



VII INTERNATIONAL SIMULIIDAE SYMPOSIUM

Zaragoza 2016

5-8 September 2016

Book of abstracts

Systematics, evolution and biogeography, Ecology and behaviour, Disease transmission, Natural enemies and symbiotic interactions, Economic impacts, control and management

Editor of the book of abstracts

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Design

bogartybacall
CREATIVE DESIGN

O.03. DNA BARCODING OF SPANISH BLACK FLIES (DIPTERA: SIMULIIDAE)



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Key Words: COI, DNA barcoding, spanish black flies, simuliidae, cryptic diversity.

Certain black flies are of medical concern because they transmit pathogens of medical or veterinary importance. However, their taxonomy is very difficult because of their morphological homogeneity. In the present study, the utility of a partial sequence of the COI gene, the DNA barcoding region, as an aid for species identification of Spanish Simuliidae is discussed. Immature specimens were collected manually and mature larvae reared to adult in the laboratory; man biting females were collected on human catches or other baits. There are recorded 5 genera and 50 species in Spain. In this paper, we analyzed 14 morphospecies collected mainly around the Aragón Region, representing a 28% of the total blackfly fauna in the country. The Neighbour Joining tree (NJ) derived from the DNA barcodes grouped most specimens according to species recognized by morphological traits. The overall genetic distance average 0.13% specific sequence divergences within morphologically distinct species ranged from 0 to 0.6%, while higher divergences (3.3% to 3.68%) suggested cryptic diversity. Highest between group mean genetic diversity averaged 20.84% between the pair *Prosimulium latimucro* (Enderlein, 1925) and *Simulium velutinum* (Santos Abreu, 1922). Regarding species complexes we only analyzed *S. ornatum* s.l. specimens from this species grouped in two groups in the NJ, indicating the presence of hidden diversity. *P. latimucro* showed deep splits in the NJ well supported by bootstraps values. In conclusion, DNA barcoding combined with a sound morphotaxonomic framework would provide an effective approach for the identification of black flies in the region.

We thank Nadya Nikilova, Biodiversity Inst of Ontario, Univ. Guelph, Canada for her validation of COI sequences and data in BOLD database.