

Deep-level phylogeny of Cicadomorpha inferred from mitochondrial genomes sequenced by NGS

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Table S1. Taxonomic information and GenBank accession numbers for the taxa included in this study.

Item	Higher Taxon	Superfamily	Family	Species	Accession number	Voucher numbers for the sequenced species
Ingroup	Cimicomorpha	Membracoidea	Aetalionidae	<i>Darthula hardwickii</i>	NC_026699	-
		Membracoidea	Membracidae	<i>Leptobelus gazella</i>	NC_023219	-
		Membracoidea	Membracidae	<i>Tricentrus</i> sp.	KY039115	EMHAU-15041605
		Membracoidea	Membracidae	<i>Tricentrus</i> sp.1	KY039118	EMHAU-15062504
		Membracoidea	Cicadellidae	<i>Alobaldia tobae</i>	KY039116	EMHAU-15062710
		Membracoidea	Cicadellidae	<i>Drabescoides nuchalis</i>	NC_028154	-
		Membracoidea	Cicadellidae	<i>Empoasca vitis</i>	NC_024838	-
		Membracoidea	Cicadellidae	<i>Exitianus indicus</i>	KY039128	EMHAU-15062706
		Membracoidea	Cicadellidae	<i>Homalodisca vitripennis</i>	NC_006899	-
		Membracoidea	Cicadellidae	<i>Illinigina</i> sp.	KY039129	EMHAU-15062817
		Membracoidea	Cicadellidae	<i>Nephotettix cincticeps</i>	NC_026977	-
		Membracoidea	Cicadellidae	<i>Norvellina</i> sp.	KY039131	EMHAU-15062816
		Membracoidea	Cicadellidae	<i>Olidiana</i> sp.	KY039119	EMHAU-15062716
		Membracoidea	Cicadellidae	<i>Orosius orientalis</i>	KY039146	EMHAU-15062705
		Membracoidea	Cicadellidae	<i>Phlogotettix</i> sp.	KY039135	EMHAU-15090801
		Membracoidea	Cicadellidae	<i>Typhlocyba</i> sp.	KY039138	EMHAU-15062510
		Membracoidea	Cicadellidae	<i>Yanocephalus yanonis</i>	KY039113	EMHAU-15062803
		Cercopoidea	Aphrophoridae	<i>Peuceptyelus minutus</i>	KY039134	EMHAU-15052918
		Cercopoidea	Aphrophoridae	<i>Philaenus spumarius</i>	AY630340	-
		Cercopoidea	Cercopidae	<i>Aphrophora</i> sp.	KY039120	EMHAU-15062701
		Cercopoidea	Cercopidae	<i>Abidama producta</i>	NC_015799	-
		Cercopoidea	Cercopidae	<i>Aeneolamia contigua</i>	KY039117	EMHAU-15070803
		Cercopoidea	Cercopidae	<i>Aphrophora alni</i>	KY039122	EMHAU-15062722
		Cercopoidea	Cercopidae	<i>Callitettix versicolor</i>	EU725832	-
		Cercopoidea	Cercopidae	<i>Callitettix bififormis</i>	NC_025496	-
		Cercopoidea	Cercopidae	<i>Callitettix braconoides</i>	NC_025497	-
		Cercopoidea	Cercopidae	<i>Callitettix</i> sp.	KY039124	EMHAU-15090607
		Cercopoidea	Cercopidae	<i>Cosmoscarta bispecularis</i>	NC_026289	-

	Cercopoidea	Cercopidae	<i>Paphnutius ruficeps</i>	NC 021100	-	
	Cicadoidea	Cicadidae	<i>Diceroprocta semicincta</i>	KM000131	-	
	Cicadoidea	Cicadidae	<i>Gaeana maculata</i>	KM244671	-	
	Cicadoidea	Cicadidae	<i>Magiccada tredecim</i>	KM000130	-	
	Cicadoidea	Cicadidae	<i>Meimuna opalifera</i>	KY039112	EMHAU-16010524	
	Cicadoidea	Cicadidae	<i>Platypleura kaempferi</i>	KY039114	EMHAU-16010602	
	Cicadoidea	Cicadidae	<i>Pomponia linearis</i>	KY039136	EMHAU-16010509	
	Cicadoidea	Cicadidae	<i>Tettigades auropilosa</i>	KM000129	-	
	Cicadoidea	Cicadidae	<i>Tettigades ulnaria</i>	KM000128	-	
Outgroup	Fulgoromorpha	Fulgoroidea	Cixiidae	<i>Oliarus</i> sp.	KY039121	EMHAU-15053033
		Fulgoroidea	Cixiidae	<i>Pentastiridius</i> sp.	KY039133	EMHAU-15062511
		Fulgoroidea	Delphacidae	<i>Nilaparvata</i> sp.	KY039125	EMHAU-15062823
		Fulgoroidea	Delphacidae	<i>Sogatella furcifera</i>	NC_021417	-
		Fulgoroidea	Derbidae	<i>Lydda</i> sp.	KY039126	EMHAU-15091903
		Fulgoroidea	Dictyopharidae	<i>Scolops</i> sp.	KY039127	EMHAU-15083115
		Fulgoroidea	Fulgoridae	<i>Lycorma delicatula</i>	EU909203	-
		Fulgoroidea	Issidae	<i>Sivaloka</i> sp.	KY039137	EMHAU-15070305
		Fulgoroidea	Issidae	<i>Sivaloka damnosus</i>	FJ360694	-
	Heteroptera	Nepoidea	Belostomatidae	<i>Diplonychus rusticus</i>	FJ456940	-
	Notonectoidea	Notonectidae	<i>Enithares tibialis</i>	FJ456949	-	
	Cimicoidea	Coreidae	<i>Hydaropsis longirostris</i>	EU427337	-	
	Miroidea	Miridae	<i>Lygus hesperus</i>	NC_024641	-	
	Pentatomoidea	Cydnidae	<i>Macroscytus gibbulus</i>	EU427338	-	
	Lygaeoidea	Berytidae	<i>Yemmalysus parallelus</i>	EU427346	-	

Note: The newly sequenced mitogenome sequences are indicated in bold.

Table S2. The information of local blast for bait sequences of each species newly determined in this study.

Species	<i>cox1</i>			<i>cytb</i>			<i>rrnS</i>		
	Score	bits	Identities	Score	bits	Identities	Score	bits	Identities
<i>Tricentrus</i> sp.	1229	619	99%	-	-	-	-	-	-
<i>Tricentrus</i> sp.1	1187	599	100%	-	-	-	-	-	-
<i>Alobaldia tobae</i>	1982	1000	99%	1134	572	100%	811	409	95%
<i>Exitianus indicus</i>	1980	999	99%	971	490	96%	835	421	96%
<i>Illinigina</i> sp.	1949	983	99%	1140	575	100%	811	409	97%
<i>Norvellina</i> sp.	-	-	-	-	-	-	906	457	98%
<i>Olidiana</i> sp.	1221	618	100%	1126	568	100%	882	445	98%
<i>Orosius orientalis</i>	1217	614	100%	-	-	-	819	413	96%
<i>Phlogotettix</i> sp.	-	-	-	-	-	-	864	436	96%
<i>Typhlocyba</i> sp.	-	-	-	706	356	91%	353	178	87%
<i>Yanocephalus yanonis</i>	1179	595	99%	-	-	-	775	391	95%
<i>Peuceptyelus minutus</i>	-	-	-	1183	597	100%	-	-	-
<i>Aphrophora</i> sp.	1225	618	100%	-	-	-	-	-	-
<i>Aeneolamia contigua</i>	1978	998	99%	-	-	-	835	421	96%
<i>Aphrophora alni</i>	1941	979	99%	1136	573	100%	85	432	96%
<i>Callitettix</i> sp.	-	-	-	1076	543	98%	406	205	93%
<i>Meimuna opalifera</i>	1233	622	99%	-	-	-	-	-	-
<i>Platypleura kaempferi</i>	1207	609	99%	-	-	-	-	-	-
<i>Pomponia linearis</i>	1243	627	99%	-	-	-	-	-	-
<i>Oliarus</i> sp.	-	-	-	-	-	-	509	257	90%
<i>Pentastiridius</i> sp.	1170	590	100%	-	-	-	-	-	-
<i>Nilaparvata</i> sp.	442	223	83%	182	92	83%	260	131	86%
<i>Lydda</i> sp.	-	-	-	-	-	-	848	428	98%
<i>Scolops</i> sp.	1237	624	99%	-	-	-	-	-	-
<i>Sivaloka</i> sp.	1241	626	99%	-	-	-	876	442	97%

Note: Gaps indicate the failure of PCR amplification or Sanger sequencing.

Table S3. (A) The partition schemes and best-fitting models selected by PartitionFinder for dataset of 52taxa_PCG.

52taxa_PCG		
Subset	Subset Partitions	Best Model
Partition 1	atp6_cp1, atp8_cp2, cox2_cp1, cytb_cp1, cox3_cp1	GTR+I+G
Partition 2	atp6_cp2, cox2_cp2, cytb_cp2, cox3_cp2	GTR+I+G
Partition 3	atp6_cp3, atp8_cp3, cox2_cp3, cytb_cp3, nad3_cp3, nad6_cp3, cox3_cp3	GTR+G
Partition 4	atp8_cp1, nad2_cp1, nad3_cp1, nad6_cp1	GTR+I+G
Partition 5	cox1_cp1	GTR+I+G
Partition 6	cox1_cp2	GTR+I+G
Partition 7	cox1_cp3	GTR+I+G
Partition 8	nad1_cp1, nad4_cp1, nad4l_cp1, nad5_cp1	GTR+I+G
Partition 9	nad1_cp2, nad4_cp2, nad4l_cp2, nad5_cp2	GTR+I+G
Partition 10	nad1_cp3, nad4_cp3, nad4l_cp3, nad5_cp3	GTR+I+G
Partition 11	nad2_cp2, nad3_cp2, nad6_cp2	GTR+I+G
Partition 12	nad2_cp3	GTR+G

Note: "cp_1" representing the first codon position, "cp_2" representing the second codon position, and "cp_3" representing the third codon position.

Abbreviations used in the Best Model: GTR, General-Time-Reversible model; I, invariant sites; G, discrete Gamma distribution; MTREV, the transition probability matrix of the REV model for mtDNA-encoded proteins; F, the actual frequencies of the protein under study.

Table S3. (B) The partition sechemes and best-fitting models selected by PartitionFinder for dataset of 52taxa_PCG_AA.

52taxa_PCG_AA		
Subset	Subset Partitions	Best Model
Partition 1	atp6, cox2, cox3, cytb	MTREV+I+G+F
Partition 2	atp8, nad2, nad3, nad6	MTREV+I+G+F
Partition 3	cox1	MTREV+I+G+F
Partition 4	nad1, nad4, nad4l, nad5	MTREV+I+G+F

Table S3. (C) The partition schemes and best-fitting models selected by PartitionFinder for dataset of 52taxa_PCGDegen.

52taxa_PCGDegen		
Subset	Subset Partitions	Best Model
Partition 1	atp6_cp1, cox2_cp1, cytb_cp1, nad3_cp1, cox3_cp1	GTR+I+G
Partition 2	atp6_cp2, cox2_cp2, cytb_cp2, cox3_cp2	GTR+I+G
Partition 3	atp6_cp3, nad2_cp3, nad3_cp3, nad6_cp3	GTR+G
Partition 4	atp8_cp1, atp8_cp3, nad2_cp1, nad6_cp1	GTR+I+G
Partition 5	atp8_cp2, nad1_cp3, nad2_cp2, nad3_cp2, nad6_cp2	GTR+G
Partition 6	cox1_cp1	GTR+G
Partition 7	cox1_cp2	GTR+I+G
Partition 8	cox1_cp3, cox2_cp3, cytb_cp3, cox3_cp3	GTR+G
Partition 9	nad1_cp1, nad4_cp1, nad4l_cp1, nad5_cp1	GTR+I+G
Partition 10	nad1_cp2, nad4_cp2, nad4l_cp2, nad5_cp2	GTR+I+G
Partition 11	nad4_cp3, nad4l_cp3, nad5_cp3	GTR+I+G

Table S3. (D) The partition schemes and best-fitting models selected by PartitionFinder for dataset of 52taxa_PCGRNA.

52taxa_PCGRNA		
Subset	Subset Partitions	Best Model
Partition 1	atp6_cp1, atp8_cp2, cox2_cp1, cytb_cp1, cox3_cp1	GTR+I+G
Partition 2	atp6_cp2, cox2_cp2, cytb_cp2, cox3_cp2	GTR+I+G
Partition 3	atp6_cp3, atp8_cp3, cox2_cp3, cytb_cp3, nad3_cp3, nad6_cp3, cox3_cp3	GTR+G
Partition 4	atp8_cp1, nad2_cp1, nad3_cp1, nad6_cp1	GTR+I+G
Partition 5	cox1_cp1	GTR+I+G
Partition 6	cox1_cp2	GTR+I+G
Partition 7	cox1_cp3	GTR+I+G
Partition 8	Ala, Cys, Ser1, Ser2, nad1_cp1, nad4l_cp1	GTR+I+G
Partition 9	nad1_cp2, nad4_cp2, nad4l_cp2, nad5_cp2	GTR+I+G
Partition 10	nad1_cp3, nad4_cp3, nad4l_cp3, nad5_cp3	GTR+I+G
Partition 11	nad2_cp2, nad3_cp2, nad6_cp2	GTR+I+G
Partition 12	nad2_cp3	GTR+G
Partition 13	nad4_cp1, nad5_cp1	GTR+I+G
Partition 14	12S	GTR+I+G
Partition 15	16S, Val	GTR+I+G
Partition 16	Arg, Asn, Gly, Leu2, Lys, Met, Thr, Trp	GTR+I+G
Partition 17	Asp, Glu, Ile, Leu1	GTR+G
Partition 18	Gln, His, Phe, Pro, Tyr	GTR+I+G

Table S3. (E) The partition schemes and best-fitting models selected by PartitionFinder for dataset of 52taxa_PCGDegenRNA.

52taxa_PCGDegenRNA		
Subset	Subset Partitions	Best Model
Partition 1	atp6_cp1, cox2_cp1, cytb_cp1, nad3_cp1, cox3_cp1	GTR+I+G
Partition 2	atp6_cp2, cox2_cp2, cytb_cp2, cox3_cp2	GTR+I+G
Partition 3	atp6_cp3, cox1_cp3, cox2_cp3, cytb_cp3, nad3_cp3, cox3_cp3	GTR+G
Partition 4	atp8_cp1, atp8_cp3, nad2_cp1, nad6_cp1	GTR+I+G
Partition 5	Ala, Cys, Val, atp8_cp2	GTR+I+G
Partition 6	cox1_cp1	GTR+I+G
Partition 7	cox1_cp2	GTR+I+G
Partition 8	nad1_cp1, nad4_cp1, nad4l_cp1, nad5_cp1	GTR+I+G
Partition 9	nad1_cp2, nad4_cp2, nad4l_cp2, nad5_cp2	GTR+I+G
Partition 10	nad1_cp3, nad2_cp2, nad3_cp2, nad6_cp2	GTR+G
Partition 11	nad2_cp3, nad6_cp3	GTR+G
Partition 12	nad4_cp3, nad4l_cp3, nad5_cp3	GTR+I+G
Partition 13	12S, 16S	GTR+I+G
Partition 14	Arg, Asn, Ile, Lys, Met, Ser1, Ser2	GTR+I+G
Partition 15	Asp, Glu, Gly, Leu1, Leu2, Thr, Trp	GTR+G
Partition 16	Gln, His, Phe, Pro, Tyr	GTR+I+G

Table S3. (F) The partition schemes and best-fitting models selected by PartitionFinder for dataset of 43taxa_PCG.

43taxa_PCG		
Subset	Subset Partitions	Best Model
Partition 1	atp6_cp1, atp8_cp2, cox2_cp1, cytb_cp1, cox3_cp1	GTR+I+G
Partition 2	atp6_cp2, cox2_cp2, cytb_cp2, cox3_cp2	GTR+I+G
Partition 3	atp6_cp3, atp8_cp3, cox2_cp3, cytb_cp3, nad3_cp3, nad6_cp3, cox3_cp3	GTR+G
Partition 4	atp8_cp1, nad2_cp1, nad3_cp1, nad6_cp1	GTR+I+G
Partition 5	cox1_cp1	GTR+I+G
Partition 6	cox1_cp2	GTR+I+G
Partition 7	cox1_cp3	GTR+I+G
Partition 8	nad1_cp1, nad4_cp1, nad4l_cp1, nad5_cp1	GTR+I+G
Partition 9	nad1_cp2, nad4_cp2, nad4l_cp2, nad5_cp2	GTR+I+G
Partition 10	nad1_cp3, nad4_cp3, nad4l_cp3, nad5_cp3	GTR+I+G
Partition 11	nad2_cp2, nad3_cp2, nad6_cp2	GTR+I+G
Partition 12	nad2_cp3	GTR+G

Table S3. (G) The partition sechemes and best-fitting models selected by PartitionFinder for dataset of 43taxa_PCG_AA.

43taxa_PCG_AA		
Subset	Subset Partitions	Best Model
Partition 1	atp6, cox2, cox3, cytb	MTREV+I+G+F
Partition 2	atp8, nad2, nad3, nad6	MTREV+I+G+F
Partition 3	cox1	MTREV+I+G+F
Partition 4	nad1, nad4, nad4l, nad5	MTREV+I+G+F

Table S3. (H) The partition schemes and best-fitting models selected by PartitionFinder for dataset of 43taxa_PCGDegen.

43taxa_PCGDegen		
Subset	Subset Partitions	Best Model
Partition 1	atp6_cp1, cox2_cp1, cytb_cp1, nad3_cp1, cox3_cp1	GTR+I+G
Partition 2	atp6_cp2, cox2_cp2, cytb_cp2, cox3_cp2	GTR+I+G
Partition 3	atp6_cp3, atp8_cp2, nad3_cp3	GTR+G
Partition 4	atp8_cp1, atp8_cp3, nad2_cp1, nad6_cp1	GTR+I+G
Partition 5	cox1_cp1	GTR+I+G
Partition 6	cox1_cp2	GTR+I+G
Partition 7	cox1_cp3, cox2_cp3, cytb_cp3, cox3_cp3	GTR+I+G
Partition 8	nad1_cp1	GTR+G
Partition 9	nad1_cp2, nad4_cp2, nad4l_cp2, nad5_cp2	GTR+I+G
Partition 10	nad1_cp3, nad4_cp3, nad4l_cp3, nad5_cp3	GTR+G
Partition 11	nad2_cp2, nad3_cp2, nad6_cp2	GTR+I+G
Partition 12	nad2_cp3, nad6_cp3	GTR+G
Partition 13	nad4_cp1, nad4l_cp1, nad5_cp1	GTR+I+G

Table S3. (I) The partition schemes and best-fitting models selected by PartitionFinder for dataset of 43taxa_PCGRNA.

43taxa_PCGRNA		
Subset	Subset Partitions	Best Model
Partition 1	Ala, Cys, Gln, Val, atp6_cp1, atp8_cp2	GTR+I+G
Partition 2	atp6_cp2, cox2_cp2, cytb_cp2, cox3_cp2	GTR+I+G
Partition 3	atp6_cp3, atp8_cp3, cox2_cp3, cytb_cp3, nad3_cp3, nad6_cp3, cox3_cp3	GTR+G
Partition 4	atp8_cp1, nad2_cp1, nad3_cp1, nad6_cp1	GTR+I+G
Partition 5	cox1_cp1	GTR+I+G
Partition 6	cox1_cp2	GTR+I+G
Partition 7	cox1_cp3	GTR+I+G
Partition 8	cox2_cp1, cytb_cp1, cox3_cp1	GTR+I+G
Partition 9	nad1_cp1, nad4_cp1, nad4l_cp1, nad5_cp1	GTR+I+G
Partition 10	nad1_cp2, nad4_cp2, nad4l_cp2, nad5_cp2	GTR+I+G
Partition 11	nad1_cp3, nad4_cp3, nad4l_cp3, nad5_cp3	GTR+I+G
Partition 12	nad2_cp2, nad3_cp2, nad6_cp2	GTR+I+G
Partition 13	nad2_cp3	GTR+G
Partition 14	12S, 16S	GTR+I+G
Partition 15	Arg, Asn, Gly, Ile, Lys, Met, Ser1, Ser2, Thr, Trp	GTR+I+G
Partition 16	Asp, Glu, His, Leu1, Leu2, Phe, Pro, Tyr	GTR+I+G

Table S3. (J) The partition schemes and best-fitting models selected by PartitionFinder for dataset of 43taxa_PCGDegenRNA.

43taxa_PCGDegenRNA		
Subset	Subset Partitions	Best Model
Partition 1	atp6_cp1, cox2_cp1, cytb_cp1, nad3_cp1, cox3_cp1	GTR+I+G
Partition 2	atp6_cp2, cox2_cp2, cytb_cp2, cox3_cp2	GTR+I+G
Partition 3	atp6_cp3, cox2_cp3, cytb_cp3, nad1_cp3, nad4_cp3, nad4l_cp3, nad5_cp3, cox3_cp3	GTR+I+G
Partition 4	atp8_cp1, atp8_cp3, nad2_cp1, nad6_cp1	GTR+I+G
Partition 5	atp8_cp2, nad2_cp2, nad3_cp2, nad3_cp3, nad6_cp2	GTR+G
Partition 6	cox1_cp1	GTR+G
Partition 7	cox1_cp2	GTR+I+G
Partition 8	cox1_cp3, nad1_cp2	GTR+G
Partition 9	nad1_cp1, nad4_cp1, nad4l_cp1, nad5_cp1	GTR+I+G
Partition 10	nad2_cp3, nad6_cp3	GTR+G
Partition 11	nad4_cp2, nad4l_cp2, nad5_cp2	GTR+I+G
Partition 12	12S, 16S, Val	GTR+I+G
Partition 13	Ala, Cys, Gln, Ser1, Ser2	GTR+I+G
Partition 14	Arg, Asn, Asp, Glu, Gly, His, Ile, Leu1, Leu2, Lys, Met, Phe, Pro, Thr, Trp, Tyr	GTR+I+G