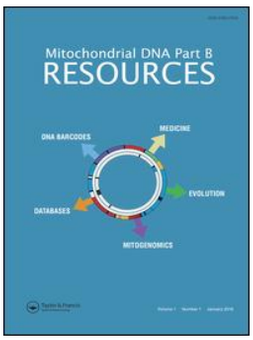

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MITOGENOME ANNOUNCEMENTS

The complete mitochondrial genome of *Idgia oculata* (Coleoptera: Cleroidea: Prionoceridae) and a related phylogenetic analysis of Cleroidea

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ABSTRACT

In this study, the complete mitochondrial genome of *Idgia oculata* Redtenbacher, 1868 was sequenced using Illumina's NovaSeq platform. The mitogenome is a double-stranded circular molecule of 15,805 bp in length with 22 transfer RNA genes, 13 protein-coding genes (PCGs), 2 ribosomal RNA genes as in other insects. To estimate the taxonomic status of Prionoceridae, total of 9 species from 5 families of Cleroidea were selected as ingroups and 2 species of Coccinellidae as outgroups for phylogenetic analysis based on 13PCGs. The results showed that three major clades were formed, including a 'Melyridae-Cleridae' clade, 'Melyridae-Trogossitidae-Phloiophilidae' clade, and 'Melyridae-Prionoceridae' clade. Prionoceridae showed more closely related to Melyridae than other families. More mitogenome of thorough taxon sampling will be needed to well understand the relationship in Cleroidea.

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Mitochondrial genome; phylogeny; Idgia oculata; Cleroidea

Idgia oculata Redtenbacher, 1868 is a species of the family Prionoceridae within the melyrid lineage ('soft-winged flower beetles') of the superfamily Cleroidea (Polyphaga: Cucujiformia) (Bouchard et al. 2011). The species is easily recognized by the large-sized body, length 15.5–18.5 mm, metallic blue head and elytra, testaceous pronotum, with a pair of blackish spots on the center of the disc.

Idgia oculata is normally encountered in large groups, feeding on various flowering shrubs and trees. Flight period centered around June with extreme dates of 25 May and 6 July (Aston 2011).

The specimens used in this study was collected by a flight interception trap (FIT) (Nie et al. 2017) from Hong Kong and deposited in the Institute of Zoology, Chinese Academy of Sciences, Beijing, China. Genomic DNA was extracted by DNeasy Blood & Tissue kit (QIAGEN, Germany) and then sequenced using Illumina's NovaSeq platform (Illumina, San Diego, CA) with 350 bp insert size and a pair-end 150 bp sequencing strategy. The sequence reads were first filtered by the programs following Zhou et al. (2013) and then the remaining high-quality reads were assembled using IDBA-UD (Yu and Henry 2012). The annotations of genes were done by Geneious 8.0.5 software (Kearse et al. 2012) and tRNAscan-SE 1.21 (Schattner et al. 2005).

The complete mitochondrial genome (mitogenome) of *I. oculata* is a double-stranded circular molecule of 15,805 bp in length (GenBank accession number: MH779812), with 22 transfer RNA genes, 13 protein-coding genes (PCGs), 2 ribosomal RNA genes, and a control region as in other insects. The overall base composition is A: 40.1%, T: 40.8%, C: 11.2%, and G: 7.9%, with a much higher A + T content.

The phylogenetic tree was reconstructed to estimate the status of Prionoceridae in Cleroidea. All available mitogenomes of families of Cleroidea were downloaded from Genbank (Table 1).

The acceptable sequences including 13 protein-coding genes and longer than 10K bp were kept. Total 8 species (JX412815.1, EU877951.1, JX412799.1, JX412833.1, JX412765.1, KX035157.1, KT808467.1, JX412752.1) from 5 families were selected as ingroups and 2 species (JQ321839.1, KU877170.1) of Coccinellidae was selected as outgroups (Table 1). The phylogenetic inference was done based on 13PCGs. Trans Align methods were used to align all protein-coding genes (Bininda-Emonds 2005). The aligned data from 13PCGs were concatenated with Sequence Matrix v.1.7.8 (Vaidya et al. 2011). Bayesian inference was performed using MrBayes v.3.2 (Ronquist et al. 2012). Data were partitioned according to loci of 13 PCGs. The MCMC search was conducted for 2,000,000 generations, and sampling was done every 100 generations until the average standard deviation of split frequencies was below 0.01. The first 25% of trees were discarded as 'burn-in' and posterior probabilities were estimated for each node.

Phylogenetic tree (Figure 1) showed that three major clades were formed, including 'Melyridae-Cleridae' clade,

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Table 1. The information of 11 species used for phylogenetic analysis.

Family	Species	Genbank No.	References
Melyridae	*Chaetosoma scaritides*	EU877951.1	Sheffield et al. (2008)
Melyridae	Malachiinae sp.	JX412799.1	Timmermans (2015) unpublished
Melyridae	*Clanoptilus assimilis*	JX412833.1	Timmermans (2015) unpublished
Melyridae	Melyridae sp.	JX412765.1	Timmermans (2016) unpublished
Cleridae	Hydnocerini sp.	KX035157.1	Linard and Andujar (2017) unpublished
Cleridae	*Trichodes sinae*	KT808467.1	Yuan and Zhang (2016) unpublished
Phloiophilidae	*Phloiophilus edwardsi*	JX412815.1	Timmermans (2015) unpublished
Prionoceridae	*Idgia oculata*	MH779812	In this study
Trogossitidae	*Temnoscheila virescens*	JX412752.1	Timmermans (2015) unpublished
Coccinellidae	*Coccinella septempunctata*	JQ321839.1	Kim et al. (2012)
Coccinellidae	*Cycloneda sanguinea*	KU877170.1	Pires (2016) unpublished

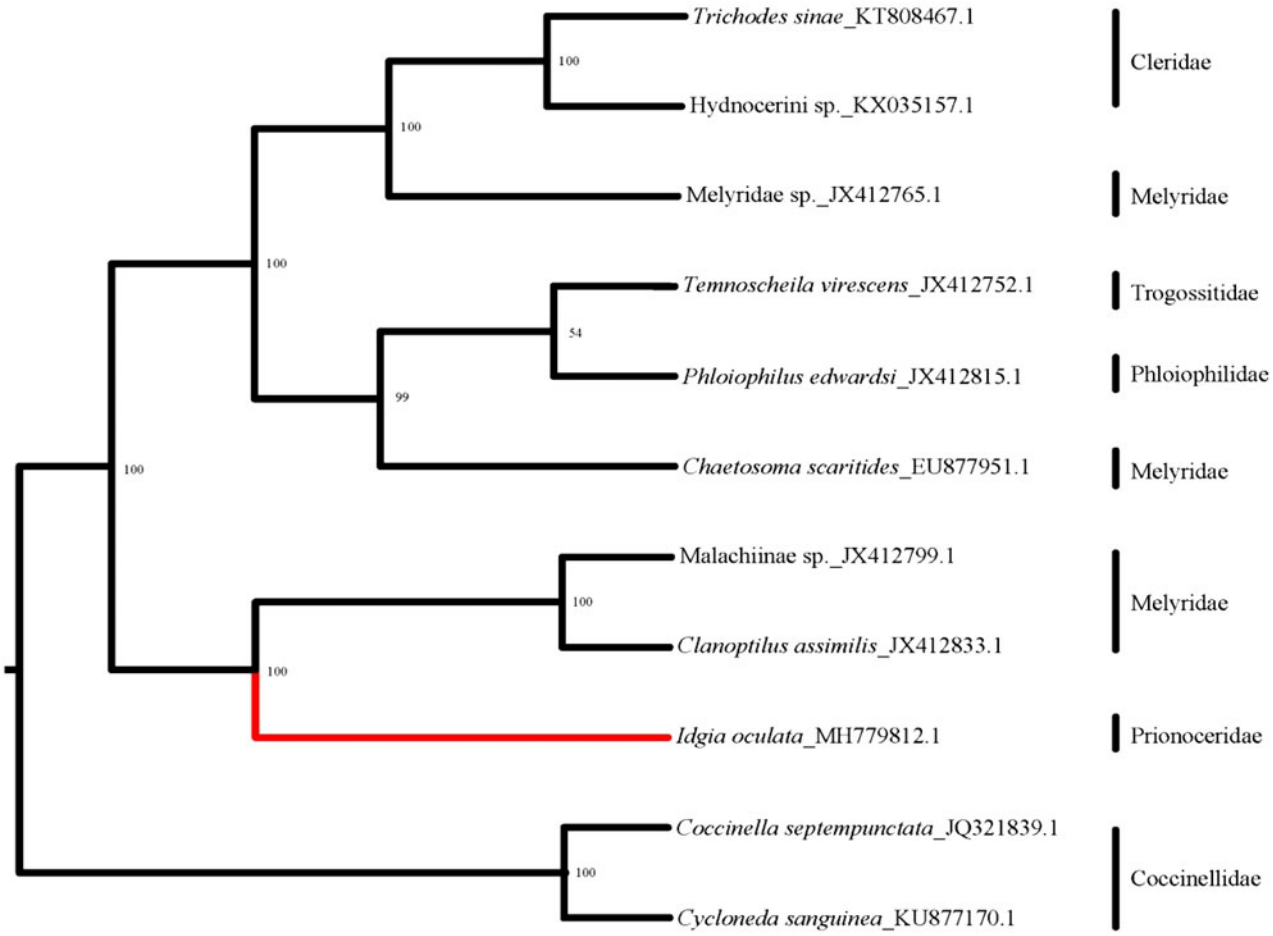

Figure 1. The Bayesian tree based on 13PCGs combined data sets. Numbers on nodes indicate Bayesian posterior probabilities. Red branch is the new data in this study.

'Melyridae-Trogossitidae-Phloiophilidae' clade, and 'Melyridae-Prionoceridae' clade. Melyridae is distributed on three branches, which suggests it is not recovered as a monophyly but a polyphyly. This result is congruent with the proposal by Majer (1987) that the Melyridae is polyphyletic based on the morphological study.

Prionoceridae seems more closely related to the melyrid subfamily Malachiinae than other taxa based on current data. But it was formed a clade with the melyrid subfamily Melyrinae based on morphological characters in the cladograms of all Cleroidea produced by Kolibáč (1999). However, few molecular data affect the further discussion on the basal relationship of Cleroidea. More mitogenome of thorough taxon sampling will be needed to resolve this question, especially the relationship between Prionoceridae and Melyridae.

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Disclosure statement

No potential conflict of interest was reported by the authors.

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