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Two new genera and three new species of the Pantheinae from East Asia and China (Lepidoptera, Noctuidae). Contribution to revision of Pantheinae VIII

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Abstract

Two new genera and three species of the Pantheinae are described. The genus *Flavala* **gen. n.** (type-species *Acronycta flavala* Moore, 1867) is separated from *Anacronicta* Warren, 1909. The new combination *Flavala flavala* (Moore, 1867) **comb. n.** is introduced. Two new species, *Flavala crypta* **sp. n.** and *F. secunda* **sp. n.** are described based on the result of barcoding of mitochondrial DNA. The new genus *Xizanga* **gen. n.** (type-species *Xizanga mysterica* **sp.n.**) is tentatively placed in Pantheinae.

Key words: Noctuidae, Pantheinae, new genera, new species, new combination, DNA barcoding, East Asia, China

Introduction

In the course of our revision of the East Asian genera of Pantheinae, we found that *Anacronicta flavala* (Moore, 1867) does not belong to the genus *Anacronicta*, nor to any other genus of the Pantheinae. However, judging by the hindwing venation with developed vein M2 and the presence of sparse hairs on the eye surface, the taxon is more appropriately placed in the subfamily Pantheinae. Herein we separate "*flavala"* from *Anacronicta* and describe the new genus *Flavala* **gen. n.** with type species *Acronicta flavala* Moore, 1867. Examination of extensive material of "*flavala*" revealed that this taxon is represented by at least three externally nearly inseparable species with similar phenotypes and male genitalia. Subsequent molecular studies of them indicates this group is a complex of species with COI differences from 2.67% to 6.13%. Two such cryptic species are described in this article. The second genus described in this article, *Xizanga* **gen. n.** with type-species *Xizanga mysterica* **sp. n.,** is of uncertain systematic position. We tentatively place it in Pantheinae due to the quadrifid venation of the hindwing with developed vein M2, arising from the middle of discal cell, the bulged frons and short proboscis.

Material and methods

Molecular analyses were performed from dry legs of collected specimens. DNA barcodes (658 base pairs of Cytochrome Oxidase Subunit I 5' region, COI-5P) were sequenced in Paul Hebert's lab (CCDB) at the University of Guelph, Canada by using standard high-throughput protocol as described in Ivanova *et al*. (2006) (see also http://www.dnabarcoding.ca/pa/ge/research/protocols for regular updates of protocols used at the CCDB). The four sequences BC ZSM Lep 48680, 48681, 48682 and 58654 with images and further details about the barcoded specimens (e.g., voucher hosting institution, GenBank accession numbers, GPS coordinates, trace files) can be obtained from the Barcode of Life Data System (BOLD; Ratnasingham & Hebert 2007) The bar-code index numbers ('BIN') are BOLD:AAU3991, BOLD:AAU3992, BOLD:AAU3993 and BOLD:ABX0042. Sequences were analyzed using BOLD v3 analysis tools. The terms 'sequence variation' and 'genetic distance' refer to the

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