



Research paper

Species identification of horse flies (Diptera: Tabanidae) in Thailand using DNA barcoding



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ABSTRACT

Horse flies (Diptera: Tabanidae) are of medical and veterinary importance because they are known to transmit pathogens. Approximately 80 species of horse flies have been reported in Thailand. Monitoring the distribution of horse fly species is important to control the spread of diseases transmitted by them. Currently, the species identification of horse flies is based on their morphology; this requires considerable skills and taxonomic expertise, and it may be difficult to identify morphologically similar species. DNA-based identification methods are increasingly being developed for rapid and accurate identification of various insect species. In this study, we used mitochondrial cytochrome oxidase subunit I (COI) for species identification of horse flies in Thailand. A 658 bp fragment of COI was amplified from 145 adult horse flies belonging to 48 morphologically distinct species and sequenced. Sequence analysis revealed an intraspecific divergence of 0.0%–4.4% and an interspecific divergence of 0.0%–16.2%. Our results showed that COI barcodes were effective in discriminating a majority of horse flies in Thailand on the basis of the barcoding gap and phylogenetic analyses. However, COI barcodes were unable to distinguish among members of the *Tabanus striatus* complex and some species within the *T. ceylonicus* group.

1. Introduction

Horse flies, members of the family Tabanidae, are haematophagous flies that feed on livestock, wildlife and occasionally humans. They act as mechanical vectors in the transmission of several causative agents of medical and veterinary importance, including helminths, protozoa, viruses and bacteria (Foil, 1989; Le Goff et al., 1991; Baldacchino et al., 2014). Several species of horse flies transmit trypanosomiasis, a major protozoan disease in livestock farm caused by *Trypanosoma evansi*, *T. brucei*, *T. congolense* and *T. vivax* (Veer et al., 2002; Baldacchino et al., 2014). The family Tabanidae comprises nearly 4500 species, of which approximately 1300 species belong to the genus *Tabanus* (Morita et al., 2016). Approximately 80 species of horse flies have been identified in Thailand (Burton, 1978). Recently, Changbunjong et al. (2018) listed of 45 species and their distribution in different habitats of Thailand.

The correct identification of horse flies is very important for determining their role in disease transmission and for planning effective vector control and management strategies. The species identification of

horse flies based on morphological characters is easy to handle and economical and does not require any complicated equipment. However, the morphological species identification requires experienced taxonomists and the specimens need to have a clear external morphological characteristics with proper preparation. Misidentification does not only affect vector control but also the control and prevention of disease transmission. Therefore, molecular-based identification can be used to solve morphological problems in terms of morphologically similar species, lacking of important morphological characters and immature life stages. DNA barcoding is a standardised method to discriminate vertebrate and invertebrate species based on the amplification of 658 bp of cytochrome oxidase subunit I (COI). COI is a mitochondrial gene, which is amplified using a set of universal primers; it is used to discriminate between a wide variety of animal species (Hebert et al., 2003). The barcoding region of COI has been shown to effectively discriminate different species of many flies, including flesh flies (Meiklejohn et al., 2011, 2013), blow flies (Nelson et al., 2007; Boehme et al., 2012), fruit flies (Blackett et al., 2012), tabanid flies (Cywinska

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