

Figure S2. The secondary cloverleaf structure for the tRNAs of *Coomaniella copipes*.

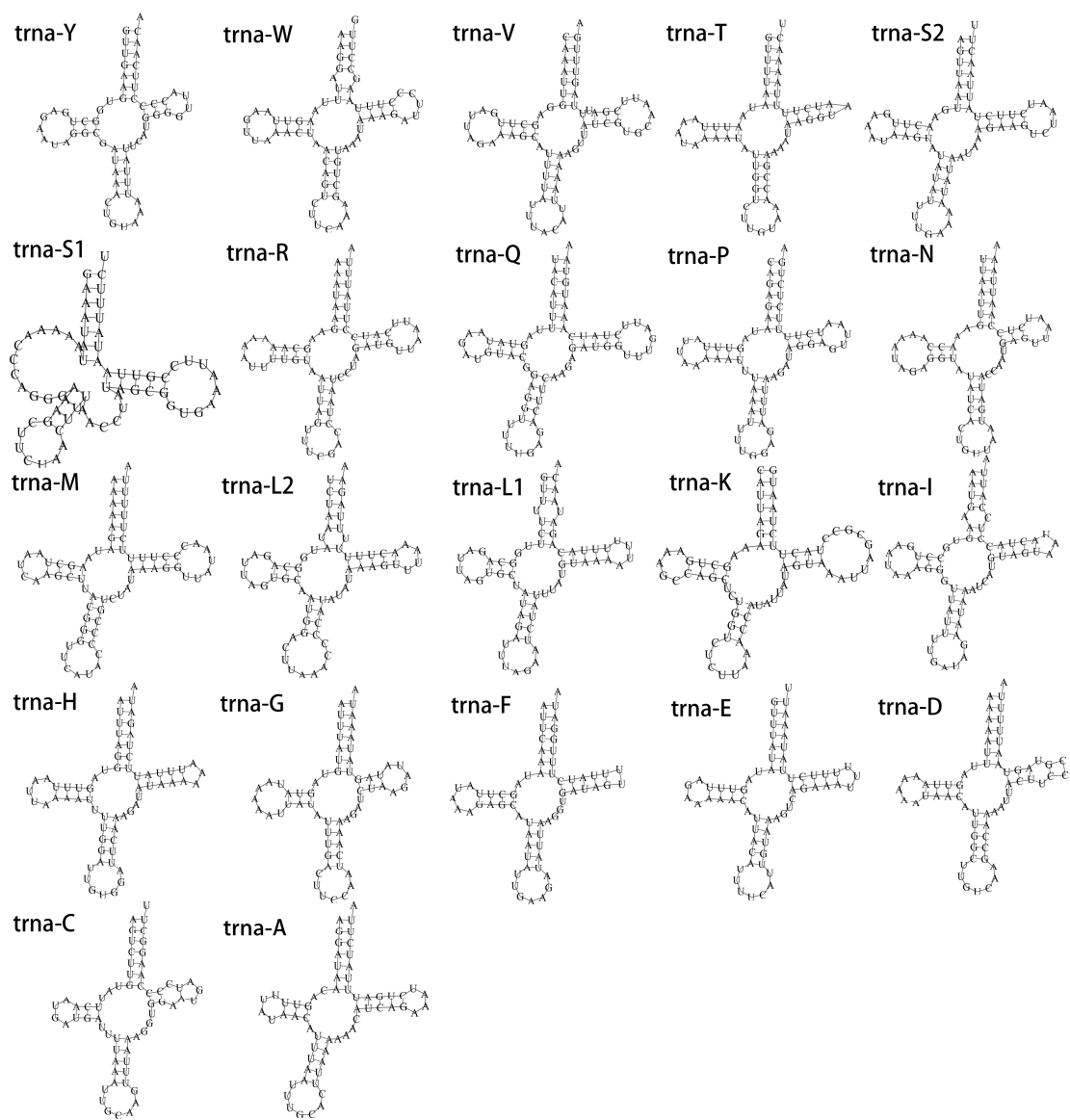


Figure S4. The secondary cloverleaf structure for the tRNAs of *Dicerca corrugata*.

Table S1. Codon usage of the protein-coding genes in *Coomaniella copipes*.

Codon	Count	RSCU	Codon	Count	RSCU	Codon	Count	RSCU	Codon	Count	RSCU
UUU(F)	291	1.6	UCU(S)	124	2.66	UAU(Y)	132	1.67	UGU(C)	28	1.65
UUC(F)	73	0.4	UCC(S)	18	0.39	UAC(Y)	26	0.33	UGC(C)	6	0.35
UUA(L)	321	3.23	UCA(S)	97	2.08	UAA(*)	0	0	UGA(W)	85	1.77
UUG(L)	35	0.35	UCG(S)	4	0.09	UAG(*)	0	0	UGG(W)	11	0.23
CUU(L)	118	1.19	CCU(P)	77	2.35	CAU(H)	51	1.46	CGU(R)	24	1.75
CUC(L)	23	0.23	CCC(P)	20	0.61	CAC(H)	19	0.54	CGC(R)	0	0
CUA(L)	91	0.92	CCA(P)	32	0.98	CAA(Q)	67	1.89	CGA(R)	29	2.11
CUG(L)	8	0.08	CCG(P)	2	0.06	CAG(Q)	4	0.11	CGG(R)	2	0.15
AUU(I)	326	1.7	ACU(T)	75	1.8	AAU(N)	152	1.63	AGU(S)	25	0.54
AUC(I)	57	0.3	ACC(T)	17	0.41	AAC(N)	35	0.37	AGC(S)	4	0.09
AUA(M)	203	1.78	ACA(T)	72	1.72	AAA(K)	80	1.52	AGA(S)	97	2.08
AUG(M)	25	0.22	ACG(T)	3	0.07	AAG(K)	25	0.48	AGG(S)	4	0.09
GUU(V)	90	2.13	GCU(A)	83	2.05	GAU(D)	55	1.51	GGU(G)	48	0.92
GUC(V)	13	0.31	GCC(A)	27	0.67	GAC(D)	18	0.49	GGC(G)	9	0.17
GUA(V)	55	1.3	GCA(A)	50	1.23	GAA(E)	69	1.75	GGA(G)	130	2.49
GUG(V)	11	0.26	GCG(A)	2	0.05	GAG(E)	10	0.25	GGG(G)	22	0.42

Table S2. Codon usage of the protein-coding genes in *Coomaniella dentata*.

Codon	Count	RSCU	Codon	Count	RSCU	Codon	Count	RSCU	Codon	Count	RSCU
UUU(F)	319	1.76	UCU(S)	123	2.62	UAU(Y)	139	1.76	UGU(C)	33	1.89
UUC(F)	44	0.24	UCC(S)	18	0.38	UAC(Y)	19	0.24	UGC(C)	2	0.11
UUA(L)	391	3.88	UCA(S)	95	2.03	UAA(*)	0	0	UGA(W)	87	1.81
UUG(L)	22	0.22	UCG(S)	1	0.02	UAG(*)	0	0	UGG(W)	9	0.19
CUU(L)	125	1.24	CCU(P)	73	2.23	CAU(H)	53	1.54	CGU(R)	21	1.56
CUC(L)	13	0.13	CCC(P)	12	0.37	CAC(H)	16	0.46	CGC(R)	2	0.15
CUA(L)	48	0.48	CCA(P)	46	1.4	CAA(Q)	69	1.89	CGA(R)	29	2.15
CUG(L)	5	0.05	CCG(P)	0	0	CAG(Q)	4	0.11	CGG(R)	2	0.15
AUU(I)	348	1.81	ACU(T)	90	2.07	AAU(N)	162	1.71	AGU(S)	28	0.6
AUC(I)	36	0.19	ACC(T)	16	0.37	AAC(N)	28	0.29	AGC(S)	3	0.06
AUA(M)	213	1.86	ACA(T)	67	1.54	AAA(K)	88	1.73	AGA(S)	100	2.13
AUG(M)	16	0.14	ACG(T)	1	0.02	AAG(K)	14	0.27	AGG(S)	7	0.15
GUU(V)	99	2.4	GCU(A)	81	2.1	GAU(D)	65	1.86	GGU(G)	44	0.87
GUC(V)	2	0.05	GCC(A)	17	0.44	GAC(D)	5	0.14	GGC(G)	4	0.08
GUA(V)	57	1.38	GCA(A)	54	1.4	GAA(E)	77	1.9	GGA(G)	137	2.7
GUG(V)	7	0.17	GCG(A)	2	0.05	GAG(E)	4	0.1	GGG(G)	18	0.35

Table S3. Codon usage of the protein-coding genes in *Dicerca corrugata*.

Codon	Count	RSCU	Codon	Count	RSCU	Codon	Count	RSCU	Codon	Count	RSCU
UUU(F)	238	1.41	UCU(S)	77	1.86	UAU(Y)	118	1.41	UGU(C)	30	1.62
UUC(F)	100	0.59	UCC(S)	31	0.75	UAC(Y)	49	0.59	UGC(C)	7	0.38
UUA(L)	268	2.72	UCA(S)	99	2.39	UAA(*)	0	0	UGA(W)	78	1.63
UUG(L)	81	0.82	UCG(S)	8	0.19	UAG(*)	0	0	UGG(W)	18	0.38
CUU(L)	114	1.16	CCU(P)	69	2.08	CAU(H)	46	1.31	CGU(R)	21	1.47
CUC(L)	19	0.19	CCC(P)	19	0.57	CAC(H)	24	0.69	CGC(R)	1	0.07
CUA(L)	90	0.91	CCA(P)	40	1.2	CAA(Q)	69	1.86	CGA(R)	25	1.75
CUG(L)	20	0.2	CCG(P)	5	0.15	CAG(Q)	5	0.14	CGG(R)	10	0.7
AUU(I)	289	1.57	ACU(T)	73	1.5	AAU(N)	140	1.51	AGU(S)	25	0.6
AUC(I)	80	0.43	ACC(T)	42	0.86	AAC(N)	45	0.49	AGC(S)	4	0.1
AUA(M)	174	1.63	ACA(T)	73	1.5	AAA(K)	69	1.38	AGA(S)	78	1.89
AUG(M)	40	0.37	ACG(T)	7	0.14	AAG(K)	31	0.62	AGG(S)	9	0.22
GUU(V)	96	1.89	GCU(A)	84	1.83	GAU(D)	55	1.47	GGU(G)	58	1.09
GUC(V)	20	0.39	GCC(A)	31	0.67	GAC(D)	20	0.53	GGC(G)	6	0.11
GUA(V)	74	1.46	GCA(A)	58	1.26	GAA(E)	58	1.55	GGA(G)	116	2.19
GUG(V)	13	0.26	GCG(A)	11	0.24	GAG(E)	17	0.45	GGG(G)	32	0.6

Table S4. Summarized A+T contents of 13 PCGs for the three buprestid species investigated in this study.

genes	A+T (%)		
	<i>C. copipes</i>	<i>C. dentata</i>	<i>D. corrugata.</i>
<i>nad2</i>	74.49	76.74	70.48
<i>cox1</i>	66.23	68.71	63.36
<i>cox2</i>	69.20	72.73	66.72
<i>atp8</i>	79.49	81.41	77.56
<i>atp6</i>	71.26	75.26	71.26
<i>cox3</i>	68.61	71.53	65.44
<i>nad3</i>	74.01	77.12	67.51
<i>nad5</i>	76.98	79.07	72.85
<i>nad4</i>	76.35	78.67	73.43
<i>nad4l</i>	77.89	77.19	74.23
<i>nad6</i>	79.80	80.78	75.25
<i>cytb</i>	69.82	71.83	66.75
<i>nad1</i>	74.42	75.97	71.40