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

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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 TIANGEN™ 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′–ATCGCCTAAACCTCAGCCAC–3′, Wang et al. 2006), HCO2198 (5′–TAAACTTCAGGGTGACCAAAAAATCA–3′, Folmer et al. 1994), *COI*-F3 (5′–C CGCAATATGRTATTTCTAC–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, 100º03' 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, 101º07' E, alt. 1200m, 27.vii.2009, fallen logs, L Wang; 1♀ (SCAU, No. 124324), Hesong, Menghai, Yunnan, 21˚49' N, 100º06' 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**


