

The *Culicoides* of the subgenus *Avaritia* (Diptera: Ceratopogonidae) in the Palaearctic region: through unsuspected diversity with epidemiologic implications

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The biting midges of the genus *Culicoides* (Diptera: Ceratopogonidae) are known vectors of pathogens especially Orbivirus of the Reoviridae family such as bluetongue, african horse sickness, epizootic hemorrhagic disease and more recently Schmallenberg viruses. The western Europe and the Mediterranean basin faced bluetongue transmission with the 6 species belonging to the *Avaritia* subgenus recorded in these areas including the species closely related to the *Obsoletus* group. To date, no study encompasses the whole number of species belonging to a subgenus at a biogeographical scale. The data presented focus on local or on country fauna scale using a classification based on subgenus and/or group of species. Among the latter, the presence of cryptic species has been pointed out by recent phylogenetic studies. These classification discrepancies between authors since decades result in a taxonomic imbroglio. Recent findings of specimens with tricky morphology related to the *Obsoletus* group in France led us to better describe the systematic and the taxonomy of the subgenus *Avaritia* in the Palaearctic region. This study focuses on investigating the phylogenetic relationships between and within the *Avaritia* species of the Palaearctic region with a special interest for the *Obsoletus* group at a world scale.

Voucher specimens were selected based on morphology, sequenced for the CO1 region (mtDNA) and then slide-mounted allowing a morphological interpretation of the results afterwards. A total of 82 CO1 sequences including 43 sequences from the GenBank database were analyzed by Bayesian inference and the resulting tree was used to study species boundaries. The Barcoding gap was evaluated for the closest related species not supported by the species delimitation analysis.

Within the *Avaritia* subgenus, we propose a new systematic scheme for the species of the *Obsoletus* group including *C. scoticus* as a basal clade with the two following complexes: the *Sanguisuga* complex with the species *C. abchazicus*, *C. gornostaevae*, *C. sanguisuga* and *C. sinanoensis*; the *Obsoletus* complex made of the species *C. obsoletus*, *C. montanus* and a new species. *Culicoides filicinus*, absent in this analysis, could not be placed in the proposed scheme. The existence of *Dewulfi* and *Chiopterus* complex is discussed. The results of the species boundaries analysis and the presence of discriminant morphological characters support the evidence of two new species under description with one in the *Obsoletus* complex. We also point out new records of *C. gornostaevae* (France, Sweden and Switzerland) and *C. aff. sanguisuga* (Sweden). The subgenus *Avaritia* includes worldwide major vectors of Orbivirus. The revealed diversity increases up to 10 species in western Europe and questions about the possible vector roles in Europe of these newly recorded species. Evaluating the vector role of the *Avaritia* species in bluetongue and other viruses transmission reaches a higher challenging level for the European teams.