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The genera *Luzonimyia* and *Pararhinoleucophenga* from China (Diptera: Drosophilidae), with DNA barcoding information

QINGSONG GAO & HONGWEI CHEN

Department of Entomology, South China Agricultural University, Tianhe, Guangzhou, Guangdong, 510642 China

Abstract

Four new species are described from Yunnan, China, which belong to two different genera within the subfamily Steganinae: *Luzonimyia hirsutina* sp. nov., *Luzonimyia setocauda* sp. nov., *Pararhinoleucophenga amnicola* sp. nov. and *Pararhinoleucophenga sylvatica* sp. nov. The DNA sequences and GenBank accession numbers of the mitochondrial *COI* gene among Chinese species are provided.

Key words: Barcoding, *COI* gene, Drosophilid, East Asia, Fauna, taxonomy

Introduction

Luzonimyia Malloch, 1926 and *Pararhinoleucophenga* Duda, 1924 are all smaller genera in the subfamily Steganinae (Brake & Bächli 2008). The genus *Luzonimyia* includes six species (Cao & Chen 2008): 1 sp. each from Australia and the Philippines, and 2 spp. each from southern China and Africa. The genus *Pararhinoleucophenga* is endemic to the Oriental region, and includes nine species: 1 sp. from Indonesia (Java, Sumatra), 1 sp. from India and Sri Lanka, and 7 spp. from southern China (Cao & Chen 2009).

In this paper, four new species are described from Yunnan, China: 2 spp. of *Luzonimyia* and 2 spp. of *Pararhinoleucophenga* species. In addition, a total of 16 DNA sequences and GenBank accession numbers of the mitochondrial *COI* gene among ten Chinese species are provided (Table 1).

Material and methods

Materials and morphological terminology. All specimens examined were collected by sweeping on tree trunks or tussocks near streams in the forest, preserved in 75% ethanol, and then dried and pinned after morphological examination and identification. The specimens are deposited in Department of Entomology, South China Agricultural University, Guangzhou, China (SCAU). We followed Zhang & Toda (1992) and Chen & Toda (2001) for the definitions of measurements, indices and abbreviations.

DNA extraction and sequencing. A total of 16 samples of 10 species were investigated for molecular work (Table 1); their total DNA was extracted from the abdominal tissue of samples after dissection of the genitalia, using the TIANGENT™ DNA extraction kit following the recommended protocol. The *COI* fragments were amplified using the cycle protocol as in Zhao *et al.* (2009). The PCR/sequencing primer pairs are *COI*-F1 (5'-ATCGCCTAAACTTCAGCCAC-3', Wang *et al.* 2006), HCO2198 (5'-TAAACTTCAGGGTGACCAAAAATCA-3', Folmer *et al.* 1994), *COI*-F3 (5'-CGCGACAATGRYTATTTCTAC-3', Li *et al.* 2013) and *COI*-R3 (5'-CCATTGCACTAATCTGCCATA-3', Li *et al.* 2013).

0.88 (0.88–0.95), vb = 0.53 (0.62–0.91), dcl = 0.42 (0.39–0.50), presctl = 0.23 (0.55–0.82), sctl = damaged (1.09–1.20), sterno = 0.77 (0.73–0.87), orbito = 2.00 (2.00–2.33), dcp = 0.27 (0.22–0.33), sctlp = 1.17 (1.00–1.19), C = 3.26 (3.38–3.78), 4c = 0.61 (0.56–0.67), 4v = 1.35 (1.45–1.59), 5x = 1.56 (1.63–1.87), ac = 2.25 (2.00–2.38), M = 0.49 (0.49–0.58), C3F = 1.00 (1.00)

Type specimens. Holotype ♂ (SCAU, No. 124320), CHINA: Yixiang, Puer, Yunnan, 27°12' N, 100°03' E, alt. 1400m, 18.xi.2012, ex. tussock, JJ Gao. Paratypes: 2♂ (SCAU, Nos. 124321, 22), same data as holotype; 1♂ (SCAU, No. 124323), Caiyanghe, Puer, Yunnan, 22°36' N, 101°07' E, alt. 1200m, 27.vii.2009, fallen logs, L Wang; 1♀ (SCAU, No. 124324), Hesong, Menghai, Yunnan, 21°49' N, 100°06' E, alt. 1900m, 17.iv.2010, ex. fallen logs, L Wang; 1♂ (SCAU, No. 124319), CHINA: Guanlei, Mengla, Yunnan, 14.xi.2012, ex. tussock, JJ Gao.

Etymology. From the Latin word: *sylvaticus*, referring to the fly dwelling in forest.

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References

- Brake, I. & Bächli, G. (2008) Drosophilidae (Diptera). *World catalogue of Insects. Vol. 9*. Apollo Books, Stenstrup, pp. 412.
- Cao, H.Z. & Chen, H.W. (2008) Discovery of the genus *Luzonimyia* Malloch in China, with descriptions of two new species (Insecta, Diptera, Drosophilidae). *The Raffles Bulletin of Zoology*, 56, 251–254.
- Cao, H.Z. & Chen, H.W. (2009) Revision of the Oriental genus *Pararhinoleucophenga* Duda (Diptera: Drosophilidae). *Zoological Studies*, 48, 125–136.
- Chen, H.W. & Toda, M.J. (2001) A revision of the Asian and European species in the subgenus *Amiota* Loew (Diptera: Drosophilidae) and establishment of species-groups based on phylogenetic analysis. *Journal of Natural History*, 35, 1517–1563.
<http://dx.doi.org/10.1080/002229301317067665>
- Duda, O. (1924) Die Drosophiliden (Dipteren) des Deutschen Entomologischen Institutes der Kaiser Wilhelm-Gesellschaft. *Archiv Naturgeschichte*, 90, 172–234.
- Folmer, O., Black, M., Hoeh, W., Lutz, R. & Vrijenhoek, R. (1994) DNA primers for amplification of mitochondrial cytochrome *c* oxidase subunit I from diverse metazoan invertebrates. *Molecular Marine Biology and Biotechnology*, 3, 294–299.
- Li, T., Gao, J.J., Lu, J.M., Ji, X.L. & Chen, H.W. (2013) Phylogenetic relationship among East Asian species of the *Stegana* genus group (Diptera: Drosophilidae). *Molecular Phylogenetics and Evolution*, 66 (1), 412–416.
<http://dx.doi.org/10.1016/j.ympev.2012.09.004>
- Malloch, J.R. (1926) Notes on oriental Diptera, with descriptions of new species. *The Philippine Journal of Science*, 31, 491–512.
- McAlpine, J.F. (1981) Morphology and terminology adults. In: McAlpine, J.F. (Ed.), *Manual of Nearctic Diptera*, 1, pp. 9–64. [Research Branch Agriculture Canada monogr. 27. Ottawa: Minister Supply and Services Canada]
- Okada, T. (1988) A revision of the genera *Pararhinoleucophenga* Duda and *Paraleucophenga* Hendel (Diptera, Drosophilidae), with special regard to archestinic characters. *Kontyû, Tokyo*, 56, 618–624.
- Tamura, K., Peterson, D., Peterson, N., Stecher, G., Nei, M. & Kumar, S. (2011) MEGA5: molecular evolutionary genetics analysis using maximum likelihood, evolutionary distance, and maximum parsimony methods. *Molecular Biology and Evolution*, 28, 2731–2739.
<http://dx.doi.org/10.1093/molbev/msr121>
- Wang, B.C., Park, J., Watabe, H., Gao, J.J., Xiangyu, J.G., Aotsuka, T., Chen, H.W. & Zhang, Y.P. (2006) Molecular phylogeny of the *Drosophila virilis* section (Diptera: Drosophilidae) based on mitochondrial and nuclear sequences. *Molecular Phylogenetics and Evolution*, 40, 484–500.
<http://dx.doi.org/10.1016/j.ympev.2006.03.026>
- Zhang, W.X. & Toda, M.J. (1992) A new species-subgroup of the *Drosophila immigrans* species-group (Diptera: Drosophilidae), with Description of two new species from China and Revision of Taxonomic Terminology. *Japanese Journal of Entomology*, 60, 839–850.
- Zhao, F., Gao, J.J. & Chen, H.W. (2009) Taxonomy and molecular phylogeny of the Asian *Paraleucophenga* Hendel (Diptera: Drosophilidae). *Zoological Journal of the Linnean Society*, 155, 616–629.
<http://dx.doi.org/10.1111/j.1096-3642.2008.00450.x>