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Characterization of the complete mitochondrial genome of *Loxocephala sichuanensis* (Hemiptera: Eurybrachidae) with the phylogenetic analyses of Fulgoromorpha

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Little is known about the mitochondrial genome of the family Eurybrachidae, with only two species sequenced. This study added one more mitogenome of *Loxocephala sichuanensis* in this family. The mitochondrial genome length of this species was 15,605 bp, consisting of 37 genes: 13 PCGs, 2 rRNAs, 22 tRNAs, and a control region. An unusually high A + T content, reaching 94.3% at the third codon position of 13 PCGs in *Loxocephala*, was found in Eurybrachidae, which was the highest among all planthoppers, especially on N-strand. Three tandem repeat regions were detected in the control region. Phylogenetic analyses based on complete mitochondrial genome sequences from 145 species (encompassing 18 planthopper families and 135 species in Fulgoromorpha as ingroup, and 6 other non-planthopper families in Auchenorrhyncha as outgroup) were conducted. Six datasets (PCG123R24, PCG123R2, PCG123, PCG12R24, PCG12R2, PCG12) were established to investigate the influence of 22 tRNAs and the third codon of the 13 PCGs of mitogenome for phylogeny analyses. Both Maximum likelihood and Bayesian trees supported the monophyly of the superfamilies Delphacoidea and Fulgoroidea. Delphacoidea, consisting of Cixiidae and Delphacidae as sister group, was in the basal position of Fulgoromorpha. In Fulgoroidea, the families Meenoplidae and Kinnaridae, Dictyopharidae and Fulgoridae, Acanaloniidae and Tropiduchidae were sister groups which were strongly supported. Caliscelidae was close to the sister group Lophopidae with Eurybrachidae. The four families Flatidae, Nogodinidae, Ricaniidae and Issidae were closely related. The position of Tettigometridae was uncertain. Derbidae and Achilidae form a sister group when 22 tRNAs were included in the phylogeny. The joining of the tRNA sequences of mitochondrial genome enhanced the stability of family-level nodes and adjusted some phylogenetic positions, highlighting the significant role of joining tRNAs in phylogenetic analyses. Including or excluding the third codon position of 13 PCGs generally did not affect the overall phylogenetic structures of Fulgoromorpha.

Keywords Auchenorrhyncha, Molecular phylogeny, Maximum likelihood, Bayesian analysis

Fulgoromorpha, a captivating insect group within the order Auchenorrhyncha, consists of 21 extant families and over 14,000 species worldwide¹. Previously classified all as Fulgoroidea Latreille, 1807 for recent taxa, it has recently been divided into two superfamilies: Delphacoidea Leach, 1815 and Fulgoroidea^{2,3}. These attractive planthoppers are all phytophagous insects, adults sucking on leaves, stems and roots, while some nymphs sucking on the fluid in fungal hyphae^{4,5}. They convert the unabsorbed sugars into a delicate substance called honeydew, which also inadvertently promotes the growth of mold, thus causing unexpected secondary damage

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to the plant⁶. Planthopper also serve as an important carrier of plant pathogens that spread plant diseases^{6,7}. Consequently, several of them have become economic pests^{6,7}.

The family Eurybrachidae Stål, 1862 is a relatively small group within the superfamily Fulgoroidea consisting of 40 genera and 210 species worldwide and divided into two subfamilies and six tribes¹. The species *Loxocephala sichuanensis* Chou and Huang, 1985 is a particular and rare species found only in the western part of Sichuan, China in genus *Loxocephala* Schaum, 1850 of tribe Loxocephalini Schmidt, 1908 in subfamily Eurybrachinae Stål, 1862 of the family Eurybrachidae⁸. This species was initially described as a subspecies *L. sinica sichuanensis* Chou and Huang, 1985⁹, however later re-evaluated and upgraded to species status based on male genitalia by Wang and Wang⁸. *L. sichuanensis* can be easily recognized by these morphological characteristics: tegmina tawny, basal 2/5 of the costal margin with a broad castaneous band, clavus area decorated with several white spots, apical part of tegmina interspersed with around 20 uniform black spots; the vertex, pronotum, and mesonotum are all tawny; frons is orange; legs are red⁸.

Previous studies in Eurybrachidae mostly focused on the description of new genera and species, but molecular studies are scarce, especially for mitochondrial gene studies. It is crucial to recognize that mitochondrial genes represent the most prevalent insect sequences in genetic data, and the entire mitochondrial genome plays a key role in various fields such as molecular systematics, population genetics, phylogeography, diagnostics, and molecular evolutionary studies¹⁰. So far, only 44 partial sequences obtained by Sanger sequencing from nine Eurybrachidae species are available on NCBI (<https://www.ncbi.nlm.nih.gov/>)¹¹, while only two species *Loxocephala perpunctata* Jacobi, 1944 (GenBank accession number: MW848343) and *Klapperibrachys cremeri* (GenBank accession number: NC_084361) with complete mitochondrial gene sequenced and published in Eurybrachidae^{12,13}.

In this study, the mitogenome of *Loxocephala sichuanensis*, a local endemic species in Sichuan, China, was added and analyzed in Eurybrachidae. A large dataset phylogeny in Fulgoromorpha, based on all the available mitochondrial genomes from NCBI, was conducted using both Maximum likelihood (ML) and Bayesian inference (BI) methods to explore the relationships within different families in planthoppers. Besides of the 13 protein coding (PCGs) genes and 2 ribosomal RNA (rRNA) genes of the mitogenome commonly used for phylogeny, the sequences of the 22 transfer RNA (tRNA) genes were also added to the phylogeny analyses which may improve the resolution and accuracy of the nodes¹⁰. Due to the high A or T bias in the third codon of the protein coding genes in the mitogenome, the inclusion or exclusion of the third codon of the 13 PCGs was also tested to examine its influence on the phylogeny of Fulgoromorpha. Finally, six different datasets (1. PCG123R24: 13 PCGs + 22 tRNAs + 2 rRNAs; 2. PCG123R2: 13 PCGs + 2 rRNAs; 3. PCG123: 13 PCGs; 4. PCG12R24: First and second codon positions of 13 PCGs + 22 tRNAs + 2 rRNAs; 5. PCG12R2: First and second codon positions of 13 PCGs + 2 rRNAs; 6. PCG12: First and second codon positions of 13 PCGs) were used for phylogenetic analyses in this study.

Results and discussion

Mitochondrial genome structure and composition of *Loxocephala sichuanensis*

The complete mitochondrial genome length of *L. sichuanensis* was 15,605 base pairs (bp) (GenBank accession number: OR663919). It included 37 genes: 13 PCGs, 2 rRNAs, 22 tRNAs, and a control region (Supplementary file 1). This finding is comparable to other reported mitochondrial genomes in insects¹⁰. Most of the genes (9 PCGs, 14 tRNAs) were located on the J-strand, while the remaining genes (4 PCGs, 2 rRNAs, 8 tRNAs) were on the N-strand (Table 1). The mitogenome's base composition was 46.5% adenine (A), 34.1% thymine (T), 12.1% cytosine (C), and 7.3% guanine (G), with an overall A + T content of 80.6%. This proportion is comparable to levels identified in other sequenced Eurybrachidae species^{12,13}. Additionally, the genome displayed a positive AT skew (0.154) and a negative GC skew (− 0.245). The strong A + T bias may result from mutational pressure, a phenomenon also observed in other mitochondrial genomes in Hemiptera¹⁴.

The combined length of the 13 PCGs of *L. sichuanensis* was 10,945 bp. The overall PCGs exhibited a negative AT skew (− 0.119) and GC skew (− 0.021), while the PCGs on J-strand had a positive AT skew (0.056). The general A + T content in the third codon position of the 13 PCGs of the two Eurybrachidae species, *L. sichuanensis* and *L. perpunctata*, was significantly higher than in other Fulgoromorpha species (Fig. 1). Both species exhibited an A + T content of 94.3% in the third codon position, which was the highest among the 135 Fulgoromorpha species (Fig. 1). Additionally, the A + T content of the third codon on the N-strand was exceptionally higher than on the J-strand (Fig. 1). All PCGs started with codons ATN, except for *nad5*, which started with the codon GTG (Table 1). The four genes *cox1*, *cox2*, *atp6* and *cox3* used an incomplete T as the stop codon (Table 1), which may be converted to TAA through polyadenylation after transcription¹⁵.

The total length of the 22 tRNAs of *L. sichuanensis* was 1,395 bp. The gene arrangement of tRNAs (Table 1) was the same as the other species *L. perpunctata* in *Loxocephala*¹². Both species exhibited positive AT skew and GC skew for the total tRNA genes. The 22 tRNAs had only 18 bp differences between the above two species. Most of the tRNAs could be folded into the typical trilobal structure, except for tRNA-Ser1 and tRNA-Val, which were missing DHU stems (Supplementary file 2). The mismatched types in the secondary structure of tRNAs contained A-A, A-C, A-G and U-U, with A-A predominating.

The two rRNA genes, respectively located between *trnL1* and *trnV*, and between *trnV* and the A + T rich region (Table 1), with a total length of 1,937 bp. They had a high A + T content (80.6%), a negative AT skew and a positive GC skew.

The control region, located between *rrnS* and *trnI* on the J-strand, was 1,192 bp (Table 1), with the A + T content reaching to 82%. It contained three tandem repeat regions: a 144 bp unit repeated 2.1 times, then a 16 bp unit repeated 2.1 times, and finally a 392 bp repeat region with the unit "TTTTTCCAAATTTTGTCACCTT"

Gene	Position		Size	Intergenic nucleotides	Codon		Strand
	From	To			Start	Stop	
<i>trnI</i>	1	63	63				J
<i>trnQ</i>	64	132	69				N
<i>trnM</i>	132	195	64	– 1			J
<i>nad2</i>	196	1161	966		ATT	TAA	J
<i>trnW</i>	1160	1228	69	– 2			J
<i>trnC</i>	1221	1281	61	– 8			N
<i>trnY</i>	1285	1345	61	3			N
<i>cox1</i>	1347	2880	1534	1	ATG	T	J
<i>trnL2</i>	2882	2948	67	1			J
<i>cox2</i>	2950	3622	673	1	ATA	T	J
<i>trnK</i>	3623	3691	69				J
<i>trnD</i>	3692	3754	63				J
<i>atp8</i>	3755	3907	153		ATA	TAA	J
<i>atp6</i>	3901	4552	652	– 7	ATG	T	J
<i>cox3</i>	4553	5333	781		ATG	T	J
<i>trnG</i>	5334	5396	63				J
<i>nad3</i>	5397	5744	348		ATA	TAG	J
<i>trnA</i>	5743	5805	63	– 2			J
<i>trnR</i>	5809	5867	59	3			J
<i>trnN</i>	5869	5932	64	1			J
<i>trnS1</i>	5932	5990	59	– 1			J
<i>trnE</i>	5990	6052	63	– 1			J
<i>trnF</i>	6051	6113	63	– 2			N
<i>nad5</i>	6113	7795	1683	– 1	GTG	TAA	N
<i>trnH</i>	7796	7857	62				N
<i>nad4</i>	8021	9349	1329	163	ATG	TAG	N
<i>nad4L</i>	9343	9615	273	– 7	ATG	TAA	N
<i>trnT</i>	9618	9682	65	2			J
<i>trnP</i>	9684	9747	64	1			N
<i>nad6</i>	9749	10,240	492	1	ATA	TAA	J
<i>cytb</i>	10,233	11,354	1122	– 8	ATG	TAG	J
<i>trnS2</i>	11,353	11,416	64	– 2			J
<i>nad1</i>	11,417	12,355	939		ATG	TAA	N
<i>trnL1</i>	12,357	12,419	63	1			N
<i>rrnL</i>	12,420	13,621	1202				N
<i>trnV</i>	13,622	13,678	57				N
<i>rrnS</i>	13,679	14,413	735				N
A + T rich region	14,414	15,605	1192				J

Table 1. Mitogenomic organization of *L. sichuanensis*.

repeated 18.7 times (Fig. 2) (Supplementary file 3). This occurrence of three repeats is uncommon in Fulgoromorpha, where most species have only one or two repeats^{16,17}, but some species in Flatidae could reach to four¹⁸.

L. sichuanensis had a total of 42 bp overlaps across 12 genes, with the longest overlaps (8 bp) occurring between *trnW* and *trnC*, and between *nad6* and *cytb* (Table 1). The total length of intergenic spacers was 178 bp, with the longest spacer (163 bp) located between *trnH* and *nad4* (Table 1).

Phylogenetic analyses of Fulgoromorpha

The tree topologies generated from six different data matrices (PCG123R24, PCG123R2, PCG123, PCG12R24, PCG12R2, PCG12) (Supplementary files 4–15) showed some variation among families in Fulgoromorpha but were generally consistent. Both Maximum likelihood (ML) and Bayesian inference (BI) analyses produced well-resolved phylogenetic trees with moderate to strong branch value support (Figs. 3, 4).

In all the analyses under the site-homogeneous models, the ingroup Fulgoromorpha was always well supported as a monophyletic group with strong Bootstrap (BS) support in ML trees and strong posterior probability (PP) support in BI trees (Figs. 3, 4). The ingroup was separated into two large clades: the first clade (BS = 100, PP = 1) included the families Cixiidae and Delphacidae, representing the monophyletic superfamily Delphacoidea which recently separated from Fulgoroidea in 2022 and 2023 by Bourgoin and Szewdo^{2,3} according to the

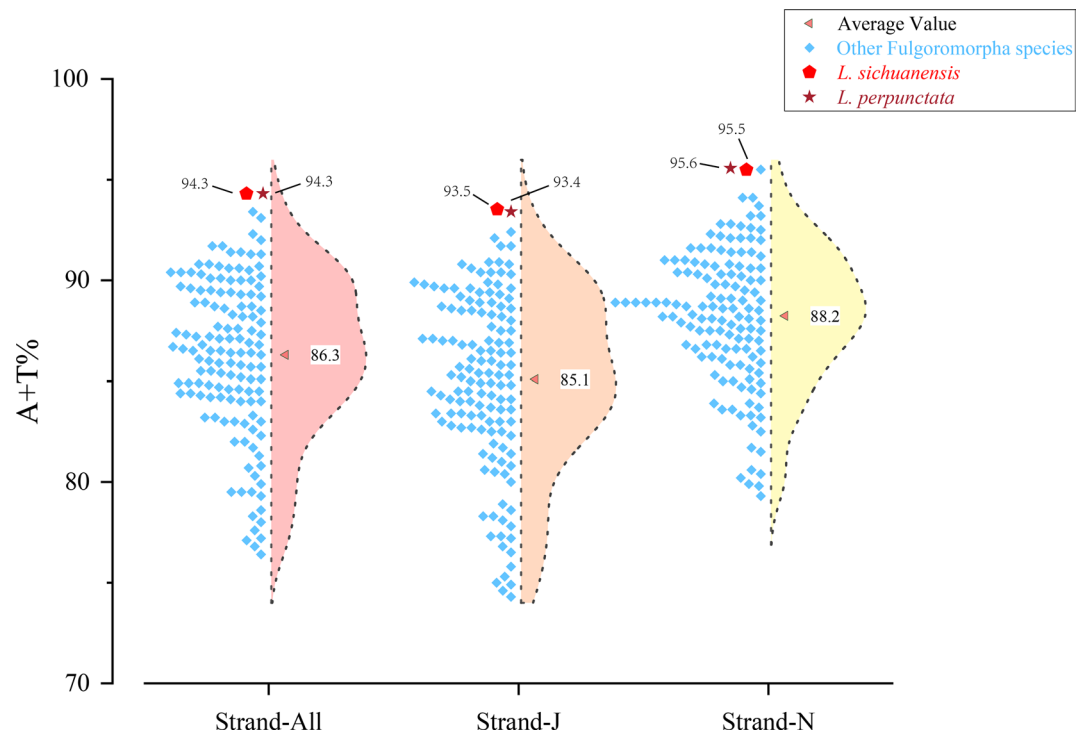


Fig. 1. The A + T content in the third codon position of 13 PCGs of 135 Fulgoromorpha species.

Loxocephala sichuanensis

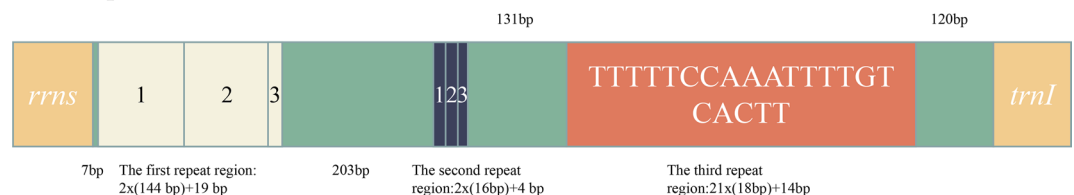


Fig. 2. Organization of the A + T rich region of *L. sichuanensis*. The light yellow box, dark blue box and red box represent respectively the first, the second and the third repeat regions; the numbers in the box represent the number of sequence repetitions, and the uppercase letters indicate the repeated sequences.

morphological characters; the second large clade (BS = 100, PP = 1) grouped the remaining 16 Fulgoromorpha families together, representing the monophyletic superfamily Fulgoroidea.

Within the superfamily Fulgoroidea, the Meenoplidae + Kinnaridae clade was consistently in the most basal position, with strong support (BS = 100, PP = 1), sister to the remaining Fulgoroidea families. The monophyly and sister relationship of Dictyopharidae and Fulgoridae were strongly supported (BS = 100, PP = 1) across all trees.

A noteworthy finding was the sister relationship between Derbidae and Achilidae, which was supported in all the BI trees and only in datasets that included 22 tRNAs in ML tree. These families were mostly sister to the Dictyopharidae + Fulgoridae clade, with strong support for their monophyly. The families Acanaloniidae and Tropiduchidae were consistently identified as sister taxa, forming a basal group (BS = 100, PP = 1) to all other families: Tettigometridae, Caliscelidae, Lophopidae, Eurybrachidae, Nogodinidae, Ricaniidae, Flatidae, and Issidae.

However, the position of Tettigometridae was uncertain within this clade. In Bayesian trees, Tettigometridae was positioned at the base of Lophopidae, Eurybrachidae, and Caliscelidae. In ML trees, this positioning was only observed in the PCG123R24, PCG123, PCG12R24, and PCG12R2 datasets. In the other two datasets (PCG123R2 and PCG12R2), Tettigometridae was sister to Flatidae.

Eurybrachidae, including *L. sichuanensis*, consistently formed a stable clade (Caliscelidae + (Lophopidae + Eurybrachidae)). This result verified the previous morphological study by Emeljanov¹⁹ and the molecular study based on 18S, 28S, H3 and *Wingless* genes for the sister group relationships of the families Eurybrachidae and Lophopidae²⁰.

The last major clade in Fulgoroidea always comprised the four families Nogodinidae, Ricaniidae, Flatidae, and Issidae. The sister relationship between Nogodinidae and Ricaniidae received strong support in all analyses, except for the ML tree based on the PCG12R24 dataset, which showed the topology

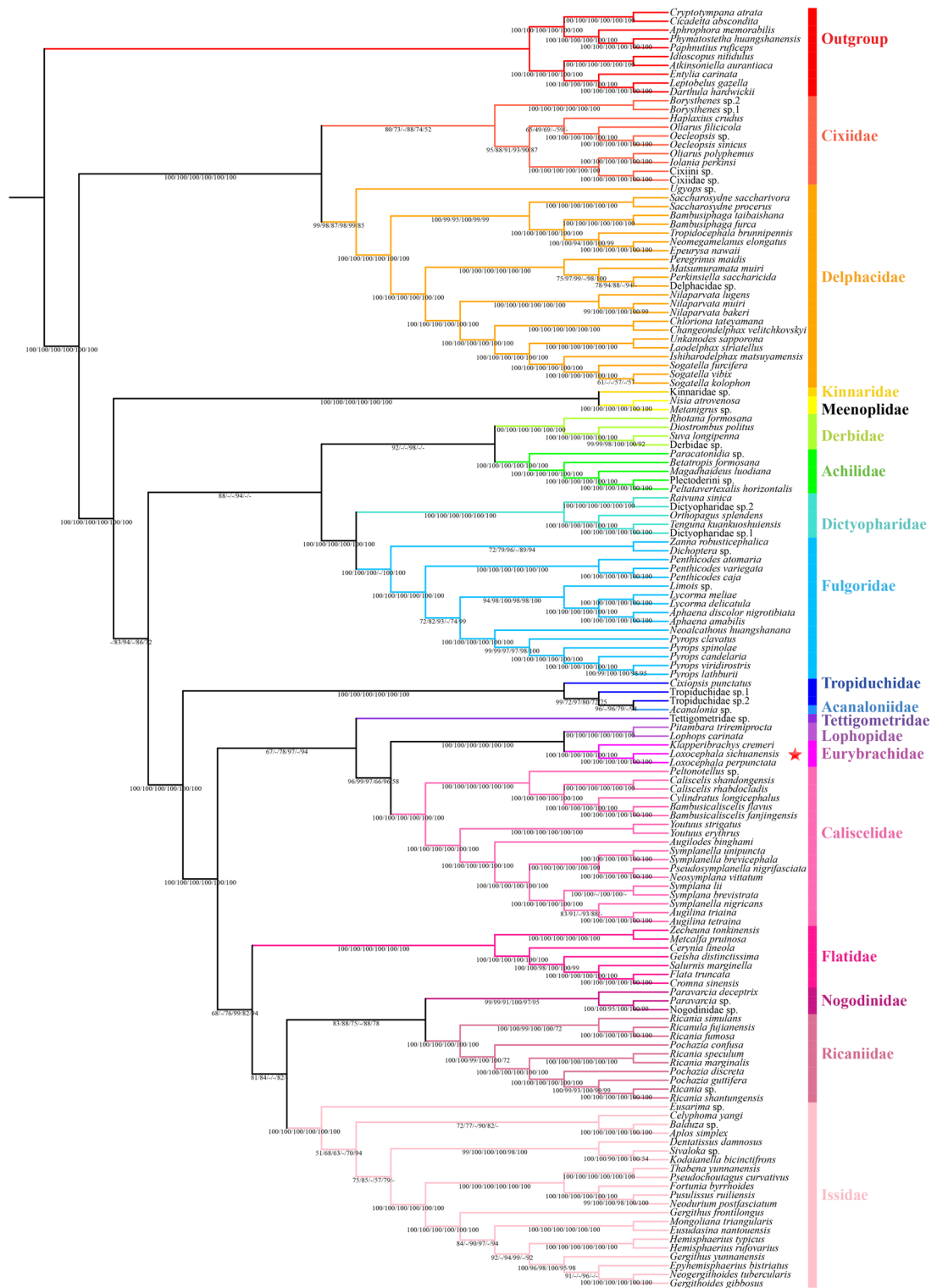


Fig. 3. Phylogenetic tree produced from ML analysis. Numbers on branches are bootstrap (BS) support values, respectively for datasets PCG123R24, PCG123R2, PCG123, PCG12R24, PCG12R2, PCG12.

(Nogodinidae + (Ricaniidae + Flatidae)) with low support, indicating that it should not be considered. The observed topologies generally supported the arrangement (Flatidae + ((Nogodinidae + Ricaniidae) + Issidae)), unless rRNAs were excluded from the datasets. The monophyly of these four families were supported in this study.

The comparative phylogeny study for different matrices

The analyses revealed that in the Bayesian tree topology which included the 22 tRNA sequences, the tree topology differed from the trees generated from other datasets. Notably, the inclusion of tRNA sequences resulted in

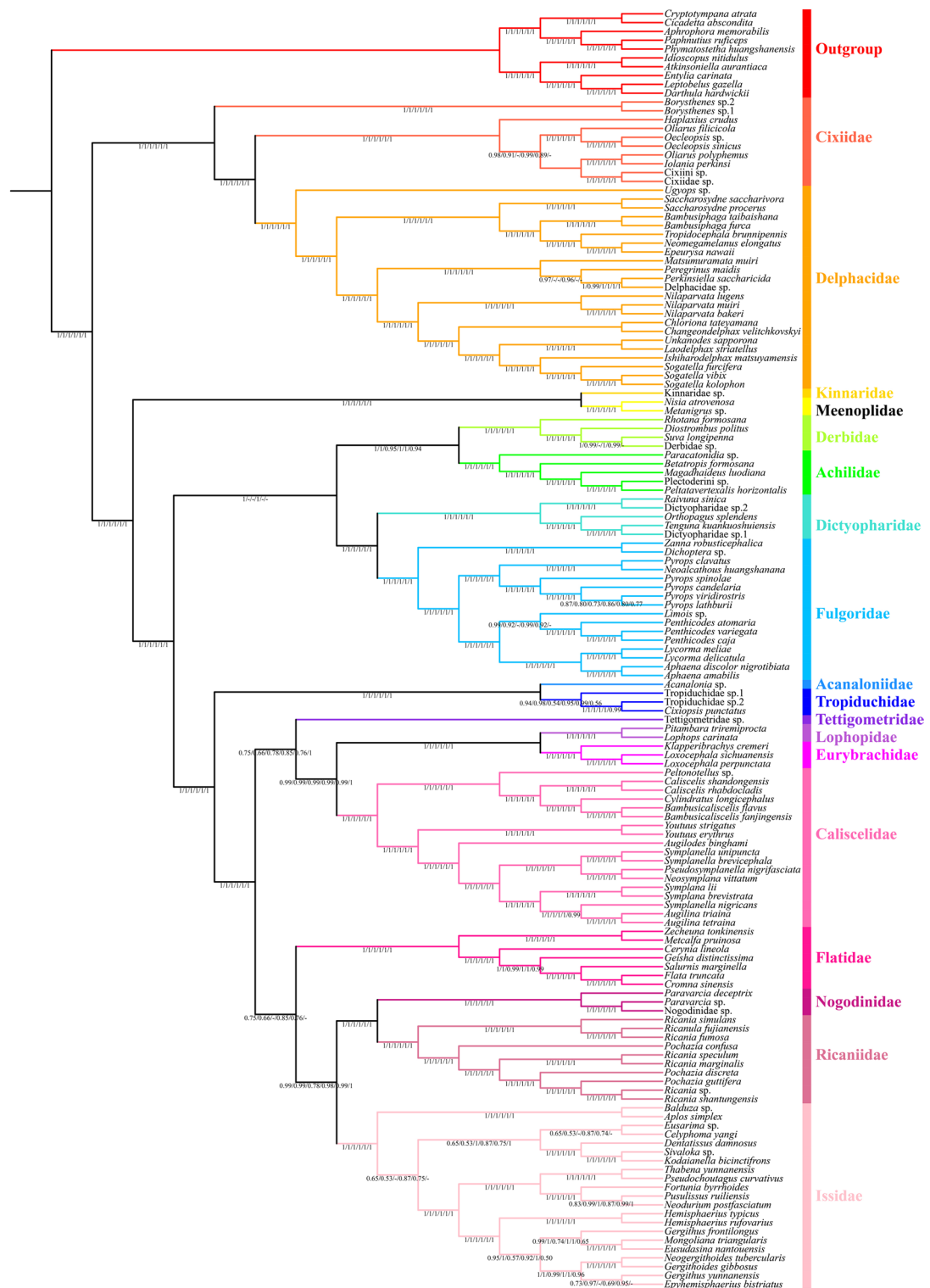


Fig. 4. Phylogenetic tree produced from BI analysis. Numbers on branches are Bayesian posterior probabilities (PP) support values, respectively for datasets PCG123R24, PCG123R2, PCG123, PCG12R24, PCG12R2, PCG12.

a large clade with the sister group relationship of (Derbidae + Achilidae) and (Fulgoridae + Dictyopharidae), an unprecedented topology found for the first time in this study.

In younger branches, joining tRNA sequences significantly altered the topology, particularly within some branches of Issidae and Tropiduchidae. The addition of tRNA sequences also increased the stability of higher-level nodes. For example, the common node of Tettigometridae, Lophopidae, Eurybrachidae, and Caliscelidae showed higher PP values, 0.75 and 0.85 in datasets PCG123R24 and PCG12R24, respectively, compared to 0.66 and 0.76 in datasets without tRNA sequences (PCG123R2 and PCG12R2) (Figs. 3, 4). Similarly, the node summarizing

showed that the (Nogodinidae + Ricaniidae + Issidae + Flatidae) cluster has PP values of 0.75 and 0.85 in the datasets PCG123R24 and PCG12R24, compared to 0.66 and 0.76 in the reduced tRNA datasets (PCG123R2, PCG12R2) (Figs. 3, 4). It is evident that a dataset comprising only 13 PCG sequences is insufficient to produce a topological structure similar to that of the trees obtained by incorporating tRNA or rRNA datasets²¹, such as the 19 nodes of the Issidae family in BI tree.

When comparing relationships across different datasets, we found that including two rRNAs and 22 tRNAs altered the position of the family Flatidae in Fulgoromorpha. It was no longer appeared as a sister group to Issidae when only 13 PCGs were used (datasets PCG123 and PCG12), but was positioned at the base of the ((Nogodinidae + Ricaniidae) + Issidae) clade in the other four datasets that included more genes, either contained tRNAs or rRNAs.

In the BI tree analyses, the structures of PCG12 and PCG123 are comparable, the same result occurred when compared PCG12R2 to PCG123R2, and PCG123R24 to PCG12R24. This similarity indicates that incorporating the third codon position did not affect the overall structure. However, the inclusion of two rRNA genes altered the structural relationships in the PCG12 and PCG123 datasets, changing the topology from (Nogodinidae + Ricaniidae) + (Issidae + Flatidae) to Flatidae + ((Nogodinidae + Ricaniidae) + Issidae). The addition of 22 tRNA genes in the PCG123R24 and PCG12R24 datasets preserved this revised branch structure but modified the (Derbidae + Achilidae) + (Fulgoridae + Dictyopharidae) branch, which was not present in the earlier datasets.

In the ML tree analyses, Derbidae was positioned at the base of Achilidae or Fulgoridae + Dictyopharidae when only PCGs included. However, with the inclusion of 22 tRNA genes in the PCG123R24 and PCG12R24 datasets, its position shifted to a (Derbidae + Achilidae) + (Fulgoridae + Dictyopharidae) structure. The branch structure of Flatidae, Nogodinidae, Ricaniidae, and Issidae also changed when joining tRNAs. The structure (Nogodinidae + Ricaniidae) + (Issidae + Flatidae) in PCG123 and PCG12 datasets changed to Flatidae + ((Nogodinidae + Ricaniidae) + Issidae) in PCG123R24 and PCG12R24 datasets, and this new topology remained consistent regardless of the addition of rRNA or tRNA genes.

Conclusion

The mitogenome of *Loxocephala sichuanensis* in family Eurybrachidae from Fulgoroidea was sequenced, assembled and annotated. The structure of mitogenome for this species was analyzed. An unexpected finding was that the notably high A + T content at the third codon position of 13 PCGs, particularly on the N-strand of *Loxocephala* in Eurybrachidae within Fulgoromorpha. Phylogenetic analysis based on the mitogenomes from 145 species, including 18 planthopper families as ingroup and 6 outgroup families, was conducted within Auchenorrhyncha. The establishment of the superfamilies Delphacoidea and Fulgoroidea was confirmed. Relationships between the different families in Fulgoromorpha were explored. Adding 22 tRNAs into dataset showed a more stable result and higher node values in the phylogenetic analyses. Although some relationships within Fulgoromorpha are still uncertain, increasing the sample size and adding more molecular data may solve these issues in the future.

Materials and methods

Sample preparation, DNA extraction and sequencing

The specimen of *L. sichuanensis* was collected from the Wolong Nature Reserve in Sichuan Province, China. After collection, the specimen was promptly conserved in alcohol and maintained at a temperature of -20 degrees at the China West Normal University, Sichuan, China. Following an accurate morphological identification under the stereomicroscope with photos of type specimen of *L. sichuanensis* in Wang and Wang⁸, the total genomic DNA was extracted from the thorax and legs of the specimen using an Animal Tissue DNA Extraction kit. The whole mitochondrial genome sequence was generated using high-throughput sequencing (Illumina NovaSeq6000 platform with insert size 400 bp and sequencing mode paired ends 2×150 bp).

Sequence assembly, annotation, and analysis

Raw paired reads were quality-trimmed ($Q \geq 20$) and assembled using Geneious 2022.1.1²². The mitochondrial genomes of *L. perpunctata* (MW848343), *Klapperibrachys cremeri* (NC_084361), *Laodelphax striatellus* (MK292916), *Zecheuna tonkinensis* (MW872013) were chosen as reference sequences. The annotation of mitogenome was made by the same software with the same reference species. When annotating, the protein coding genes were identified by Geneious using Open Reading Frame, then checked if could translate to continuous proteins under the invertebrate genetic code; the tRNA genes were identified through the online websites tRNA Scan-SE server (<http://lowelab.ucsc.edu/tRNAscan-SE/>) and MITOS2 (<http://mitos2.bioinf.uni-leipzig.de/index.py>) and their secondary structure predicted meanwhile^{23,24}; the rRNA genes and control region were identified by the boundaries of tRNA genes and the comparison with other mitogenomes in Fulgoromorpha. The mitogenome map was produced using Proksee (<https://proksee.ca/>)²⁵. The A + T content of the third codon position for Fulgoromorpha (135 species) was made with software Origin. The mitogenomic information, nucleotide base composition, A + T/G + C content, AT skew/GC skew were analyzed with PhyloSuite²⁶ (Supplementary file 16). Strand asymmetry was calculated in terms of formulae: AT skew = $(A - T)/(A + T)$ and GC skew = $(G - C)/(G + C)$ ²⁷. The secondary structure of tRNAs was manually mapped using Adobe Illustrator CS6 based on the structure predicted by MITOS2. Tandem repeats of A + T rich region was identified by Tandem Repeats Finder (<https://tandem.bu.edu/trf/trf.basic.submit.html>)²⁸.

Phylogenetic analysis

The mitogenomes of 145 species from Auchenorrhyncha (Supplementary file 17) were used for phylogenetic analysis, of them, 135 Fulgoromorpha species (Delphacoidea and Fulgoroidea) as ingroup, while three species from Cercopoidea (representing by families Aphrophoridae and Cercopidae), two species from Cicadoidea

(representing by family Cicadidae), and five species from Membracoidea (representing by families Membracidae, Aetalionidae & Cicadellidae) as the outgroup. Except for the species *L. sichuanensis* sequenced, assembled and annotated in this study, the rest mitogenomes were downloaded from NCBI (<https://www.ncbi.nlm.nih.gov/>)¹¹. The 13 PCGs, 22 tRNAs and 2 rRNAs from mitogenomes were extracted automatically using PhyloSuite²⁶, then MAFFT²⁹ aligned for each gene. The alignments were subsequently refined using the codon-aware program MACSE v2.06³⁰ for 13 PCGs, ambiguously aligned fragments were removed in batches using Gblocks 0.91b³¹, gap sites were removed with trimAl v1.2rev57³², and then concatenated into different datasets. To investigate the influence of 22 tRNAs and the third codon of the 13 PCGs of mitogenome for phylogeny analyses, this study established six different data matrices:

1. PCG123R24: 13 PCGs + 22 tRNAs + 2 rRNAs
2. PCG123R2: 13 PCGs + 2 rRNAs
3. PCG123: 13 PCGs
4. PCG12R24: First and second codon positions of 13 PCGs + 22 tRNAs + 2 rRNAs
5. PCG12R2: First and second codon positions of 13 PCGs + 2 rRNAs
6. PCG12: First and second codon positions of 13 PCGs).

Modelfinder was used to identify appropriate partitions and select suitable models for each partition under the Bayesian information criterion (BIC)(Supplementary file 18).

Both Maximum likelihood (ML) and Bayesian inference (BI) methods were used for phylogenetic analyses based on the full mitochondrial genomes except for control region. Maximum likelihood analysis was performed by IQ-TREE³³, using the Ultrafast bootstrap algorithm with 300,000 replicates, partitions with Edge-linked. Bayesian analysis was performed with MrBayes³⁴. Two simultaneous runs were performed, each with one cold and three hot chains. Markov Chain Monte Carlo (MCMC) sampling estimated the posterior probability with 800,000 generations, sampling every 1000 generations once, with an average standard deviation of split frequencies below 0.05 and a relative burn-in rate of 25%, partitions with Edge-unlinked. Phylogenetic trees were visualized using the online website itol (<https://itol.embl.de/>)³⁵.

Data availability

Data associated with this study has been deposited at NCBI under the accession number OR663919 (<https://www.ncbi.nlm.nih.gov/nucleotide/OR663919.1/>). All data generated or analysed during this study are included in this published article and its Supplementary Information files.

Received: 10 April 2024; Accepted: 2 September 2024

Published online: 20 September 2024

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Acknowledgements

We sincerely thank the specimen collectors for their hard work in the field collection.

Author contributions

Shaobo FENG: Conceptualization, Data curation, Formal analysis, Visualization, Writing—original draft & Writing—review & editing. Menglin WANG: Conceptualization, Supervision & Writing—review & editing.

Funding

This study was supported by the National Natural Science Foundation of China (32100369).

Competing interests

The authors declare no competing interests.

Additional information

Supplementary Information The online version contains supplementary material available at <https://doi.org/10.1038/s41598-024-71948-5>.

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