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Article



Preliminary use of DNA sequences for *Dohrniphora* (Diptera: Phoridae) phylogeny and taxonomy

JOHN M. HASH¹, BRIAN V. BROWN² & PAUL T. SMITH¹

¹Department of Biology, California State University, Bakersfield, 9001 Stockdale Hwy, Bakersfield, CA 93311, USA. E-mail: psmith3@csub.edu ²Entomology Section, Natural History Museum of Los Angles County, 900 Exposition Boulevard, Los Angeles, CA 90007, USA. E-mail: bbrown@nhm.org

Abstract

Phylogenetic analysis of DNA sequence data from the nuclear CAD (rudimentary) and mitochondrial NDI, COI, and 16S gene regions (2817 bp total) recovered exemplars of the genus *Dohrniphora* as a monophyletic lineage. The data also supported the sister-group relationship of *Dohrniphora* + *Diplonevra* and were used to associate a morphologically dissimilar male and female of the species *D. ecitophila*. Further, we discuss the implications of this designation and provide support for the synonymy of *D. ecitophila* and *D. geminata* as proposed by Borgmeier (1968).

Key words: phylogenetics, parsimony, humpbacked flies, taxonomy, Dohrniphora, Diplonevra

Introduction

The genus *Dohrniphora* Dahl is estimated to be the third largest genus in the family Phoridae with approximately 175 described species (Brown & Kung 2007). *Dohrniphora* larvae exhibit diverse life histories including the following: parasitism, kleptoparasitism, predation, and scavenging (Disney 1994). Morphologically, the genus is characterized as having one dorsal longitudinal setal palisade on the hind tibia, absence of long wing setae, and a reduced epandrial ring on the dorsal surface (Brown 1992). The genus *Dohrniphora*, along with its hypothesized sister-taxon, *Diplonevra* Lioy, is classified in the tribe Diplonevrini and subfamily Aenigmatiinae (Brown 1992). *Dohrniphora* and *Diplonevra* can be distinguished from each other by the presence of two or more dorsal longitudinal setal palisades found on the hind tibia in *Diplonevra* (Brown 1992).

Similar to other phorid genera, *Dohrniphora* males and females exhibit extreme sexual dimorphism and often cannot be associated as the females exhibit few distinguishing characteristics. As such, the recognition of species and currently available taxonomic keys are based almost exclusively on male specimens only. Recently, Brown and Kung (2007) completed a partial revision of the New World *Dorhniphora* (i.e., those with hind tibial setae), and Brown & Kung (2010) revised the New World species without hind tibial setae. It is not known if each of the two groups represents monophyletic lineages or if hind tibial setae have been gained or lost independently on multiple occasions. A rigorous phylogenetic analysis using an independent character set, such as DNA sequence data, would be useful toward understanding the importance and evolution of hind tibial setation and intrageneric relationships within *Dohrniphora* in general.

Previous research on phorids has shown that molecular data are useful for species-level phylogeny estimation (Brown & Smith 2011; Smith & Brown 2010) and also for assigning unknown male phorids with their known female counterparts (Smith & Brown 2008). In Smith & Brown (2008), direct sequence comparison of the mito-chondrial 12S and ND1 genes was used to determine the identity of an unknown male from a database of known female *Melaloncha* DNA sequences. Similarly, known males and unknown females of the genus *Phora* have been associated using mitochondrial rDNA sequence data (Cook & Mostovski 2002). In the genus *Phora*, however, it is the male specimens that may be distinguished, based on the structure of the hypopygium, but female specimens are largely uniform in structure.