pISSN: 0259-9996 – eISSN: 2783-3968

Journal of Entomological Society of Iran

2026, 46 (4), 449-459

Short Communication

First description of the pupa of the endemic biting midge *Forcipomyia whitcombei* Boorman, 1989 (Dip., Ceratopogonidae) from Southern Oman

Hamed Al-Nadabi[1], Ali A. Al-Jahdhami[2], Ahmed Al Sidairi[1], Ahmed Al-Raeesi[1], Khalifa Al-Zeidi[1], Mohammed Akaak[3], Fatema Al-Shahri[3], Husam Al-Hinaai[4] & Ali Al-Wahaibi[4]

1. *Center for Environmental Studies and Research (CESAR), Sultan Qaboos University, P.O. Box 34, Al-Khoud 123, Muscat, Sultanate of Oman*

2. *Department of Plant Development, Ministry of Agricultural, Fisheries, and Water Resources, Muscat, Sultanate of Oman*

3. *Dhofar Municipality, Salalah, Sultanate of Oman*

4. *Department of Plant Sciences, College of Agricultural and Marine Sciences, Sultan Qaboos University, Muscat, Sultanate of Oman*

Abstract. *Forcipomyia whitcombei* Boorman, 1989 (Diptera: Ceratopogonidae) is a biting midge known only from the monsoon season-affected Dhofar region of southern Oman. Although the adult stage has been described previously, the immature stages have remained unknown for more than 35 years. In this study, the pupa is described for the first time from specimens collected in several humid microhabitats and reared to adults to confirm their identity. The pupa is readily recognized by its large smooth dorsal apotome and short, laterally directed respiratory organs. The distinctive number and distribution pattern of pupal tubercles, particularly on the cephalothorax and abdominal tergites, constitute important diagnostic features that readily distinguish pupae of *F. whitcombei* from related sympatric species of *Forcipomyia*. Molecular identification based on the *ITS1* region was incorporated to genetically confirm the taxonomic identity of the pupae, discriminate them from morphologically similar species within the group, and complement the morphological characterization. The description presented here provides useful morphological characters for identifying the immature stages of the species and may facilitate their recognition in future field and laboratory studies.

Keywords: Endemic, *Lasiohelea*, cephalothorax, genital lobe, midge, larval exuviae

Article info
Received: 13 August 2026
Accepted: 20 September 2026
Published: 30 October 2026

Subject Editor: Mehdi Esfandiari

Corresponding authors: Ali A. Al-Jahdhami

E-mail: entomologistali96@gmail.com

DOI : https://doi.org/10.22034/jesi.46.4.5

The Ceratopogonidae is one of the most diverse families of flies, comprising more than 6300 described species worldwide, with many additional species still awaiting discovery and formal description (Borkent, 2016, 2024). Members of this family have successfully colonized an extraordinary range of environments, their distribution extends from tropical ecosystems to the High Arctic, and from lowland habitats to some of the world's highest mountain regions (Alwin *et al.*, 2016). This remarkable ecological and geographical breadth highlights their adaptability and evolutionary success across diverse environmental conditions. Immature stages of Ceratopogonidae are poorly known, which hampers species identification and limits their use in ecological and conservation studies, with most aquatic surveys identifying them only to family or subfamily level. Because larvae and pupae provide unique insights into habitat, development, feeding, seasonality, and survival that adults cannot, studying immature stages is essential for a complete understanding of a species' ecology and life history (Borkent, 2014). Pupae provide a greater number of stable and readily observable diagnostic characters such as respiratory horns and abdominal tubercles, which are likely to be more diagnostic than larval features. The larval stage often exhibits subtle characters that require high magnification, and comprehensive larval descriptions are lacking for

©2026 by Author(s), Published by the Entomological Society of Iran
This Work is Licensed under Creative Commons Attribution-Non-Commercial 4.0 International Public License.

many species of the genus (Saunders, 1924, 1964; Lewańczyk *et al.*, 2009). Borkent (2014) made the first attempt to develop a comprehensive generic identification key for the pupae of Ceratopogonidae. He included 45 out of the 111 genera recognized worldwide within the family. However, he emphasized that the key was incomplete due to the limited availability of material for many taxa. He also highlighted that many, if not most, of the early descriptions of ceratopogonid pupae are of uncertain identity and should therefore be treated with caution. The inclusion of distributional information for related species may help exclude certain taxa and facilitate specimen identification within a restricted geographic region (Koch *et al.*, 2022).

Several genera of hematophagous biting midges occur in Oman, including *Atrichopogon*, *Leptoconops*, *Culicoides*, and two species of *Forcipomyia*. Accurate identification of their immature stages is therefore important for recognizing and differentiating the breeding habitats of the different biting taxa. The pupa of *Forcipomyia* can be separated from these other hematophagous ceratopogonid genera by the lack of a prothoracic extension, a distinctive condition among Ceratopogonidae. They are further characterized by labium lacking an elongate median suture and the terminal processes closely abut basally (see figs. 10A–H in Borkent, 2014). The hematophagous biting midge, *Forcipomyia whitcombei* Boorman, is endemic to the monsoon influenced region of Dhofar, southern Oman (Boorman, 1989). In the taxonomy of the immature stages of *Forcipomyia*, pupae provide the most informative and have reliable taxonomic features for distinguishing members of the subgenus *Lasiohelea* from closely related congeners in the Dhofar region (Borkent, 2014). Present study represents the first attempt to document the pupa of *F. whitcombei,* in both morphological and genetic aspects, and evaluate characters that may assist in distinguishing it from related taxa, thereby facilitating future investigations of its biology, breeding habitats, and management.

Specimen collection and data analysis

Pupae of *Forcipomyia whitcombei* were collected during July–August 2025 from a wide range of microhabitats within the monsoon-influenced region of Dhofar, Oman. Sampling focused on humid and shaded habitats where pupae were frequently encountered (fig.5). Most pupae were attached to thin algal films covering rocks, soil surfaces, and other substrates (fig.6). Individuals were carefully removed using fine-tipped forceps to avoid damaging delicate morphological structures. Collected specimens were placed individually or in small groups in ventilated rearing containers containing moist substrate from the collection site. A subset of specimens was preserved directly in 95–100% ethanol for future molecular studies. In addition to pupae, late fourth-instar larvae were collected from the same microhabitats and transferred to rearing containers. These larvae were maintained under laboratory conditions and monitored daily until pupation. Newly formed pupae were retained for morphological examination or allowed to complete development to adulthood. Part of the collected pupal material was reared to obtain associated adults and to confirm species identity through successful adult emergence. Emerged adults were preserved and associated with their corresponding pupal exuviae whenever possible. Pupae and pupal exuviae were slide-mounted using standard entomological techniques. The morphological terminology follows Borkent (2014). Identification of the genus and subgenus was based on the generic pupal keys for Ceratopogonidae presented by Borkent (2014). Voucher specimens are deposited in the Department of Plant Sciences, Sultan Qaboos University, and the private collection of the second author.

DNA was extracted from pupal specimens using Tissue DNA Preparation – Column Kit (Jena Bioscience GmbH, Jena, Germany). Internal transcribed spacer 1 (*ITS1*) region of nuclear ribosomal DNA was amplified, with forward PanCulF (GTAGGTGAACCTGCGGAAGG) and reverse PanCulR (TGCGGTCTTCATTCGAACCCAT) primers (Perrin *et al.*, 2006; Elbers *et al.*, 2012). The resulting sequence was BLASTed at NCBI database and similar sequences were retrieved for analysis. A total of 23 *ITS1* sequences were aligned using BioEdit v. 7.7.1 (Hall, 1999). *Leptoconops nipponensis* Tokunaga (LC662811) was chosen as the outgroup taxon. Maximum likelihood analysis was performed using IQ-Tree (Nguyen *et al.*, 2015) with 1000 bootstrap replicates. FigTree v.1.4.2 (Rambaut, 2012) was used for tree visualization, and annotated the final tree with Adobe Illustrator CC2019. One *ITS1* sequence was produced in this study with 363 bp in length, which has been submitted to GenBank (QB161996).

Material examined: Oman, Dhofar, Taqa, Ayn Athom 22.vii.2025, Ali Al-Jahdhami leg. 15♀2♂, 17°06′45″N, 54°21′55″E, 304m; 4.viii.2026, Ali Al-Jahdhami leg. 74♀14♂.

Description: Habitus as in (fig.1) pupa brown (specimens preserved in 95% ethanol showed slightly faded coloration), slender, gradually tapering posteriorly. Total body elongate, consisting of a broad cephalothorax, occupying approximately one-third of total body length.

Head and cephalothorax: Dorsal apotome large, subtriangular to broadly oval, smooth, without conspicuous dorsomedial tubercle. Surface weakly ornamented with minute granulation. Eye sheaths large and conspicuous, extending laterally along the cephalothorax.

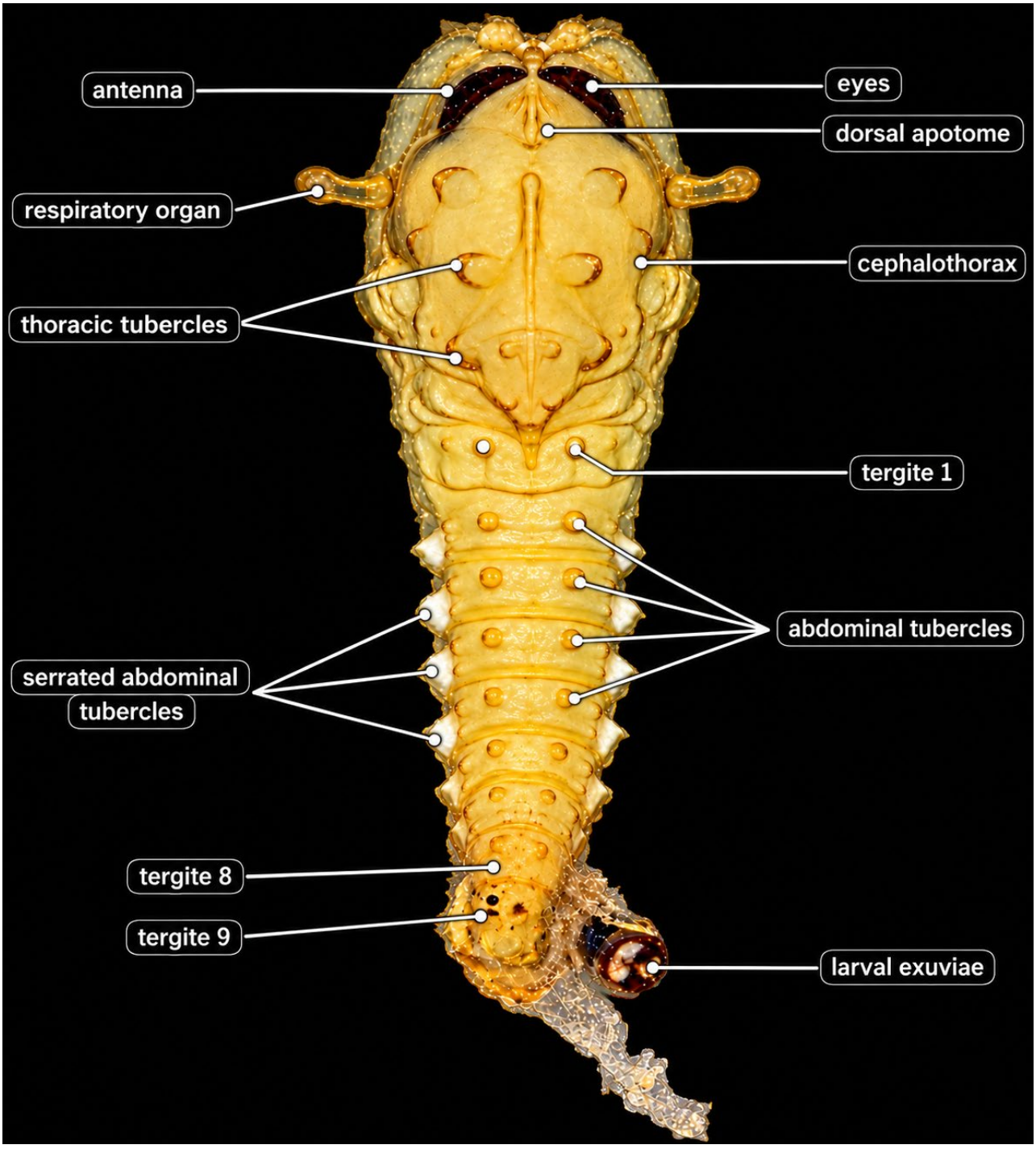


Fig. 1. Habitus of pupae of female *Forcipomyia whitcombei*, in dorsal view.

Cephalothorax with one median dorsomedial tubercle and four paired lateral tubercles, dorsomedial tubercle situated immediately posterior to the dorsal apotome; anterolateral tubercles located near the bases of the respiratory organs; dorsolateral and mediolateral tubercles arranged symmetrically on the central cephalothorax; posterolateral tubercles situated near the posterior margin (fig.2). All tubercles low, rounded, and bearing short sensilla or setae. Abdominal margins with well-developed serrate tubercles along laterally, paired rounded dorsal tergal tubercles. Wing and leg sheaths closely appressed to the body and reaching the anterior abdominal segments.

Abdomen: Consisting of nine apparent segments, gradually becoming narrower and tapering posteriorly, particularly from segments 6–9. Tergites 2–7 each with a pair of rounded dorsal tubercles arranged in two longitudinal submedian rows, approximately one tubercle on each side of the midline per segment. Lateral margins of abdominal segments with prominent, strongly projecting serrate tubercles, arranged in a repeated posterolateral series; serration most distinct on the middle abdominal segments. Dorsal tubercles low, rounded and smaller than lateral serrate tubercles. Tergite 8 narrower than preceding segments; tergite 9 constitute the terminal abdominal segment. Larval exuviae retained posteriorly.

Description of respiratory organ (fig.3)

The respiratory organ is short to moderately elongate, cylindrical, and slightly curved outward, arising laterally from the cephalothorax. The apex is expanded into a rounded to slightly oval disc bearing approximately 9–10 apical pores arranged radially around the margin. The respiratory organ is transparent, smooth, and connected to the cephalothorax by a short basal stalk. No secondary branches are present.

Description of Terminal Processes (fig.4)

Terminal processes paired, strongly sclerotized, short, directed posterolaterally and diverging distinctly from one another. Each process broadly triangular, gradually narrowing to a pointed apex, with the outer margin slightly curved. Processes originate from the posterior margin of segment 9 and separated medially by a shallow concavity; each process is about 2–3 times as long as its basal width and extends distinctly beyond the posterior margin of segment 9.

Diagnosis. Pupae of *Forcipomyia* can be distinguished from those of other ceratopogonid genera (*Atrichopogon*, *Leptoconops*, and *Culicoides*) by the absence of a prothoracic extension and the labium undivided medially by an elongate suture, with terminal processes closely abutting basally.

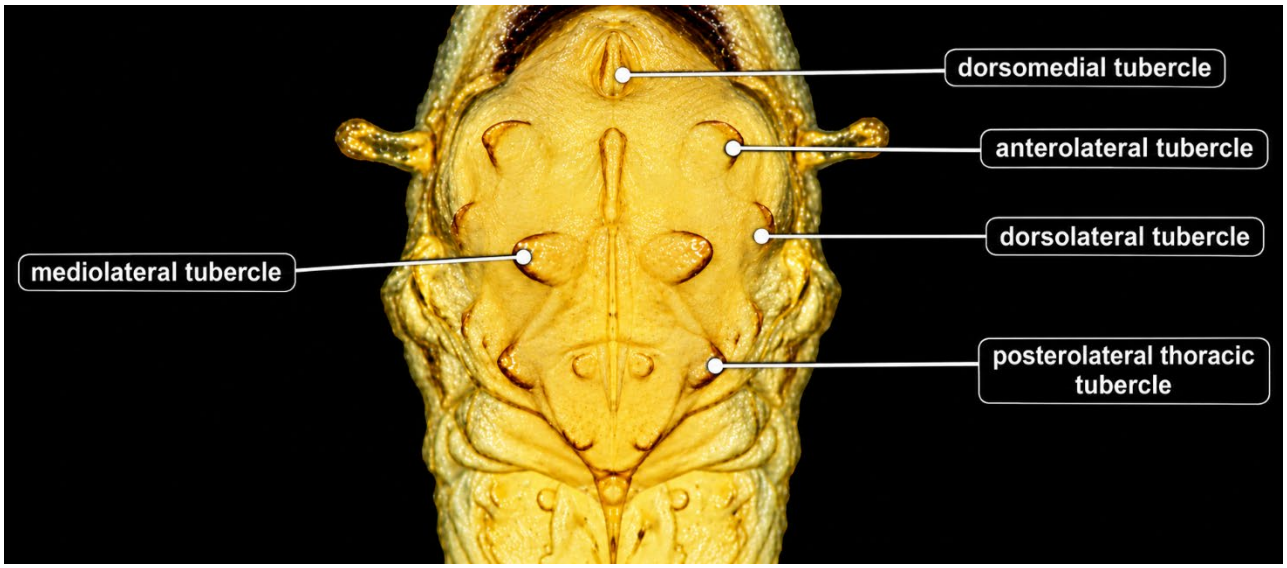


Fig. 2. Cephalothorax in dorsal view.

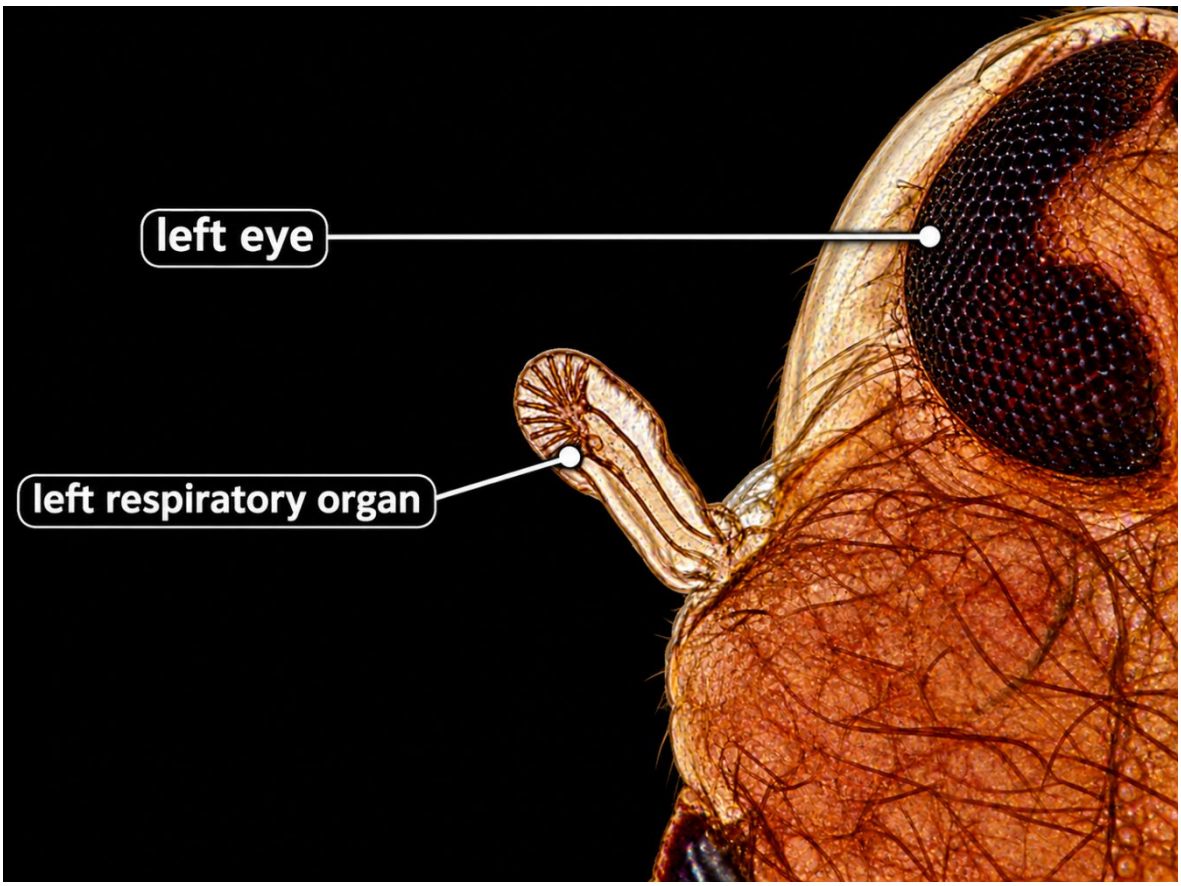


Fig. 3. Left respiratory organ in dorsal view.

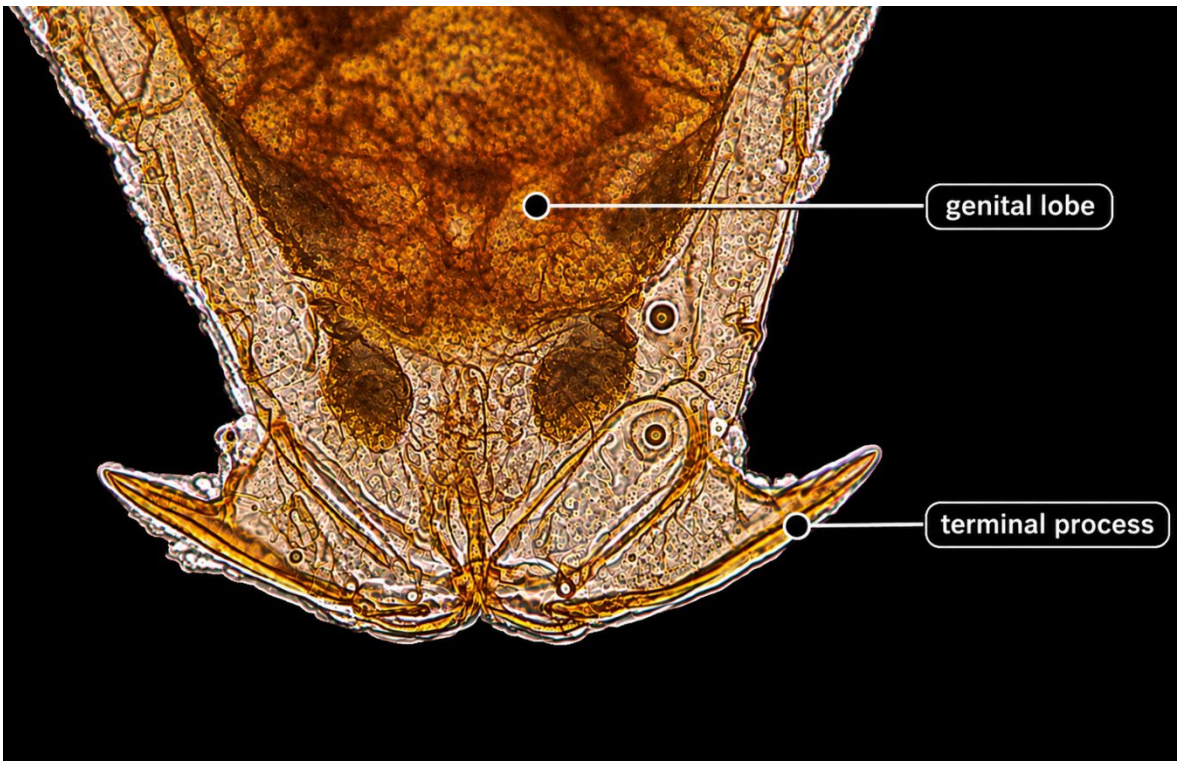


Fig. 4. Abdominal segment 9 in dorsal view.



Fig. 5. Typical habitat of *Forcipomyia whitcombei.*

The subgenus (*Lasiohelea*) is present in Oman by two species (*F. whitcombei* and *F. baltea* Boorman, 1989) while several subgenera of *Forcipomyia* occur in Dhofar, namely (*Microhelea)*, (*Euprojoannisia)*, (*Synthyridomyia)*, (*Lepidohelea)*, (*Forcipomyia)*, and (*Lasiohelea)*. The subgenus (*Microhelea)* is distinguished by very elongate, slender setae arising directly from the cuticle of the head and mesonotum, without tubercles. In (*Euprojoannisia)* respiratory organ pores are elongate and arranged in a semicircle at the apex, whereas the other subgenera have round to oblong pores arranged in a single or slightly undulating row. (*Synthyridomyia)* differs from other by no retaining the larval exuviae on the pupal abdomen. (*Lepidohelea)* and (*Forcipomyia)* have elongate terminal processes directed posteriorly, with the male genital lobes positioned dorsally to them, whereas (*Lasiohelea)* has short terminal processes directed laterally, with the male genital lobes positioned ventral to the terminal processes.

Molecular analysis

The *ITS1* region has previously been used for molecular identification in species of *Forcipomyia* (Lu *et al.*, 2025). Maximum likelihood tree based on *ITS1* sequences of *Forcipomyia* and *Culicoides*, along with the outgroup *Leptoconops nipponensis*, indicates that the pupa belongs to *Forcipomyia whitcombei* (Fig. 7). The *ITS1* sequence generated in this study from the pupal stage grouped with sequences generated from the adult and larval stage of *F. whitcombei*. Our unpublished DNA barcoding analysis further supported our findings. The pupal morphology of *F. whitcombei* includes a combination of plesiomorphic and apomorphic character states within the broader phylogenetic framework proposed by Borkent (2014). One notable feature is that the larval exuviae remain attached to the posterior portion of the pupal abdomen. Borkent (2014) considered the absence of retained larval exuviae as plesiomorphic and retention of the larval exuviae as apomorphic. Within *Forcipomyia*, loss of the retained larval exuviae in several subgenera was interpreted as a secondary state. Therefore, retention of the larval

exuviae in *F. whitcombei* represents a derived character condition and may reflect the evolutionary specialization of terrestrial pupation within this lineage. In contrast, several cephalic characters retain more plesiomorphic conditions. Borkent (2014) considered the presence of a well-developed lacinia as plesiomorphic and reported this condition in *Lasiohelea*. Likewise, an entire labium, rather than one divided medially by a longitudinal suture, represents as the plesiomorphic condition in the broader phylogenetic analysis of Ceratopogonidae. These features indicate that the pupa of *F. whitcombei* combines ancestral character states together with the derived retaining of the larval exuviae. Other conspicuous features of *F. whitcombei*, including the well-developed but short abdominal tubercles, serrate lateral abdominal tubercles, and short terminal processes directed posterolaterally, are informative taxonomically but should not be interpreted independently as plesiomorphic or apomorphic.



Fig. 6. Pupa of *Forcipomyia whitcombei* photographed in situ within its breeding habitat.

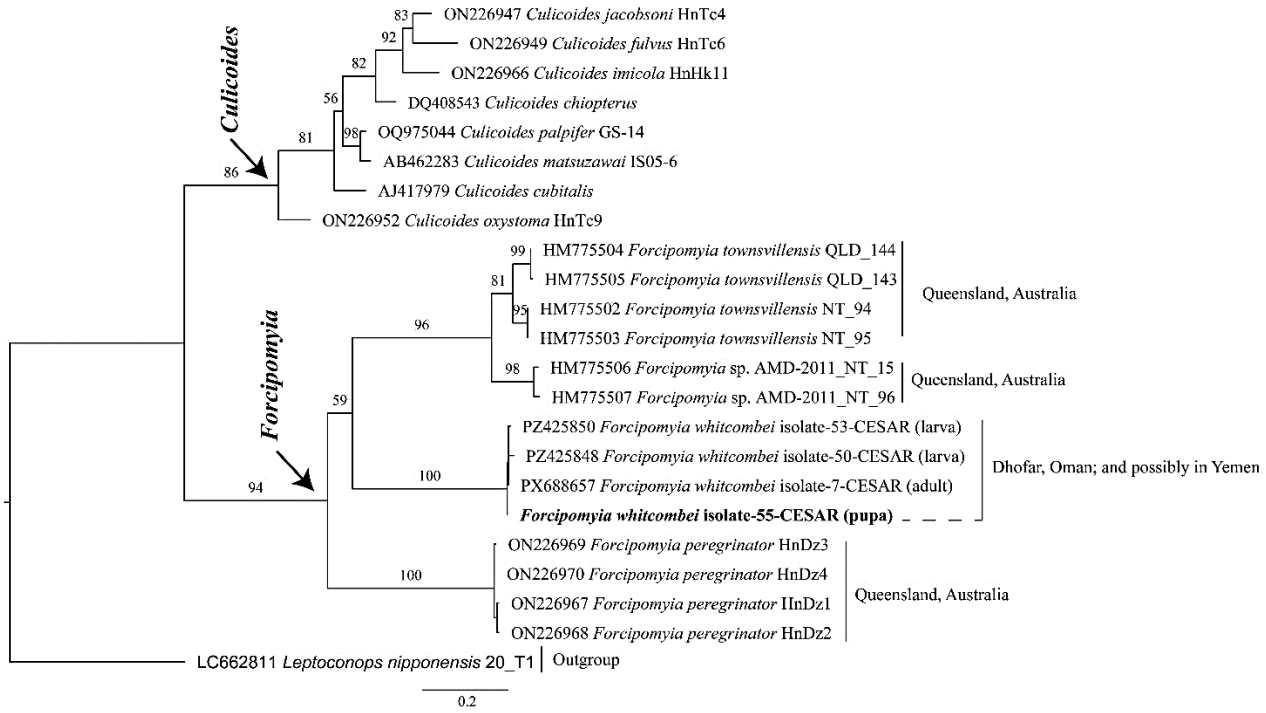


Fig. 7. Maximum likelihood tree based on *ITS1* sequences of *Forcipomyia* and *Culicoides*. The studied specimen indicated in bold font, nested within the clade comprised of *Forcipomyia whitcombei*.

The geographical and ecological characteristics of *F. whitcombei* provide useful supplementary biogeographical information, but they should not be considered primary evidence for species identification. Both *F. whitcombei* and *F. baltea* are endemic to the eastern Arabia and Oman. *F. baltea* confined to northern Oman, whereas *F. whitcombei* is restricted to Dhofar region particularly in the influenced habitats by monsoon. Consequently, the *F. whitcombei* is allopatrically separated from the *F. baltea* providing a clear biogeographical distinction within the subgenus members. Ecologically, both species are greatly variable in their habitats, seasonal activity and adult emergence, environmental condition, microclimatic preferences, larval food resources and dormancy behavior.

Author's Contributions

Hamed Al-Nadabi: Conceptualization, Methodology, Visualization, Investigation, Data curation, Formal analysis, Writing – original draft, Writing – review and editing, Final review and editing supervision, project administration and funding acquisition; **Ali A. Al-Jahdhami:** Conceptualization, Methodology, Visualization, Investigation, Data curation, Formal analysis, Writing – original draft, Writing – review and editing, Final review and editing, supervision, and project administration; **Ahmed Al Sidairi:** Conceptualization, Methodology, Investigation, Data curation, Final review and editing, supervision, project administration and funding acquisition.; **Ahmed Al-Raeesi:** Methodology, Visualization, and Investigation; **Khalifa Al-Zeidi:** Methodology, Visualization, and Investigation; **Mohammed Akaak:** Conceptualization, Methodology, Visualization, Investigation, funding acquisition; **Fatema Al-Shahri:** Methodology, Visualization, Investigation, funding acquisition **Husam Al-Hinaai:** Methodology, Visualization, Investigation, Final review and editing; **Ali Al-Wahaibi:** Conceptualization, Methodology, Visualization, supervision, project administration and funding acquisition.

Author's Information

Hamed Al-Nadabi ✉ hamed@squ.edu.om https://orcid.org/0000-0002-6759-2392
Ali A. Al-Jahdhami ✉ entomologistali96@gmail.com https://orcid.org/0000-0003-1204-0491
Ahmed Al Sidairi ✉ sidairi@squ.edu.om https://orcid.org/0009-0008-5476-2621

Ahmed Al-Raeesi ✉ aalraeesi@squ.edu.om https://orcid.org/0009-0008-7720-1181
Khalifa Al-Zeidi ✉ alzeidi@squ.edu.om https://orcid.org/0009-0008-0552-8767
Mohammed Akaak ✉ akaak2020@hotmail.com https://orcid.org/0009-0002-3719-8420
Fatema Al-Shahri ✉ fm.alshahri@gmail.com https://orcid.org/0009-0009-9890-4393
Husam Al-Hinaai ✉ h.alhinaai@squ.edu.om https://orcid.org/0009-0009-3095-0086
Ali Al-Wahaibi ✉ awahaibi@squ.edu.om https://orcid.org/0009-0000-7677-6970

Funding

This research was funded by Dhofar Municipality and Research and Innovation Authority and was executed by Center for Environmental Studies and Research, Sultan Qaboos University (Grant number: RC/SR/DVC/CES/24/183).

Data Availability Statement

All data supporting the findings of this study are available on paper. The pupal specimens of *Forcipomyia whitcombei* examined in this study are deposited in the collection of the Laboratories of Plant Science, Sultan Qaboos University, and the private collection of the second author.

Acknowledgments

The authors thank the two reviewers for their valuable comments and suggestions, which helped improve the manuscript. We also thank the staff of the Municipality of Dhofar for facilitating the fieldwork in the Dhofar region. We sincerely thank Dr. Shah Husain for his valuable assistance with the molecular analyses conducted in this study.

Ethics Approval and Consent to Participate

Insects were used in this study. All applicable international, national, and institutional guidelines for the care and use of animals were followed. This article does not contain any studies with human participants performed by any of the authors.

Conflict of Interest

The authors declare that there is no conflict of interest regarding the publication of this paper.

Generative AI statement

The authors declare that no Gen AI was used in the creation of this manuscript.

REFERENCES

Alwin, A., Szadziewski, R. & Szwedo, J. (2016) Biting midges of the subfamily *Forcipomyiinae* (Diptera: Ceratopogonidae) from the Middle East, with keys and descriptions of new species. *Zootaxa* 4173(4): 351-378. https://doi.org/10.11646/zootaxa.4173.4.2

Boorman, J. (1989) Two new *Forcipomyia* (*Lasiohelea*) sp. (Diptera, Ceratopogonidae) from Oman. *Journal of Oman Studies*, 10, 125–130.

Borkent, A. (2014). The pupae of the biting midges of the world (Diptera: Ceratopogonidae), with a generic key and analysis of the phylogenetic relationships between genera. *Zootaxa*, 3879(1), 1–327.https://doi.org/10.11646/zootaxa.3879.1.1

Borkent, A. (2016). World Species of Biting Midges (Diptera: Ceratopogonidae). Available from: http://www.inhs.illinois.edu/research/FLYTREE/CeratopogonidaeCatalog.pdf (accessed 24 September 2026).

Borkent, A. (2024). The phylogeny of the genera of biting midges (Diptera: Ceratopogonidae) of the world. *Zootaxa* 5438(1), 1–274. https://doi.org/10.11646/zootaxa.5438.1.1

Elbers, A .R, Meiswinkel, R., Van Weezep, E., Kooi, E. A. & Van der Poel, W. H. (2012) Schmallenberg Virus in Culicoides Biting Midges in the Netherlands in 2012. *Transboundary and Emerging Diseases* 62(3):339–342. https://doi.org/10.1111/tbed.12128

Hall, T. A. (1999) BioEdit: a user-friendly biological sequence alignment editor and analysis program for Windows 95/98/NT. *Nucleic Acids Symposium Series* 41: 95–98.

Koch, W., Elven, H. & Finstad, A. G. (2022) Clavis: An open and versatile identification key format. *PLoS ONE*, 17(12), e0277752. https://doi.org/10.1371/journal.pone.0277752

Lewańczyk, A., Szadziewski, R. & Dominiak, P. (2009) Diagnosis of *Forcipomyia sahariensis* Kieffer (Diptera: Ceratopogonidae) with the first description of immature stages. *Fragmenta Faunistica*, 52(2), 149–155. https://doi.org/10.3161/00159301ff2009.52.2.149

Lu, Y., Su, J., Cheng, S., Hu, Y. & Xia, Q. (2025)Molecular identification and genetic diversity of biting midges (Diptera: Ceratopogonidae) in the tropical environment on Hainan Island, China. *Journal of Vector Borne Diseases* 62(1):45–50. https://doi.org/10.4103/JVBD.JVBD_100_23

Nguyen, L. T., Schmidt, H. A, Von Haeseler, A. & Minh, B. Q. (2015) IQ-TREE: a fast and effective stochastic algorithm for estimating maximum-likelihood phylogenies. *Molecular Biology and Evolution* 32(1):268–274. https://doi.org/10.1093/molbev/msu300

Perrin, A., Cetre-Sossah, C., Mathieu, B., Baldet, T., Delecolle, J. C. & Albina, E. (2006)Phylogenetic analysis of Culicoides species from France based on nuclear ITS1-rDNA sequences. *Medical and Veterinary Entomology* 20(2):219–228. https://doi.org/10.1111/j.1365-2915.2006.00616.x

Rambaut, A. (2012) FigTree Tree Figure Drawing Tool Version 131, Institute of Evolutionary Biology, University of Edinburgh. Available online: http://treebioedacuk/software/figtree/ (accessed on 30 December 2022).

Saunders, L. G. (1924) On the life history and the anatomy of the early stages of *Forcipomyia* (Diptera, Nemat., Ceratopogoninae). *Parasitology*, 16, 164–213. https://doi.org/10.1017/s0031182000020011

Saunders, L. G. (1964) New species of *Forcipomyia* in the *Lasiohelea* complex described in all stages (Diptera, Ceratopogonidae). *Canadian Journal of Zoology*, 42, 463–482. https://doi.org/10.1139/z64-040

Citation: Hamed Al-Nadabi, H. A., Al-Jahdhami, A, A., Al Sidairi, A., Al-Raeesi, A., Al-Zeidi, K., Akaak, M., Al-Shahri, F., Al-Hinaai, H., Al-Wahaibi, A. (2026) First description of the pupa of the endemic biting midge Forcipomyia whitcombei Boorman, 1989 (Dip., Ceratopogonidae) from Southern Oman. *J. Entomol. Soc. Iran*, 46(4), 449–459.

DOI :https://doi.org/10.22034/jesi.46.4.5

URL: https://jesi.areeo.ac.ir/article_136453.html

pISSN: 0259-9996 – eISSN: 2783-3968

Journal of Entomological Society of Iran

2026, 46 (4), 449-459

Short Communication

نخستین توصیف شفیره پشه گزنده بومی *Forcipomyia whitcombei* Boorman, 1989 (Dip., Ceratopogonidae) از جنوب عمان

حامد النادبی[۱]، علی ع. الجهدهمی[۲]، احمد السیدایری[۱]، احمد الرئیسی[۱]، خلیفه الزایدی[۱]، محمد اکاک[۳]، فاطمه الشهری[۳]، حسام الحنائی [٤] و علی الوهابی [٤]

۱. مرکز مطالعات و پژوهش‌های زیست‌محیطی، دانشگاه سلطان قابوس، مسقط، عمان

۲. بخش توسعه گیاهی، وزارت کشاورزی، شیلات و منابع آب، مسقط، عمان

۳. گروه علوم گیاهی، دانشکده علوم کشاورزی و دریایی، دانشگاه سلطان قابوس، مسقط، عمان

۴. شهرداری ظفار، صلاله، عمان

چکیده: *Forcipomyia whitcombei* Boorman, 1989 (Diptera: Ceratopogonidae) یک پشه گزنده است که فقط در منطقه ظفار در جنوب عمان که تحت تأثیر فصل باران‌های موسمی قرار دارد، شناخته شده است. اگرچه مرحله بالغ قبلاً شرح توصیف شده است، مراحل نابالغ بیش از ۳۵ سال ناشناخته مانده است. در این مطالعه، شفیره برای اولین بار از نمونه‌های جمع‌آوری‌شده در چندین ریزیستگاه مرطوب و پرورش‌یافته تا بلوغ برای تأیید هویت آنها توصیف می‌شود. شفیره به راحتی توسط آپوتوم پشتی صاف و بزرگ و اندام‌های تنفسی کوتاه و جانبی خود قابل تشخیص است. تعداد و الگوی توزیع متمایز برآمدگی‌های شفیرگی، به ویژه روی سفالوتوراکس و ترژیت‌های شکمی، ویژگی‌های تشخیصی مهمی را تشکیل می‌دهند که به راحتی شفیره‌های *F. whitcombei* را از گونه‌های همبوم مرتبط *Forcipomyia* متمایز می‌کنند. شناسایی مولکولی بر اساس ناحیه *ITS1* برای تأیید ژنتیکی هویت تاکسونومیک شفیره‌ها، تمایز آنها از گونه‌های مشابه از نظر ریخت‌شناسی در داخل گروه و تکمیل توصیف ریخت‌شناسی گنجانده شد. شرح ارائه شده در اینجا، ویژگی‌های ریخت‌شناسی مفیدی را برای شناسایی مراحل نابالغ گونه ارائه می‌دهد و ممکن است تشخیص آنها را در مطالعات میدانی و آزمایشگاهی آینده تسهیل کند.

کلمات کلیدی: بومی، *Lasiohelea*، سرسینه، لوب تناسلی، پشه‌ریز ، پوسته لاروی

اطلاعات مقاله

دریافت: ۱۴۰۵/۰۵/۲۲

پذیرش: ۱۴۰۵/۰۷/۱۸

انتشار: ۱۴۰۵/۰۸/۰۸

دبیر تخصصی: مهدی اسفندیاری

نویسنده مسئول: علی ع. الجهدهمی

ایمیل: entomologistali96@gmail.com

DOI :https://doi.org/10.22034/jesi.46.4.5

©2026 by Author(s), Published by the Entomological Society of Iran
This Work is Licensed under Creative Commons Attribution-Non-Commercial 4.0 International Public License.