The complete mitochondrial genome of Syrista parreyssii (Spinola, 1843) (Hymenoptera: Cephidae) and its phylogenetic analyses

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ABSTRACT

The complete mitochondrial genome of Syrista parreyssii (Spinola, 1843) was described. The circular genome is 18,666 bp with an A + T content of 82.60%. It contains 37 genes and a 1921 bp control region. The CR-trnI (+)-trnQ (-)-trnM (+) cluster is rearranged as trnM (+)-CR-trnQ (-)-trnI (+) cluster. Phylogenetic analysis demonstrates that European Syrista and Asian Neosyrista were not sister groups. Neosyrista is a valid genus and should be re-established. Moreover, a preliminary study based on COI showed there are at least three valid Syrista species within the European and Mediterranean regions. Whether the known Syrista parreyssii (Spinola, 1843) is a complex or there are more cryptic species needs further study.

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and in agreement with almost all Cephidae mitogenomes reported previously (e.g. Dowton et al. 2009; Korkmaz et al. 2016; Korkmaz et al. 2017). However, the gene order is different from *Syrista parreyssii* (KX907845). In the latter, *trnM (+)-trnA (–)-trnI (+)-trnQ (–) cluster was detected, which is the only case reported in Cephidae. Besides, *trnP* is absent, and *trnT* is directly connected to the flanking PCGs (Korkmaz et al. 2018).

The A + T content of the whole mitochondrial genome is 82.60% (40.70% A, 11.20% C, 6.20% G, and 41.90% T), indicating significant A + T bias. Four start codons for PCGs are used, ATG (*atp6, cox2, cob, nad4, nad4l, nad5, and nad6*); ATA (*nad3*); ATT (*atp8, cox1, cox3, and nad1*) and ATC (*nad2*). All PCGs use TAA as a stop codon except for *nad5* (TAG). Part of *nad4* (from position 1308 to position 1353) of *S. parreyssii* (KX907847) has the difference in aligning when conducting the multiply alignment of 17 Cephidae, whereas, *S. parreyssii* (OK104785) reported here has no such problem.

Trees for BI and ML were the same in topology; Figure 1 shows the BI tree with nodal supports. Phylogenetic inference fully resolved *S. parreyssii* as a basal branch of Hartigiinae of Cephidae (Figure 1). While *Neosyrista incisa* (Wei & Nie 1996) was a sister group of *Janus megamuculatus* Liu & Wei, 2017 (Liu et al. 2017) and it was not a sister group of *S. parreyssii*. Besides, the monophyly of the genus *Janus* and the tribe Pachycephini, which was erected by Benson (1946) and composed of *Characopygus* and *Pachycephus*, were also problematic as shown in Figure 1. *Characopygus* was a sister group of (*Cephus + Trachelus*) and a member of Cephinae. While *Pachycephus* was a sister group of *Phylloicus* and a member of Hartigiinae. The phylogenetic relationship of the genera in the family Cephidae needs more sampling to be clarified.

Phylogenetic reconstruction using the barcoding sequence showed that the eight samples were divided into three branches corresponding to their collection places: Turkey, Iran, and Greece. The genetic distances between these three branches were 2.1%, 5.2%, and 4.3%, respectively, as in Figure 1. While no genetic distance was found within the clades. This result clearly shows that at least three species are bearing the name of *S. parreyssii*. However, this species is recorded in many localities (Wei and Smith 2010), spanning the Mediterranean Region, and reaching into the Caucasus. Therefore, it is possible that there are more species and provokes further questions.

The accumulation of the mitochondrial genome exposes inaccurate taxonomy problems (Yang et al. 2021), which will promote the progress of integrative taxonomy to a certain extent. Combining morphological and molecular evidence, more and more crypt species will be discovered. An increasing sample matrix makes it possible to construct genus-level phylogeny, thus providing conditions for solving the problem of complex species.

**Ethics statement**

The collection of specimen conformed to the requirement of International ethics, which are unrestricted species. The collection was approved by the local authorities. The process and purpose of this experimental research were in line with the rules and regulations of our institute. There are no ethical issues and other conflicts of interest in this study.

**Author contributions**

Conceptualization, M.W.; methodology, M.W.; validation, Ö.D.; formal analysis, Z.S., and M.L.; investigation, M.L.; resources, M.W.; data curation, M.L.; writing-original draft, M.L. and L.L.; writing-review and editing, M.L. and Ö.D.; visualization, L.L. and Z.S.; supervision, M.W.; project administration, M.W.; funding acquisition, M.L. and M.W. All authors have read and agreed to the published version of the manuscript.

**Figure 1.** A Bayesian inference (BI) tree based on 17 Cephidae sequences from the 13 PCGs (left). Numbers on the branches correspond to Bayesian posterior probabilities. The accession number is given after each species. A maximum-likelihood (ML) tree based on eight COI sequences of *Syrista* species (right). P-distances between clades are provided.
Acknowledgements

We thank the Lab of Insect Systematics and Evolutionary Biology (LISEB) from Jiangxi Normal University, notable Zhang Yiwen and He Huimin, for their kind assistance on calculation. We are grateful to members of Evolutionary Bioinformatics Research Groups (EBRG) from Sivas Cumhuriyet University for stimulating discussions. The valuable comments of the anonymous reviewers are gratefully acknowledged.

Disclosure statement

No potential conflict of interest was reported by the authors. The authors alone are responsible for the content and writing of the article.

Funding

This work was supported by the National Natural Science Foundation of China [31970447], Starting Fund for Doctoral Research of Lishui University [6004LM012], and Special Fund for Scientific Research of Postdoctoral Research Station Assessment in Zhejiang Province, China [2021].

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Data availability statement

The genome sequence data that support the findings of this study are openly available in GenBank (https://www.ncbi.nlm.nih.gov) under the accession number OK104785 and gb file in Science Data Bank under the DOI:10.11922/sciencedb.01114. The associated BioProject, SRA, and BioSample numbers are PRJNA761906, SRR15850959, and SAMN21247251, respectively. All related files had been uploaded to figshare (https://figshare.com/account/home/#/projects/123556).

References

Abascal F, Zardoya R, Telford MJ. 2010. TranslatorX: multiple alignment of nucleotide sequences guided by amino acid translations. Nucleic Acids Res. 38(Web Server issue):W7–W13.
Boore JL. 1999. Animal mitochondrial genomes. Nucleic Acids Res. 27(8): 1767–1780.
Bernt M, Donath A, Juhling F, Externbrink F, Florentz C, Fritzsch G, Putz J, Middendorf M, Stadler PF. 2013. MITOS: improved de novo metazoan mitochondrial genome annotation. Mol Phylogenet Evol. 69(2): 313–319.
Benson RB. 1935. On the genera of the Cephidae and the erection of a new family Syntestidae (Hymenoptera: Tenthredinidae). Ann Mag Nat Hist. 16(95):535–533.
Benson RB. 1946. Classification of the Cephidae (Hymenoptera: Symphyta). Trans R Entomol Soc Lond. 96(6):89–108.
Dowton M, Cameron SL, Dowavic JI, Austin AD, Whiting MF. 2009. Characterization of 67 mitochondrial tRNA gene rearrangements in the hymenoptera suggests that mitochondrial tRNA gene position is selectively neutral. Mol Biol Evol. 26(7):1607–1617.
Korkmaz EM, Budak M, Ordek MN, Başbüyük HH. 2016. The complete mitogenomes of Calaneuta filiformis (Eversmann, 1847) and Calaneuta idolon (Rossi, 1794) (Hymenoptera: Cephidae); the remarkable features of the elongated A+T rich region in Cephini. Gene. 576(1 Pt 3):404–411.
Korkmaz EM, Aydıner HB, Temel B, Budak M, Başbüyük HH. 2017. Mitogenome evolution in Cephini (Hymenoptera: Cephidae); evidence for parallel adaptive evolution. Biochem Syst Ecol. 71:137–146.
Korkmaz EM, Doğan Ö, Durel BS, Temel Altun B, Budak M, Başbüyük HH. 2017. Mitogenome organization and evolutionary history of the subfamily Ciphinae (Hymenoptera: Cephidae). Syst Entomol. 43(3): 606–618.
Konow FW. 1896. Ueber Blattwespen, Tribus Cephini (Tenthredinarum). Wiener Entomol Zeitung. 15:26–31.
Liu L, Chu B, Wei MC. 2017. Two new species of Janus Stephens (Hymenoptera: Cephidae) from China with a key to Chinese species. Entomotaxonomia. 39(3):238–246.
Mocsáry A. 1904. Siricidurum species quinque novae. Annal Hist Nat Musel Ntat Hung. 2:496–498.
Meng G, Li Y, Yang C, Liu S. 2019. MitoZ: a toolkit for animal mitochondrial genome assembly, annotation and visualization. Nucleic Acids Res. 47(11):e63.
Nguyen LT, Schmidt HA, von Haeseler A, Minh BQ. 2015. IQ-TREE: a fast and effective stochastic algorithm for estimating maximum-likelihood phylogenies. Mol Biol Evol. 32(1):268–274.
Ronquist F, Teslenko M, van der Mark P, Ayres DL, Darling A, Höhna S, Larget B, Liu L, Suchard MA, Huelsenbeck JP. 2012. MrBayes 3.2: efficient Bayesian phylogenetic inference and model choice across a large model space. Syst Biol. 61(3):539–542.
Spinola M. 1843. Notes sur quelques Hyménoptères peu connus, recueillis en Espagne, pendant l’anée 1842, par M. Victor Ghiliani, voyageur-naturaliste. Ann Soc Entomol France. 1:111–129.
Tozlu E, Kotan R, Tozlu G. 2017. The investigation of Beauveria bassiana (Ascomycota: Hypocreales) as a biocontrol agent of rose-stem sawfly, Syrissa parreyssii (Spinola, 1843) (Hymenoptera: Symphyta: Cephidae) larvae. Fresenius Environ Bull. 26:7091–7100.
Wei MC. 2007. On the genus Syrissa Konow, with the description of a new species from China (Hymenoptera: Tenthredinidae). Entomol News. 118(5):450–458.
Wei MC, Nie HY. 1996. Studies of Chinese Cephidae V. The genus Sinicephus Maa and its allies (Hymenoptera: Cephidae: Hartigiini). J Central South Forest Univ. 16(4):18–23.
Wei MC, Smith DR. 2010. Review of Syrissa Konow (Hymenoptera: Cephidae). Proc Entomol Soc Washington. 112(2):302–316.
Yang YJ, Sun ZM, Niu GY. 2021. The complete mitochondrial genome of Allantus togatus (Panzer, 1801), in view of possible cryptic species. Mitochondrial DNA B Resour. 6(3):1114–1115.
Zhang D, Gao F, Jakovic I, Zou H, Zhang J, Li WX, Wang GT. 2020. PhylSoSuite: an integrated and scalable desktop platform for streamlined molecular sequence data management and evolutionary phylogenetics studies. Mol Ecol Resour. 20(1):348–355.