

Table S1. List of taxonomic groups used for the phylogenetic analyses in this study.

Family	Species	Accession number	Reference
Chrysopidae	<i>Abachrysa eureka</i>	KY587199	[13]
	<i>Ankylopteryx gracilis</i>	OQ269716	This study
	<i>Ankylopteryx octopunctata</i>	OM510943	This study
	<i>Apochrysa matsumurae</i>	NC_015095	[30]
	<i>Chrysopa pallens</i>	NC_019618	[31]
	<i>Chrysoperla externa</i>	NC_030341	
	<i>Chrysoperla nipponensis</i>	NC_015093	[30]
	<i>Italochrysa insignis</i>	KY587200	[13]
	<i>Leucochrysa pretiosa</i>	KY587201	[13]
	<i>Nothancyla verreauxi</i>	KP264629	[13]
	<i>Nothochrysa sinica</i>	NC_060341	[12]
	<i>Nothochrysa</i> sp.	KP264630	
	<i>Parankylopteryx</i> sp.	KY587202	[13]
Hemerobiidae	<i>Neuronema laminatum</i>	NC_028153	[32]
	<i>Micromus angulatus</i>	NC_042677	[33]
Mantispidae	<i>Ditaxis biseriata</i>	NC_013257	[34]
	<i>Mantispa japonica</i>	NC_039771	[35]
Myrmeleontidae	<i>Layahima yangi</i>	NC_071191	
	<i>Myrmeleon formicarius</i>	NC_047285	[36]

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Table S2. Organization of *Ankylopteryx gracilis* mitogenome.

Gene	Direction	Location		Size	Anticodon	Codon		Intergenic nucleotides
		Start	End			Start	Stop	
<i>trnI</i>	J	1	69	69	GAT			136
<i>trnQ</i>	N	274	206	69	TTG			2
<i>trnM</i>	J	277	344	68	CAT			0
<i>nad2</i>	J	345	1353	1009		ATT	T-tRNA	0
<i>trnC</i>	N	1416	1354	63	GCA			3
<i>trnW</i>	J	1420	1484	65	TCA			1
<i>trnY</i>	N	1549	1486	64	GTA			3
<i>cox1</i>	J	1553	3086	1534		TCG	T-tRNA	0
<i>trnL2</i>	J	3087	3150	64	TAA			4
<i>cox2</i>	J	3155	3838	684		ATG	TAA	2
<i>trnK</i>	J	3841	3910	70	CTT			0
<i>trnD</i>	J	3911	3975	65	GTC			0
<i>atp8</i>	J	3976	4134	159		ATT	TAA	-7
<i>atp6</i>	J	4128	4805	678		ATG	TAA	-1
<i>cox3</i>	J	4805	5593	789		ATG	TAA	2
<i>trnG</i>	J	5596	5660	65	TCC			0
<i>nad3</i>	J	5661	6012	352		ATT	T-tRNA	0
<i>trnA</i>	J	6013	6078	66	TGC			0
<i>trnR</i>	J	6079	6140	62	TCG			0
<i>trnN</i>	J	6141	6208	68	GTT			0
<i>trnS1</i>	J	6209	6275	67	TTC			1

<i>trnE</i>	J	6277	6340	64	TTC			-2
<i>trnF</i>	N	6404	6339	66	GAA			0
<i>nad5</i>	N	8130	6405	1726		ATT	T-tRNA	0
<i>trnH</i>	N	8193	8131	63	GTG			0
<i>nad4</i>	N	9530	8194	1337		ATG	TA-tRNA	-7
<i>nad4L</i>	N	9820	9524	297		ATG	TAA	2
<i>trnT</i>	J	9823	9886	64	TGT			0
<i>trnP</i>	N	9952	9887	66	TGG			2
<i>nad6</i>	J	9955	10464	510		ATT	TAA	-1
<i>cob</i>	J	10464	11598	1135		ATG	T-tRNA	0
<i>trnS2</i>	J	11599	11665	67	TGA			24
<i>nad1</i>	N	12628	11690	939		ATA	TAA	13
<i>trnL1</i>	N	12704	12642	63	TAG			0
<i>rrnL</i>	N	14023	12705	1319				0
<i>trnV</i>	N	14093	14024	70	TAC			0
<i>rrnS</i>	N	14868	14094	775				0
Control region		14869	18284	3416				

Table S3. Organization of *Ankylopteryx octopunctata* mitogenome.

Gene	Direction	Location		Size	Anticodon	Codon		Intergenic nucleotides
		Start	End			Start	Stop	
<i>trnI</i>	J	328	394	67	GAT			137
<i>trnQ</i>	N	600	532	69	TTG			2
<i>trnM</i>	J	603	670	68	CAT			0
<i>nad2</i>	J	671	1679	1009		ATT	T-tRNA	0
<i>trnC</i>	N	1743	1680	64	GCA			1
<i>trnW</i>	J	1745	1808	64	TCA			1
<i>trnY</i>	N	1874	1810	65	GTA			2
<i>cox1</i>	J	1877	3410	1534		TCG	T-tRNA	0
<i>trnL2</i>	J	3411	3474	64	TAA			3
<i>cox2</i>	J	3478	4159	682		ATG	T-tRNA	0
<i>trnK</i>	J	4160	4230	71	CTT			-1
<i>trnD</i>	J	4230	4295	66	GTC			0
<i>atp8</i>	J	4296	4454	159		ATC	TAA	-7
<i>atp6</i>	J	4448	5125	678		ATG	TAA	-1
<i>cox3</i>	J	5125	5913	789		ATG	TAG	3
<i>trnG</i>	J	5917	5981	65	TCC			0
<i>nad3</i>	J	5982	6333	352		ATT	T-tRNA	0
<i>trnA</i>	J	6334	6399	66	TGC			-1
<i>trnR</i>	J	6399	6462	64	TCG			3
<i>trnN</i>	J	6466	6531	66	GTT			0
<i>trnS1</i>	J	6532	6598	67	TTC			8

<i>trnE</i>	J	6607	6671	65	TTC			-2
<i>trnF</i>	N	6732	6670	63	GAA			0
<i>nad5</i>	N	8458	6733	1726		ATT	T-tRNA	0
<i>trnH</i>	N	8521	8459	63	GTG			0
<i>nad4</i>	N	9855	8522	1334		ATG	TA-tRNA	-7
<i>nad4L</i>	N	10145	9849	297		ATG	TAA	2
<i>trnT</i>	J	10148	10211	64	TGT			0
<i>trnP</i>	N	10277	10212	66	TGG			1
<i>nad6</i>	J	10279	10788	510		ATT	TAA	-1
<i>cob</i>	J	10788	11922	1135		ATG	T-tRNA	0
<i>trnS2</i>	J	11923	11989	67	TGA			30
<i>nad1</i>	N	12949	12020	930		ATA	TAA	22
<i>trnL1</i>	N	13034	12972	63	TAG			

Table S4. Nucleotide composition and skews in the complete mitogenomes of Chrysopidae.

Species	T(U)	C	A	G	Total	A+T%	AT-Skew	GC-Skew
<i>Ankylopteryx gracilis</i>	41.05	10.70	40.69	7.56	18284.0	81.75	0.00	-0.17
<i>Apochrysa matsumurae</i>	40.95	12.36	38.07	8.62	16214.0	79.02	-0.04	-0.18
<i>Chrysopa pallens</i>	39.63	11.71	39.92	8.74	16723.0	79.54	0.00	-0.15
<i>Chrysoperla externa</i>	39.89	11.87	38.88	9.36	16509.0	78.76	-0.01	-0.12
<i>Chrysoperla nipponensis</i>	39.71	12.01	39.17	9.10	16057.0	78.89	-0.01	-0.14
<i>Nothochrysa sinica</i>	41.26	11.48	38.64	8.62	16166.0	79.90	-0.03	-0.14

Table S5. Nucleotide composition and skews in the complete PCGs of Chrysopidae.

Species	T(U)	C	A	G	Total	A+T%	AT-Skew	GC-Skew
<i>Abachrysa eureka</i>	45.6	9.8	33.8	10.8	11133.0	79.39	-0.15	0.05
<i>Ankylopteryx gracilis</i>	45.3	9.8	33.9	11.0	11145.0	79.19	-0.15	0.06
<i>Ankylopteryx octopunctata</i>	45.1	10.1	33.7	11.1	11127.0	78.86	-0.14	0.05
<i>Apochrysa matsumurae</i>	44.2	10.7	33.3	11.8	11142.0	77.54	-0.14	0.05
<i>Chrysopa pallens</i>	44.6	10.4	33.5	11.5	11154.0	78.11	-0.14	0.05
<i>Chrysoperla externa</i>	45.3	10.4	31.7	12.6	11151.0	77.00	-0.18	0.09
<i>Chrysoperla nipponensis</i>	45.0	10.5	32.7	11.9	11151.0	77.66	-0.16	0.06
<i>Nothancyla verreauxi</i>	44.9	10.2	33.6	11.3	11132.0	78.49	-0.14	0.05
<i>Nothochrysa sinica</i>	44.6	10.4	33.6	11.3	11136.0	78.27	-0.14	0.04
<i>Nothochrysa</i> sp.	44.7	10.6	33.2	11.5	11145.0	77.94	-0.15	0.04



Table S6. Nucleotide composition at the three codon sites in the complete PCGs of Chrysopidae.

Species	T-1	C-1	A-1	G-1	T-2	C-2	A-2	G-2	T-3	C-3	A-3	G-3
<i>Abachrysa eureka</i>	39.0	9.7	34.2	17.3	47.0	17.8	21.5	14.1	52.0	2.0	45.5	1.0
<i>Ankylopteryx gracilis</i>	38.0	9.7	34.5	17.6	47.0	17.4	21.8	13.9	51.0	2.3	45.3	1.5
<i>Ankylopteryx octopunctata</i>	38.0	9.9	34.9	17.4	47.0	17.8	21.6	14.2	51.0	2.5	44.8	1.6
<i>Apochrysa matsumurae</i>	38.0	10.6	33.3	18.3	46.0	18.4	21.1	14.2	49.0	3.0	45.4	2.8
<i>Chrysopa pallens</i>	38.0	10.1	33.2	18.4	46.0	18.2	21.3	14.2	49.0	3.0	46.0	1.9
<i>Chrysoperla externa</i>	39.0	10.0	32.5	18.9	46.0	18.6	21.3	14.2	51.0	2.8	41.3	4.6
<i>Chrysoperla nipponensis</i>	39.0	9.9	32.2	19.3	46.0	18.7	21.0	14.4	51.0	2.8	44.7	1.9
<i>Nothancyla verreauxi</i>	38.0	9.9	34.1	18.1	46.0	18.3	21.5	14.1	51.0	2.4	45.2	1.7
<i>Nothochrysa sinica</i>	38.0	10.3	33.9	18.0	46.0	18.5	21.5	14.1	50.0	2.5	45.5	1.8
<i>Nothochrysa</i> sp.	37.0	10.5	33.8	18.3	46.0	18.7	21.3	14.3	51.0	2.6	44.6	1.9

Table S7. Encoded amino acids composition in the complete PCGs of Chrysopidae.

Species	Ala	Cys	Asp	Glu	Phe	Gly	His	Ile	Lys	Leu	Met	Asn	Pro	Gln	Arg	Ser	Thr	Val	Trp	Tyr
<i>Abachrysa eureka</i>	4.11	1.00	1.78	2.05	8.89	5.46	1.97	10.86	2.35	16.10	6.94	6.19	3.43	1.89	1.54	9.00	4.65	3.94	2.76	5.11
<i>Ankylopteryx gracilis</i>	4.02	0.92	1.67	2.10	8.76	5.50	2.00	11.00	2.32	15.97	6.93	6.47	3.43	1.81	1.51	8.79	4.53	4.29	2.72	5.26
<i>Ankylopteryx octopunctata</i>	4.08	1.05	1.84	2.00	8.64	5.48	2.00	10.99	2.38	15.74	7.16	6.10	3.38	1.84	1.54	8.91	4.86	4.05	2.67	5.29
<i>Apochrysa matsumurae</i>	4.43	0.97	1.78	2.05	9.12	5.51	2.08	10.26	2.51	15.76	6.61	5.59	3.43	1.92	1.57	9.20	4.91	4.59	2.70	5.02
<i>Chrysopa pallens</i>	4.34	1.00	1.91	2.08	8.95	5.55	2.00	10.51	2.37	16.10	6.39	5.88	3.50	1.78	1.54	9.09	4.69	4.53	2.72	5.07
<i>Chrysoperla externa</i>	4.53	0.97	1.89	2.10	8.79	5.72	1.97	9.98	2.27	16.40	6.18	5.88	3.45	1.83	1.54	8.90	5.02	4.69	2.72	5.18
<i>Chrysoperla nipponensis</i>	4.53	0.97	1.97	2.10	8.76	5.72	2.00	9.76	2.21	16.26	6.18	5.66	3.48	1.86	1.54	9.09	5.07	5.04	2.75	5.04
<i>Nothancyla verreauxi</i>	4.43	1.03	1.84	2.05	8.65	5.59	1.97	10.38	2.43	15.89	7.08	6.05	3.46	1.81	1.49	8.78	4.94	4.24	2.73	5.16
<i>Nothochrysa sinica</i>	4.32	0.97	1.84	2.13	8.51	5.59	1.94	10.80	2.46	15.91	6.62	5.97	3.54	1.81	1.54	9.07	4.89	4.21	2.73	5.16
<i>Nothochrysa</i> sp.	4.35	0.94	1.86	2.11	8.53	5.59	1.94	10.53	2.48	15.90	6.45	5.72	3.54	1.84	1.54	9.23	5.16	4.40	2.73	5.18

Table S8. Start codons and stop codons of PCGs in Chrysopidae.

	<i>ATP6</i>	<i>ATP8</i>	<i>COX1</i>	<i>COX2</i>	<i>COX3</i>	<i>CYTB</i>	<i>ND1</i>	<i>ND2</i>	<i>ND3</i>	<i>ND4</i>	<i>ND4L</i>	<i>ND5</i>	<i>ND6</i>
Start codon													
<i>Abachrysa eureka</i>	ATG	ATT	TCG	ATG	ATG	ATG	ATA	ATT	ATG	ATG	ATG	ATT	ATT
<i>Ankylopteryx gracilis</i>	ATG	ATT	TCG	ATG	ATG	ATG	ATA	ATT	ATT	ATG	ATG	ATT	ATT
<i>Ankylopteryx octopunctata</i>	ATG	ATC	TCG	ATG	ATG	ATG	ATA	ATT	ATT	ATG	ATG	ATT	ATT
<i>Apochrysa matsumurae</i>	ATG	ATT	TCG	ATG	ATG	ATG	ATA	ATT	ATC	ATG	ATG	ATA	ATT
<i>Chrysopa pallens</i>	ATG	ATT	ATT	ATG	ATG	ATG	ATA	ATT	ATT	ATG	ATG	ATT	ATT
<i>Chrysoperla externa</i>	ATG	ATG	TCG	ATG	ATG	ATG	ATG	ATG	ATG	ATG	ATG	ATG	ATG
<i>Chrysoperla nipponensis</i>	ATG	ATT	TCG	ATG	ATG	ATG	ATG	ATT	ATT	ATG	ATG	ATA	ATT
<i>Italochrysa insignis</i>	ATG	ATT	TCG	ATG	ATG	ATG	ATA		ATT	ATG	ATG	ATT	ATT
<i>Leucochrysa pretiosa</i>	ATG	ATT	TCG	ATG	ATG	ATG	ATA		ATT	ATG	ATG	ATT	ATT
<i>Nothancyla verreauxi</i>	ATG	ATT	TCG	ATG	ATG	ATG	ATA	ATT	ATT	ATG	ATG	ATT	ATT
<i>Nothochrysa sinica</i>	ATG	ATT	TCG	ATG	ATG	ATG	ATT	ATT	ATT	ATG	ATG	ATT	ATT
<i>Nothochrysa</i> sp.	ATG	ATT	TCG	ATG	ATG	ATG	ATT	ATT	ATT	ATG	ATG	ATT	ATT
<i>Parankylopteryx</i> sp.	ATG	ATT	ATT	ATG	ATG	ATG	ATA		ATT	ATG	ATG	ATT	ATT
Stop codon													
<i>Abachrysa eureka</i>	TAA	TAA	T-tRNA	T-tRNA	TAA	TAA	TAA	TAA	TAG	T-tRNA	TAA	T-tRNA	TAA
<i>Ankylopteryx gracilis</i>	TAA	TAA	T-tRNA	TAA	TAA	T-tRNA	TAA	T-tRNA	T-tRNA	TA-tRNA	TAA	T-tRNA	TAA
<i>Ankylopteryx octopunctata</i>	TAA	TAA	T-tRNA	T-tRNA	TAA	T-tRNA	TAA	T-tRNA	T-tRNA	TA-tRNA	TAA	T-tRNA	TAA
<i>Apochrysa matsumurae</i>	TAA	TAA	T-tRNA	T-tRNA	TAA	TAA	TAA	TAA	TAG	T-tRNA	TAA	T-tRNA	TAA
<i>Chrysopa pallens</i>	TAA	TAA	T-tRNA	T-tRNA	TAA	TAA	TAA	TAA	TAG	T-tRNA	TAA	T-tRNA	TAA
<i>Chrysoperla externa</i>	TAA	TAA	T-tRNA	T-tRNA	TAA	TAA	TAA	TAA	TAG	TAA	TAA	T-tRNA	T-tRNA
<i>Chrysoperla nipponensis</i>	TAA	TAA	T-tRNA	T-tRNA	TAA	TAA	TAA	TAA	TAG	T-tRNA	TAA	T-tRNA	TAA
<i>Italochrysa insignis</i>	TAA	TAA	T-tRNA	T-tRNA	TAA	TAA	TAA		TAG	T-tRNA	TAA	T-tRNA	TAA
<i>Leucochrysa pretiosa</i>	TAA	TAA	T-tRNA	T-tRNA	TAA	TAA	TAA		TAG	T-tRNA	TAA	T-tRNA	TAA
<i>Nothancyla verreauxi</i>	TAA	TAA	T-tRNA	T-tRNA	TAA	TAA	TAA	TAA	TAG	T-tRNA	TAA	T-tRNA	TAA
<i>Nothochrysa sinica</i>	TAA	TAA	TAA	T-tRNA	TAA	TA-tRNA	TAA	TAA	TAA	T-tRNA	TAA	T-tRNA	TAA
<i>Nothochrysa</i> sp.	TAA	TAA	TAA	T-tRNA	TAA	TAA	TAA	TAA	TAA	T-tRNA	TAA	T-tRNA	TAA
<i>Parankylopteryx</i> sp.	TAA	TAA	T-tRNA	T-tRNA	TAA	TAA	TAA		TAA	T-tRNA	TAA	T-tRNA	TAA

Table S9. Relative synonymous codon usages (RSCUs) of PCGs of *Ankylopteryx gracilis*.

Codon	Count	RSCU	Codon	Count	RSCU
UUU(F)	315	1.94	UCU(S)	107	2.10
UUC(F)	10	0.06	UCC(S)	5	0.10
UUA(L)	539	1.94	UCA(S)	90	1.76
UUG(L)	17	0.06	UCG(S)	2	0.04
UAU(Y)	185	1.90	UGU(C)	31	1.82
UAC(Y)	10	0.10	UGC(C)	3	0.18
UAA(*)	7	2.00	UGA(W)	97	1.92
UAG(*)	0	0.00	UGG(W)	4	0.08
CUU(L)	19	2.11	CCU(P)	76	2.39
CUC(L)	0	0.00	CCC(P)	7	0.22
CUA(L)	16	1.78	CCA(P)	43	1.35
CUG(L)	1	0.11	CCG(P)	1	0.03
CAU(H)	70	1.89	CGU(R)	24	1.71
CAC(H)	4	0.11	CGC(R)	0	0.00
CAA(Q)	65	2.00	CGA(R)	32	2.29
CAG(Q)	2	0.00	CGG(R)	0	0.00
AUU(I)	395	1.94	ACU(T)	95	2.26
AUC(I)	13	0.06	ACC(T)	5	0.12
AUA(M)	244	1.90	ACA(T)	66	1.57
AUG(M)	13	0.10	ACG(T)	2	0.05
AAU(N)	233	1.94	AGU(S)	47	1.54
AAC(N)	7	0.06	AGC(S)	4	0.13
AAA(K)	83	1.93	AGA(S)	71	2.33
AAG(K)	3	0.07	AGG(S)	0	0.00
GUU(V)	69	1.74	GCU(A)	93	2.50
GUC(V)	2	0.05	GCC(A)	10	0.27
GUA(V)	85	2.14	GCA(A)	45	1.21
GUG(V)	3	0.08	GCG(A)	1	0.03
GAU(D)	58	1.87	GGU(G)	73	1.43
GAC(D)	4	0.13	GGC(G)	2	0.04
GAA(E)	77	1.97	GGA(G)	123	2.41
GAG(E)	1	0.03	GGG(G)	6	0.12

\*: Stop codon

Table S10. Relative synonymous codon usages (RSCUs) of PCGs of *Ankylopteryx octopunctata*.

Codon	Count	RSCU	Codon	Count	RSCU
UUU(F)	308	1.93	UCU(S)	102	2.01
UUC(F)	12	0.08	UCC(S)	8	0.16
UUA(L)	530	1.97	UCA(S)	91	1.79
UUG(L)	8	0.03	UCG(S)	2	0.04
UAU(Y)	182	1.86	UGU(C)	39	2.00
UAC(Y)	14	0.14	UGC(C)	0	0.00
UAA(*)	5	1.67	UGA(W)	97	1.96
UAG(*)	1	0.00	UGG(W)	2	0.04
CUU(L)	22	1.96	CCU(P)	84	2.69
CUC(L)	0	0.00	CCC(P)	4	0.13
CUA(L)	23	2.04	CCA(P)	37	1.18
CUG(L)	0	0.00	CCG(P)	0	0.00
CAU(H)	68	1.84	CGU(R)	23	1.61
CAC(H)	6	0.16	CGC(R)	0	0.00
CAA(Q)	68	2.00	CGA(R)	34	2.39
CAG(Q)	0	0.00	CGG(R)	0	0.00
AUU(I)	390	1.92	ACU(T)	112	2.49
AUC(I)	17	0.08	ACC(T)	4	0.09
AUA(M)	249	1.88	ACA(T)	63	1.40
AUG(M)	16	0.12	ACG(T)	1	0.02
AAU(N)	217	1.92	AGU(S)	46	1.45
AAC(N)	9	0.08	AGC(S)	4	0.13
AAA(K)	82	1.86	AGA(S)	77	2.43
AAG(K)	6	0.14	AGG(S)	0	0.00
GUU(V)	66	1.76	GCU(A)	92	2.44
GUC(V)	0	0.00	GCC(A)	12	0.32
GUA(V)	82	2.19	GCA(A)	45	1.19
GUG(V)	2	0.05	GCG(A)	2	0.05
GAU(D)	64	1.88	GGU(G)	80	1.58
GAC(D)	4	0.12	GGC(G)	0	0.00
GAA(E)	72	1.95	GGA(G)	106	2.09
GAG(E)	2	0.05	GGG(G)	17	0.33

\*: Stop codon

Table S11. The count of microsatellite-like sequence in the complete control regions of Chrysopidae.

microsatellite-like sequence	<i>Ankylopteryx gracilis</i>	<i>Apochrysa matsumurae</i>	<i>Chrysoperla nipponensis</i>	<i>Chrysopa pallens</i>	<i>Chrysoperla externa</i>	<i>Nothochrysa sinica</i>
(TA) <sub>2</sub>	125	43	62	95	63	60
(TA) <sub>3</sub>	54	11	19	34	14	25
(TA) <sub>4</sub>	18	5	7	10	5	9
(TA) <sub>5</sub>	10	4	4	4	5	5
(TA) <sub>6</sub>	6	1	3	3	2	4
(TA) <sub>7</sub>	4	1	2	2	0	2
(TA) <sub>8</sub>	3	0	2	1	0	2
(TA) <sub>9</sub>	3	0	0	1	0	1
(AT) <sub>2</sub>	140	36	50	84	61	69
(AT) <sub>3</sub>	45	7	17	24	8	21
(AT) <sub>4</sub>	17	5	8	7	6	10
(AT) <sub>5</sub>	9	3	4	3	5	4
(AT) <sub>6</sub>	5	1	2	2	0	3
(AT) <sub>7</sub>	5	1	2	2	0	2
(AT) <sub>8</sub>	3	0	2	1	0	1
(AT) <sub>9</sub>	3	0	0	1	0	0
(TAA) <sub>2</sub>	43	10	13	12	11	8
(TAA) <sub>3</sub>	8	2	2	1	0	1
(ATT) <sub>2</sub>	10	5	6	7	10	4
(TAT) <sub>2</sub>	9	7	12	15	14	9
(TAT) <sub>3</sub>	2	1	2	4	5	1
(ATA) <sub>2</sub>	31	11	13	16	19	8
(ATA) <sub>3</sub>	10	2	0	1	1	1
(TTAA) <sub>2</sub>	5	2	2	2	3	2
(AATT) <sub>2</sub>	4	6	1	1	3	1
(TTAAA) <sub>2</sub>	1	0	0	1	0	1
(TTTAAA) <sub>2</sub>	2	0	0	0	1	0

Table S12. Nucleotide composition and skews in the complete control regions of Chrysopidae.

Species	T(U)	C	A	G	Total	A+T%	AT-Skew	GC-Skew
<i>Ankylopteryx gracilis</i>	43.93	8.15	45.45	2.46	3416.0	89.38	0.02	-0.54
<i>Apochrysa matsumurae</i>	45.14	10.43	41.38	3.05	1409.0	86.52	-0.04	-0.55
<i>Chrysoperla nipponensis</i>	41.08	8.76	45.66	4.50	1244.0	86.74	0.05	-0.32
<i>Chrysopa pallens</i>	40.47	8.66	45.56	5.30	1905.0	86.04	0.06	-0.24
<i>Chrysoperla externa</i>	42.80	7.97	45.02	4.21	1355.0	87.82	0.03	-0.31
<i>Nothochrysa sinica</i>	45.79	6.29	44.45	3.46	1271.0	90.24	-0.01	-0.29

rRNA	Species	T(U)	C	A	G	Total	A+T%	AT-Skew	GC-Skew
<i>rrnL</i>	<i>Abachrysa eureka</i>	41.55	6.04	41.62	10.79	1307.0	83.17	0.00	0.28
	<i>Ankylopteryx gracilis</i>	42.23	5.99	41.62	10.16	1319.0	83.85	-0.01	0.26
	<i>Apochrysa matsumurae</i>	39.57	6.24	42.54	11.64	1314.0	82.12	0.04	0.30
	<i>Chrysopa pallens</i>	41.25	6.57	40.49	11.69	1309.0	81.74	-0.01	0.28
	<i>Chrysoperla externa</i>	40.00	6.41	41.83	11.76	1310.0	81.83	0.02	0.29
	<i>Chrysoperla nipponensis</i>	40.55	6.50	41.09	11.86	1307.0	81.64	0.01	0.29
	<i>Italochrysa insignis</i>	40.28	6.30	41.89	11.53	1301.0	82.17	0.02	0.29
	<i>Leucochrysa pretiosa</i>	41.37	6.06	41.37	11.20	1303.0	82.73	0.00	0.30
	<i>Nothancyla verreauxi</i>	41.60	6.41	40.53	11.45	1310.0	82.14	-0.01	0.28
	<i>Nothochrysa sinica</i>	41.09	5.99	41.93	10.99	1319.0	83.02	0.01	0.29
	<i>Nothochrysa</i> sp.	40.40	6.04	42.54	11.02	1307.0	82.94	0.03	0.29
	<i>Parankylopteryx</i> sp.	41.50	5.99	42.03	10.47	1318.0	83.54	0.01	0.27
	<i>rrnS</i>	<i>Abachrysa eureka</i>	41.47	6.72	39.92	11.89	774.0	-0.02	18.60
<i>Ankylopteryx gracilis</i>		40.77	6.32	41.55	11.35	775.0	0.01	17.68	0.28
<i>Apochrysa matsumurae</i>		39.43	6.70	40.98	12.89	776.0	0.02	19.59	0.32
<i>Chrysopa pallens</i>		41.21	6.93	40.31	11.55	779.0	-0.01	18.49	0.25
<i>Chrysoperla externa</i>		40.41	7.08	40.67	11.84	777.0	0.00	18.92	0.25
<i>Chrysoperla nipponensis</i>		39.69	7.22	40.46	12.63	776.0	0.01	19.85	0.27
<i>Italochrysa insignis</i>		40.88	6.73	40.75	11.64	773.0	0.00	18.37	0.27
<i>Nothochrysa sinica</i>		39.92	6.89	41.33	11.86	784.0	0.02	18.75	0.27