

The first mitochondrial genome of spongillafly from Asia (Neuroptera: Sisyridae: *Sisyra aurorae* Navás, 1933) and phylogenetic implications of Osmyloidea

Xiumei Lu^a, Aili Lin^b, Dongsheng Wang^a and Xingyue Liu^b

^aInstitute of Ecological and Environmental Protection, Shanghai Academy of Agricultural Sciences, Shanghai, China; ^bDepartment of Entomology, China Agricultural University, Beijing, China

ABSTRACT

The spongillafly species *Sisyra aurorae* Navás, 1933 (Neuroptera: Sisyridae) is an endemic species in China and is first recorded from Shanghai. The mitogenome of this species is sequenced, representing the first mitogenome of Sisyridae from Asia. The nearly complete mitogenome is 15,634 bp, which contains 13 protein-coding genes (PCGs), 22 transfer RNA genes (tRNAs), two ribosomal RNA genes (rRNAs), and a control region. The gene order and arrangement are similar to other lacewing mitogenomes. Both Bayesian and maximum likelihood analyses based on 13 PCGs recovered the interfamilial phylogeny within Osmyloidea as Sisyridae + (Nevrorthidae + Osmylidae).

ARTICLE HISTORY

Received 20 May 2021
Accepted 29 June 2021

KEYWORDS

Mitogenome; Sisyridae; Osmyloidea; phylogeny

Sisyridae (spongillaflies) is a small lacewing family (Neuroptera: Osmyloidea), comprising about 70 species in four genera worldwide (Oswald 2020). The larvae are exclusively aquatic as a specialist predator of freshwater sponges and can be used as indicators of freshwater quality (Parfin and Gurney 1956; Weissmair 1994, 2005). Hitherto, only two partial mitochondrial genomes have been determined for the sisyrids respectively from Europe and North America, namely *Sisyra nigra* (Retzius 1783) and *Climacia areolaris* Hagen, 1861 (Wang et al. 2017). Currently, only six sisyrid species in two genera are recorded from China (Oswald 2020). Here, the mitochondrial genome of the Chinese endemic species *Sisyra aurorae* Navás, 1933 is sequenced, which represents the first mitogenome of Sisyridae from Asia.

The specimen was collected from Zhuanghang town, Fengxian District, Shanghai, China (121.39174°E, 30.89438°N), representing the first record of Sisyridae from Shanghai. It is deposited at the Pest Control Lab of Shanghai Academy of Agricultural Sciences under the voucher number SAAS20190624 (contact: Xiumei Lu, lxm2361892563@126.com). The genomic DNA was extracted from tissues of the thorax and legs using Hipure Universal DNA Kit, Magen. The mitogenome was sequenced by Illumina NovaSeq with 250 bp paired-end reads, assembled with A5-miseq and SPAdes, and annotated with MITOs WebServer. The phylogenetic tree is conducted under CIPRES and IQtree WebServers.

The mitochondrial genome of *S. aurorae* is a typical circular DNA with 15,634 bp in length, which consists of a set of 37 genes (13 PCGs, 22 tRNAs, and two rRNAs) and a control

region. The length is longer than previous two sisyrid mitogenomes, while the 16S rRNA and control region are not completely sequenced here. The gene order is identical to that of the putative ancestral arrangement of insects. The H chain codes 23 genes, while the other 14 genes are coded by the L chain. The nucleotide composition of the mitogenome is biased toward A and T, with 79.8% of A + T content (A = 40.6%, T = 39.2%, C = 11.6%, G = 8.5%). There are 616 bp intergenic nucleotides in nine locations, ranging from 1 to 586 bp in length, while only 51 bp overlapped nucleotides in 15 locations, ranging from 1 to 9 bp in length. All PCGs are started with ATN (ATG in *cox2*, *atp6*, *cox3*, *nd4*, *nd4l*, *cytb*; ATT in *nd2*, *cox1*, *atp8*, *nd5*, *nd6*; ATA in *nd3*) except *nd1* started with TTG. The typical stop codon TAA is adopted by eight PCGs (*nd2*, *cox1*, *atp8*, *atp6*, *cox3*, *nd4l*, *nd6*, *cytb*), and TAG occurs in two PCGs (*nd3* and *nd1*); the stop codon remains unknown in three PCGs (*cox2*, *nd5* and *nd4*). The 22 tRNA genes range from 63 to 72 bp in length, and all could be folded into canonical cloverleaf structure. Notably, the size of TΨC loop varies and is truncated in *trnI*, *trnF* and *trnL1*.

The superfamily Osmyloidea includes three families, i.e., Sisyridae, Nevrorthidae and Osmylidae. The larvae of these families are aquatic or semi-aquatic, while the adults are terrestrial. Though recent molecular studies support the close affinities among these three families, the phylogenetic relationship among them are still elusive with inconsistent results recovered from different data (Aspöck and Aspöck 2008; Winterton et al. 2010, 2018; Wang et al. 2017; Vasilikopoulos et al. 2020). Here, the phylogenetic relationship of Osmyloidea were inferred based on 13 PCGs from 14 species

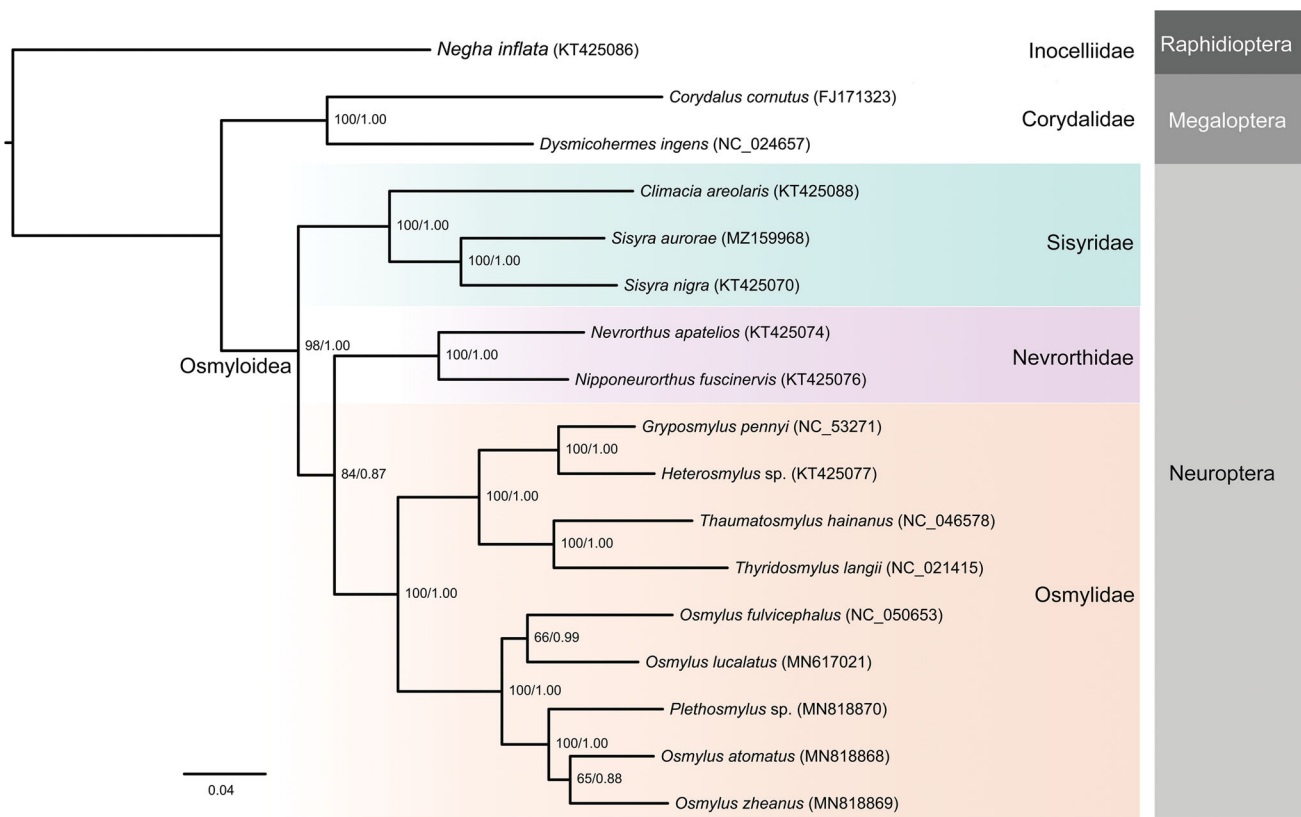


Figure 1. Phylogenetic relationship of Osmyloidea inferred based on 13 PCGs using Bayesian and maximum likelihood (ML) methods. The ML bootstrap support values and posterior probabilities are shown above each. Genbank accession numbers for the sequences are indicated next to the species names.

using Bayesian and maximum likelihood methods (Figure 1). The monophyly of these families are strongly supported. The result shows that Sisyridae is sister to the clade including Nevrorthidae and Osmylidae, being consistent with that previously recovered in Winterton et al. (2018).

Disclosure statement

The authors claimed that there is no potential conflict of interest.

Nucleotide sequence accession number

The mitogenome sequence that supports the findings of this study is openly available in GenBank of NCBI at (<https://www.ncbi.nlm.nih.gov/nucleotide/MZ159968>) under the accession number MZ159968. The associated BioProject, BioSample and sequence read archive (SRA) numbers are PRJNA729218, SAMN19114475 and SRR14508920 respectively.

Funding

The present study was funded by the Shanghai Sailing Program [No. 19YF1443000] and the National Natural Science Foundation of China [No. 31900348].

References

Aspöck U, Aspöck H. 2008. Phylogenetic relevance of the genital sclerites of Neuropterida (Insecta: Holometabola). *Syst Entomol.* 33(1):97–127.
Hagen HA. 1861. Synopsis of the Neuroptera of North America, with a list of the South American species. *Smithsonian Miscellan Collect.* 4:xx + 1–347.

Navás L. 1933. Névroptères et insectes voisins. Chine et pays environnants. Quatrième [IV] Série Notes D'Entomol CHS. 1:1–22.
Oswald JD. 2020. Neuropterida species of the world. Lacewing Digital Library, Research Publication No. 1. [accessed 2021 May 27]. <http://lacewing.tamu.edu/SpeciesCatalog/Main>
Parfin SI, Gurney AB. 1956. The spongilla-flies, with special reference to those of the western hemisphere (Sisyridae, Neuroptera). *Proc. U.S. Nat. Muse.* 105(3360):421–529.
Retzius AJ. 1783. *Caroli Lib. Bar. De Geer ... Genera et species insectorum e generosissimi avtoris scriptis scriptis extraxit, digessit, latine quoad partem reddidit, et terminologiam insectorum Linneanam addidit Anders lahan Retzivs.* 220 + 32 [index] pp.
Vasilikopoulos A, Misof B, Meusemann K, Lieberz D, Flouri T, Beutel RG, Niehuis O, Wappler T, Rust J, Peters RS, et al. 2020. An integrative phylogenomic approach to elucidate the evolutionary history and divergence times of Neuropterida (Insecta: Holometabola). *BMC Evol Biol.* 20(1):64.
Wang YY, Liu XY, Garzón-Orduña IJ, Winterton SL, Yan Y, Aspöck U, Aspöck H, Yang D. 2017. Mitochondrial phylogenomics illuminates the evolutionary history of Neuropterida. *Cladistics.* 33(6):617–636.
Weissmair W. 1994. Eidonomie und Ökologie zweier europäischer Schwammfliegen-Arten (Neuroptera: Sisyridae). *Entomol General.* 18: 261–727.
Weissmair W. 2005. Schwammhafte (Insekta: Neuroptera: Sisyridae) - Parasiten der Moostiere (Bryozoa). *Denisia.* 16:299–304.
Winterton SL, Hardy NB, Wiegmann BM. 2010. On wings of lace: phylogeny and Bayesian divergence time estimates of Neuropterida (Insecta) based on morphological and molecular data. *Syst Entomol.* 35(3):349–378.
Winterton SL, Lemmon A, Gillung JP, Garzon IJ, Badano D, Bakkes DK, Breitkreuz LCV, Engel MS, Lemmon EM, Liu XY, Machado RJP, et al. 2018. Evolution of lacewings and allied orders using anchored phylogenomics (Neuroptera, Megaloptera, Raphidioptera). *Syst Entomol.* 43(2):330–354.