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Description of a new species and new country distribution records of *Bactrocera* (Diptera: Tephritidae: Dacinae) from Cambodia

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Abstract

Bactrocera (*Bactrocera*) *kohkongiae* Leblanc (Diptera: Tephritidae: Dacinae), from the Koh Kong Province of Cambodia, is described as new. This species belongs to the Oriental fruit fly (*B. dorsalis*) complex. Genetic sequences (mitochondrial *COI* and nuclear *EF1α* and *Period*) are deposited in GenBank. A haplotype network, based on the *COI* sequences for 21 specimens, shows high genetic diversity. New country records from Cambodia are included for 22 species.

Key words: *Bactrocera*, Cambodia, Cardamom Mountains, Koh Kong, *kohkongiae*

Introduction

The fruit fly genus *Bactrocera* Macquart consists of at least 652 described species, including 73 pests of commercial/edible fruits and cucurbits (Vargas *et al.* 2015). Whereas the Australasian and Oceanian faunas were revised over two decades ago (Drew 1989), the tropical Asian species were poorly known until a recent comprehensive revision (Drew & Romig 2013). Much of the fresh material used in the Asian revision was collected from Malaysia, Thailand, Bhutan, Vietnam and Indonesia (Linder & McLeod 2008). Other regional countries were not as thoroughly surveyed, and likely harbour additional diversity. Such is the case for Cambodia, where only four species are officially known to be present (Leblanc *et al.* 2015b).

Material and methods

Traps baited with fruit fly male lures (cue-lure and methyl eugenol) were maintained for two days in 2011, along a road transect in Cambodia, to collect dacine fruit flies in forest and agricultural land. Collected specimens, preserved in 95% ethanol in a freezer, were identified to species using available literature (Drew & Hancock 1994, Drew & Romig 2013). For each species, DNA was extracted and the mitochondrial *COI* gene and nuclear *EF1α* and *Period* genes were sequenced, following the procedure described by San Jose *et al.* (2013). The *COI* sequences helped confirm species identifications and facilitated detection of cryptic species and matching of morphological variants across different geographic regions. Species determinations were confirmed by comparing pinned representatives with large series of identified species in the Queensland Department of Agriculture and Fisheries insect collection (Ecosciences Precinct, Brisbane, Australia) and the Bishop Museum (Honolulu, Hawaii). The *COI* dataset for 21 specimens of *B. kohkongiae*, described as new in this paper, was used to reconstruct a haplotype network using statistical parsimony (Templeton *et al.* 1992), as implemented in TCS version 1.21 (Clement *et al.* 2000), in order to visualize genetic variation. All sequences referred to in this publication are deposited on GenBank (Table 1). The 1464 base pair *COI* sequences on GenBank include the barcode region.

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