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Revision of the *Culicoides (Avaritia) Imicola* complex Khamala & Kettle (Diptera: Ceratopogonidae) from the Australasian region

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Abstract

The monophyly of the *Imicola* complex, a natural species complex within subgenus *C. subgen. Avaritia* Fox of the biting midge genus *Culicoides* Latreille, is supported using morphological and molecular analyses. A diagnosis for the group along with comparative redescriptions of the male and female of the species represented in Australasia, *C. brevitaris* Kieffer and *C. nudipalpis* Delfinado and a description of *C. asiatica* Bellis sp. nov., are presented together with keys for their specific determination and molecular support for their status.

Key words: Biting midges, taxonomy

Introduction

Several species belonging to *Culicoides* subgen. *Avaritia* Fox are of considerable veterinary importance as vectors of important arboviruses (Wirth and Dyce 1985; Meiswinkel *et al.* 2004b). There are varied opinions about the status of *C. subgen. Avaritia*. Yu *et al.* (2005) recently adopted a relatively broad definition of the group to include a number of species previously placed by Wirth & Hubert (1989) into a variety of other subgeneric groupings. Dyce *et al.* (2007) subsequently removed the species represented in Australasia back into the groupings proposed by Wirth & Hubert (1989) but the remainder are still placed within *C. subgen. Avaritia* (Borkent 2013). Meiswinkel *et al.* (2004a) suggested that a total of about 70 species belong to *C. subgen. Avaritia* sensu Wirth & Hubert (1989) and placed these into nine species complexes, namely the *Imicola*, *Obsoletus*, *Orientalis*, *Grahamii* (= *Actoni* sensu Dyce *et al.* 2007), *Pusillus*, *Suzukii* (= *Boophagus* sensu Dyce *et al.* 2007), *Gulbenkiani*, *Chiopterus* and *Dewulfi* complexes. To these Dyce *et al.* (2007) added the *Jacobsoni* complex bringing the total to ten complexes within the subgenus. Of these, the complex containing the greatest number of economically important species is the *Imicola* complex.

Meiswinkel (2004) provided a synopsis of this exclusively Old World complex offering a differential diagnosis between the *Imicola* and *Orientalis* Complexes and a list of the nine described species belonging to the complex, only two of which occur within Australasia. Dyce *et al.* (2007) subsequently placed four species present in Australasia, namely *Culicoides brevipalpis* Delfinado, *C. brevitaris* Kieffer, *C. nudipalpis* Delfinado and an undescribed species, into the *Imicola* complex.

In common with other subgeneric groupings within the genus *Culicoides*, there have been no attempts to test the monophyly of the *Imicola* complex. Borkent and Grogan (2009) noted that no phylogenetic analyses based on

antenna. This STI distribution is found in all species placed into the *Imicola* complex by Meiswinkel (2004) but does not occur in any other Australasian species of *C. subgen. Avaritia*, nor in the European species *C. obsoletus*, *C. scoticus* Downes & Kettle 1952, *C. chiopterus* or *C. dewulfi* (Delécolle 1985). Examination of the remaining species of *C. subgen. Avaritia* is necessary to confirm the phylogenetic importance of all of these characters within the subgenus. Within the Australasian fauna, each of the characters listed by Meiswinkel (2004), excepting the shape of the apex of the peg of the aedeagus and the STI distribution of the male antenna, which are herein proposed as synapomorphies for the *Imicola* complex, are present in some species belonging to the Actoni, Boophagus, Jacobsoni and Orientalis complexes sensu Dyce *et al.* (2007) and in *C. brevialpis*, although no single species in any of these complexes has the full suite of characters outlined by Meiswinkel (2004).

Linton *et al.* (2002) suggested that the grouping of known vector species of bluetongue virus towards the base of trees constructed using COI sequence data indicated that vector competence for the virus was ancestral within the *Imicola* complex. The lack of vector competence data for all but four species in the complex makes it difficult to draw conclusions but our analyses, using a wider range of species and two different genes, did not consistently place the four species implicated in the transmission of bluetongue virus, *C. imicola*, *C. bolitinos*, *C. brevitarsis* and *C. asiatica*, either together nor at the base of phylogenetic trees. This suggests that vector competence for this virus is either more widespread within the complex or that it has evolved on several occasions as has occurred with the vector capacity for malaria in the *Anopheles gambiae* complex (Kamali *et al.* 2012) and for *Leishmania* spp. in the Phlebotominae (Ready 2011).

Cryptic species which are genetically distinct but inseparable morphologically (Bickford *et al.* 2007) have been described from a range of different insect orders, including the Diptera, although none have thus far been identified within the genus *Culicoides*. Using a single molecular marker (COI), Pagés *et al.* (2009) discovered the presence of several morphologically similar species within *C. subgen. Culicoides* in Spain although they were able to separate these new species using morphometrics so they do not represent truly cryptic species. The absence of reliable morphological differences in either sex of *C. brevitarsis* and *C. bolitinos* indicates these two species are the first truly cryptic species so far known in the genus *Culicoides*.

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