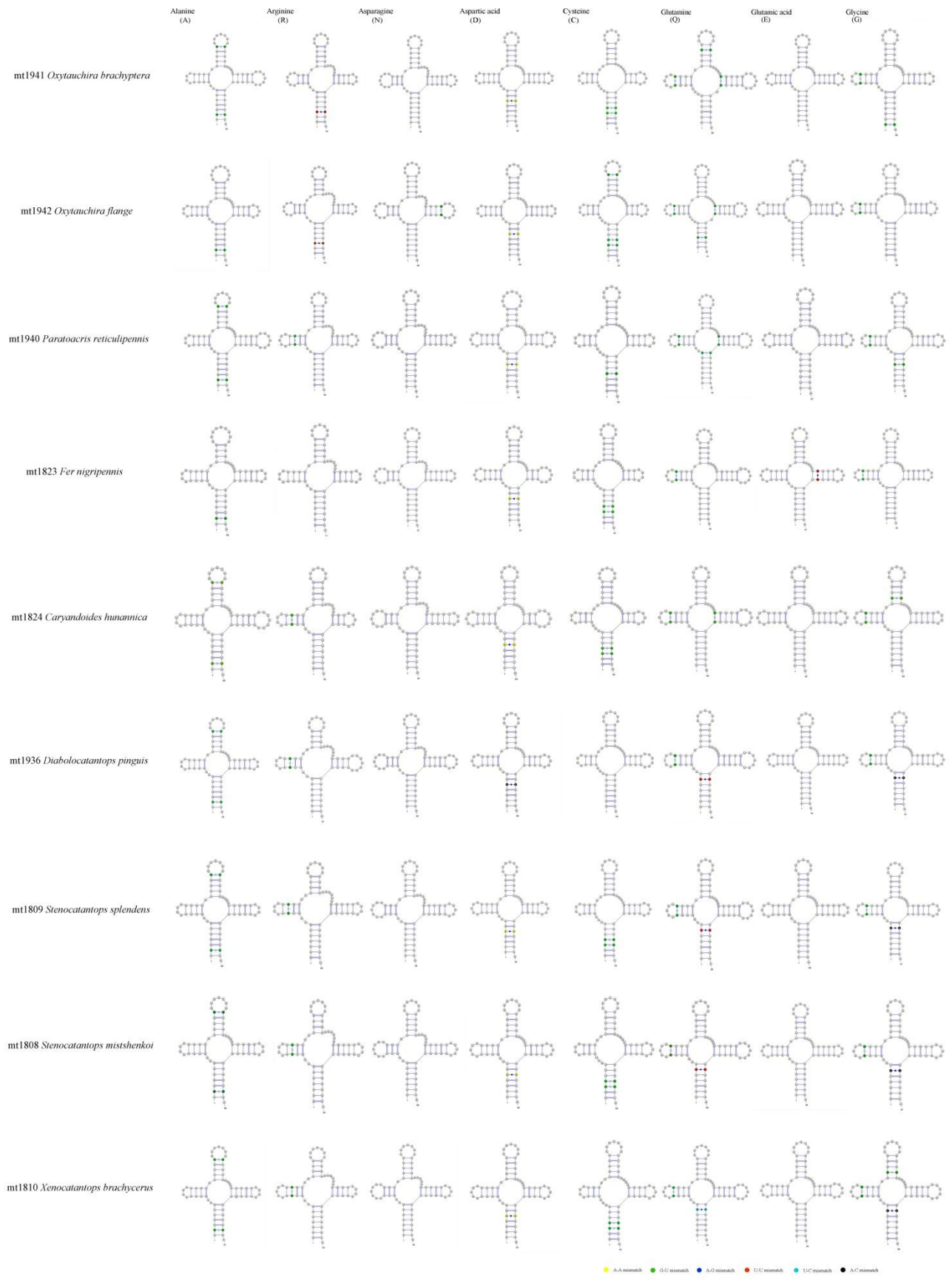
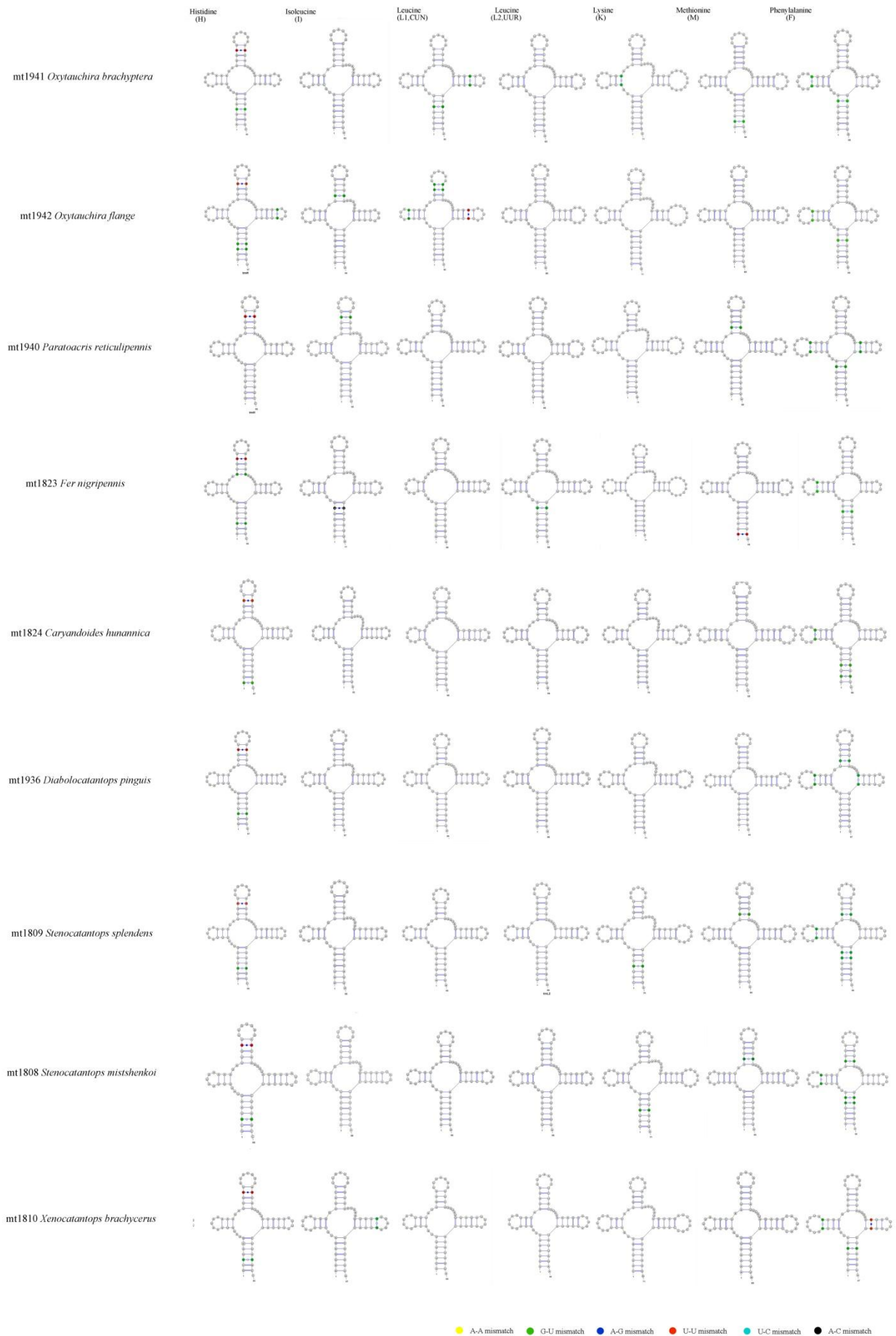


Fig. S2. Secondary structures of 22 tRNAs of the nine newly sequenced mitogenomes.



● A-A mismatch ● G-U mismatch ● A-G mismatch ● U-U mismatch ● U-C mismatch ● A-C mismatch

Fig. S2. (Cont.)



Fig. S2. (Cont.)

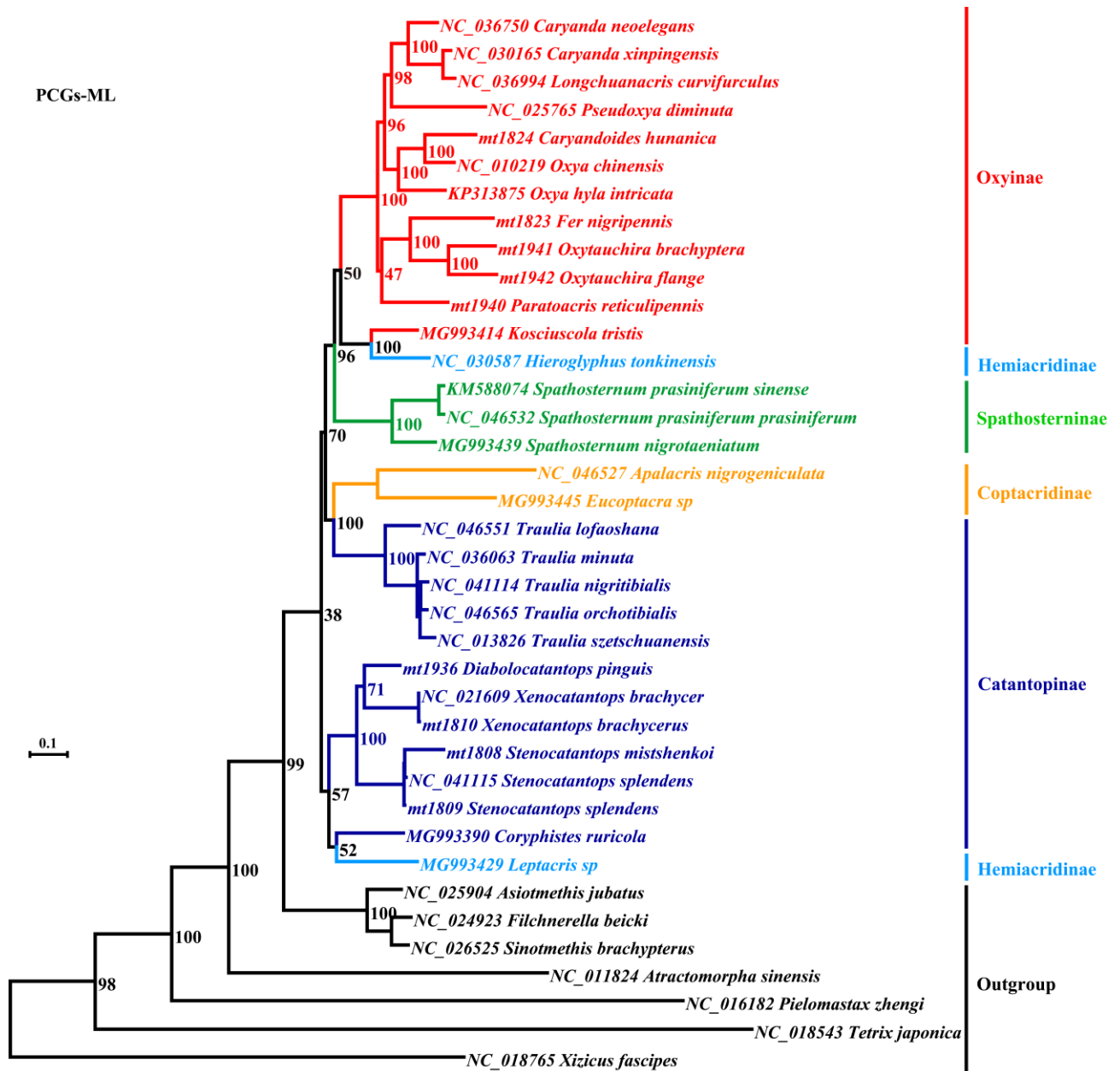


Fig. S3. Phylogenetic tree deduced from sequences of the 13 mitogenome protein coding genes (PCGs) using maximum likelihood (ML).

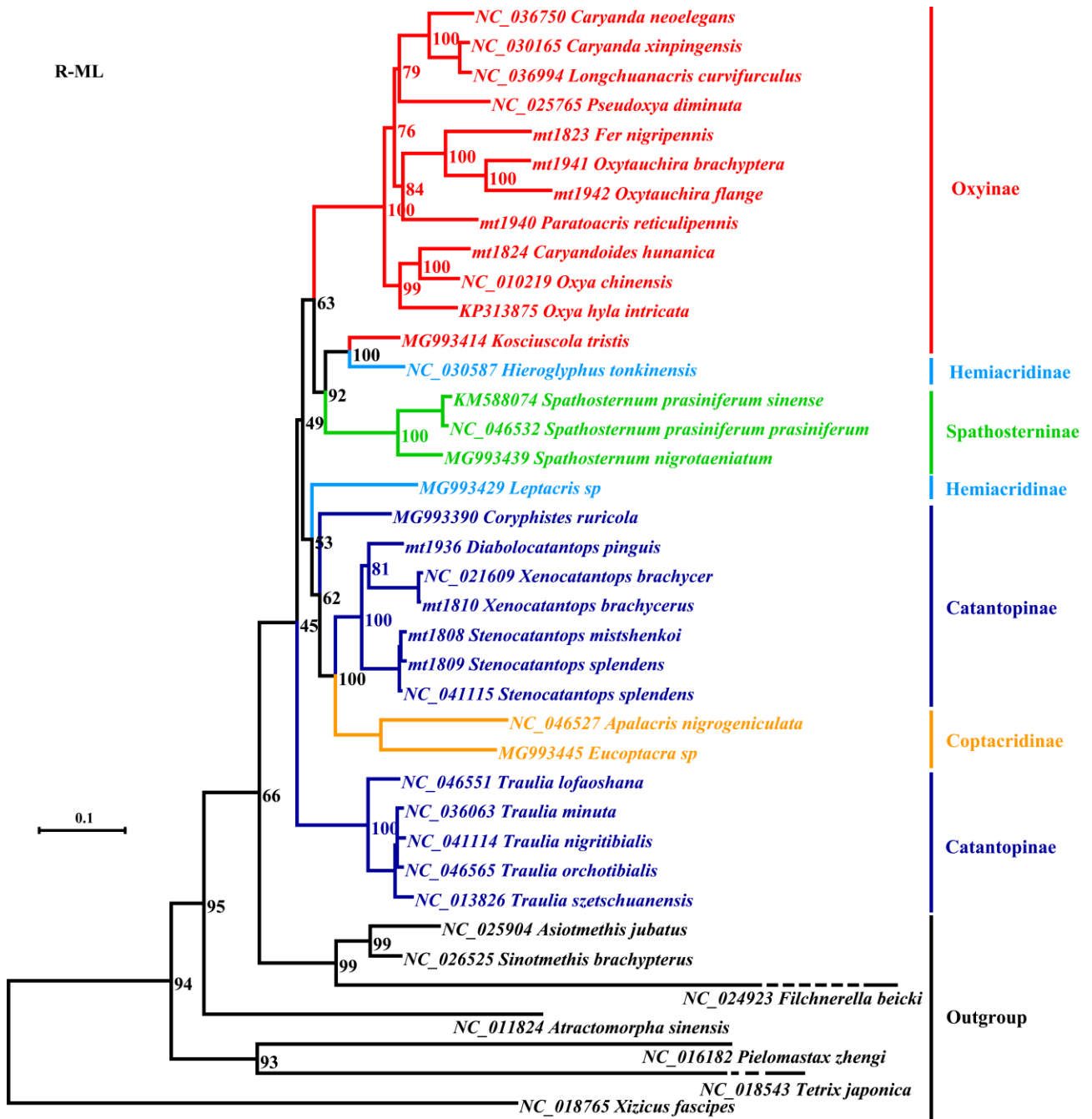


Fig. S4. Phylogenetic tree deduced from sequences of the 2 mitogenome rRNAs using maximum likelihood (ML).

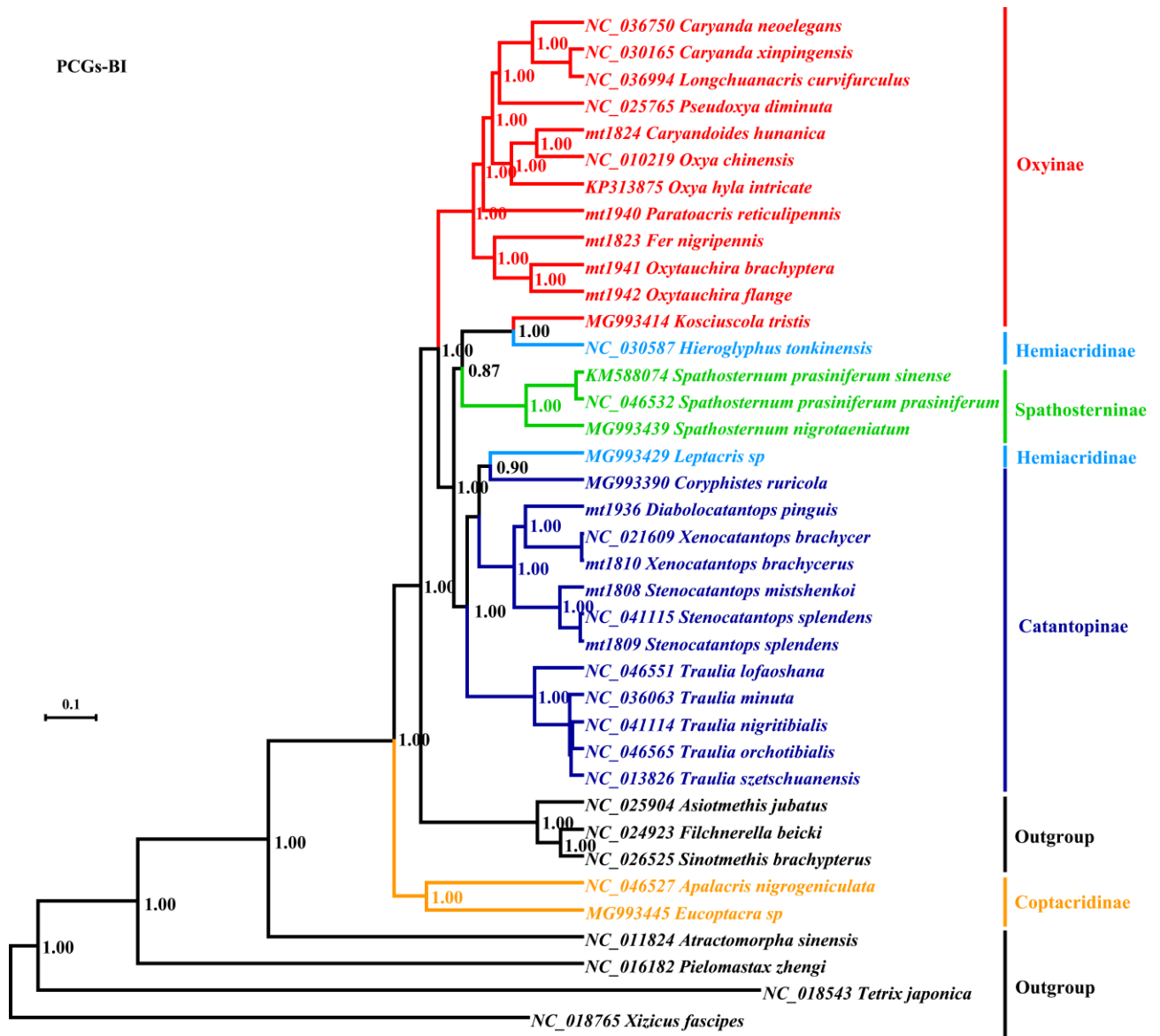


Fig. S5. Phylogenetic tree deduced from sequences of the 13 mitogenome protein coding genes (PCGs) using Bayesian Inference (BI).

