A brief review on the molecular markers for Phlebotominae taxonomy (Diptera, Psychodidae)

Bruno Leite Rodrigues[1]*& Eunice Aparecida Bianchi Galati[1]

[1] Programa de Pós-graduação em Saúde Pública, Faculdade de Saúde Pública (FSP/USP), São Paulo – SP, Brasil.

*apresentador; e-mail: brunno2310@gmail.com

Traditionally, the use of morphological traits has been the main line of evidence for the definition of sand fly species and their evolutionary relationships, but the use of molecular tools is useful as an integrative approach. Thus, we assess the current status of the molecular taxonomy of sand flies, including their most sequenced molecular markers. For this, we searched for original papers on the molecular taxonomy of sand flies using electronic databases and several key words on this topic. We also searched for the available molecular markers for each nominally described sand fly taxa in the NCBI GenBank nucleotide database, and in the Barcode of Life Data Systems – BOLD (last consulted on 10th Oct, 2022). Our survey identified that isoenzymes, microsatellites, and more recently the protein-based MALDI-TOF approaches have been used for taxonomic purposes, but the sanger sequencing and analysis of specific molecular markers are most used in the study of the taxonomy and systematics of sand flies. Of the 1,026 current sand fly species, 376 (37%) have been sequenced for at least one molecular marker, being 204 of them from the western hemisphere (New World) and 172 from the eastern one (Old World). Some genera are well-sampled, such as *Phlebotomus*, *Psychodopygus*, and *Nyssomyia*, which have 61%, 60%, and 66% of their species processed, respectively. All these genera are involved in the transmission of pathogens that causes the leishmaniases, which increases the interest in studying the integrative taxonomy of these groups. On the other hand, less than 25% of the species within the genera *Sergentomyia*, *Trichopygomyia*, and *Trichophoromyia* have been sampled, representing a major gap in the knowledge of these groups. These genera should be better sampled, especially in the case of *Trichophoromyia* due to their vectorial role, and the lack of morphological diagnostic characters to identify female specimens. Moreover, the genera *Deanemyia*, *Edentomyia* and *Hertigia* do not yet have any sequences for any of their species recorded, and despite the small number of the taxa described, their sequences will be of great relevance in the elucidation of the evolutionary relationships of American sand flies. The most sequenced molecular markers are those within mtDNA, especially the DNA barcoding fragment of *COI* gene, which has shown promising results in detecting cryptic diversity within species. At least one quarter of all sand fly species have a *COI* sequence. However, few sequences of conserved marker such as the rRNA 28S have been generated, which hampers higher-level phylogenetic inferences. We argue that the molecular taxonomy of sand flies continues to be investigated, as it has provided valuable information in detecting cryptic diversity, and may help to elucidate evolutionary patterns at the suprageneric level as different groups and markers are evaluated.

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