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The genus *Leucophenga* (Diptera, Drosophilidae), part I: the *abbreviata* species group from the Oriental region with morphological and molecular evidence

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Abstract

A new species group, the *abbreviata* group is established within the genus *Leucophenga* based on one known and three new species, all of which are endemic to the Oriental region: *L. abbreviata* (de Meijere, 1911), *L. brevivena* **sp. nov.**, *L. sujuanae* **sp. nov.** and *L. zhenfangae* **sp. nov.** A key to four species of the *abbreviata* group and the DNA barcoding are provided. Twenty-three mtDNA *COI* sequences belonging to the above species are analyzed; the molecular data are used as interactive evidence to evaluate the species boundaries defined by the morphological data.

Key words: DNA barcoding, *Leucophenga abbreviata* species group, new species, Oriental region

Introduction

A total 203 species of the genus *Leucophenga* Mik, 1886 (Diptera: Drosophilidae) have been reported from the world, 69 spp. from the Afrotropical region, 40 spp. from the Australasian region, eight spp. from the Nearctic region, 21 spp. from the Neotropical region, 75 spp. from the Oriental region and 25 spp. from the Palearctic region (Brake & Bächli 2008); and approximately 142 species of these are organized in the following ten species groups established (Bächli 1971; Okada 1990; Bächli *et al.* 2002): the *argentata* group (6 spp.), the *cuthbertsoni* group (2 spp.), the *flaviseta* group (4 spp.), the *flavopuncta* group (9 spp.), the *maculata* group (22 spp.), the *mutabilis* group (37 spp.), the *ornata* group (25 spp.), the *proxima* group (17 spp.), the *sorii* group (3 spp.) and the *subpollinosa* group (18 spp.) (Bächli 2012), the rest can not be placed to any of the above species groups.

In the present study, three new species from southern China and Nepal are described; they are morphologically similar to *Leucophenga abbreviata* (de Meijere, 1911) in wing M_1 vein distally abbreviated, not reaching wing margin (Fig. 2), which is unique in the genus. Thus, a new species group is established here, the *abbreviata* group, based on one known and three new species. Two Afrotropical species: *Leucophenga apicifera* (Adams, 1905) and *L. subvittata* Duda, 1939, share wing M_1 vein being distally abbreviated (Bächli 1971; Fig. 38, t, u), but the postocellar seta are longer than the inner vertical seta distinctly at least in *L. apicifera* (Bächli 1971; Fig. 17, k), while the postocellar seta are as long as the inner vertical seta in all the Oriental species; we provisionally exclude the two Afrotropical species in the *abbreviata* group to avoid further confusion.

It's widely accepted that molecular data have the potential to facilitate both the identification of known species and the discovery of new ones. DNA barcoding, initially proposed by Hebert *et al.* (2003a), is the use of a standardized segment of the genome for rapid species identification. The 5' end region of the mitochondrial cytochrome *c* oxidase I (*COI*) gene is recommended as the universal and standard barcoding marker for species identification (Hebert *et al.* 2004a; Ward *et al.* 2005; Ratnasingham & Hebert 2007). Various methods for DNA barcoding analysis are available and these include genetic distances, phylogenies and character attribute evaluation (Hebert *et al.* 2003b; DeSalle *et al.* 2005; Rach *et al.* 2008; Yassin *et al.* 2010; Reid *et al.* 2011; Zou *et al.* 2011). In this research, we analyze twenty-three barcode sequences of *COI* gene belonging to the one known and three new species in order to evaluate these species hypotheses.