

Molecular characterization of *Fannia* (Insecta, Diptera, Fanniidae) species of medical and forensic importance

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Fannia is the largest genus in the Fanniidae (Insecta, Diptera) family, with worldwide distribution and well diversified feeding habits. Some species can be found both in urban and rural environments and are synanthropic. For this reason and because they frequent garbage and stool are vectors of pathogens for humans and other domestic animals. In addition, they can carry eggs of *Dermatobia hominis* (the “berne” fly) contributing to the establishment of myiasis. Due to the necrophagous habit, some species may also be relevant in the forensic context with respect to the estimation of the postmortem interval. The correct identification of these species, either in the epidemiological or forensic context, is an essential step in the progress of the knowledge of the group's diversity or their ecological role, to obtain useful information for population control or for direct application in forensics. Morphological diagnosis is usually difficult because there is a great lack of descriptions and registers for these species and few taxonomic keys available. Molecular techniques have been promising to complement, aid and expedite the morphological identification of species. The objective of this study was to evaluate the effectiveness of the use of molecular techniques in the identification of *Fannia* species and their potential contribution in recognizing new species or morphological misidentification. Nucleotidic sequences of 658 bp of the mitochondrial cytochrome oxidase I (COI) gene from *Fannia* species were obtained from the GenBank database and from DNA extractions, amplification (PCR) and sequencing in the laboratory. A total of 192 sequences, representing 39 *Fannia* species, were analyzed based on the DNA Barcode method, following the methodology proposed by the International Barcode of Life Project (IBoL). The divergence relationships (intra and interspecific) of those sequences were analyzed with the Neighbor-Joining (NJ) phylogenetic reconstruction method, using the 2-parameter Kimura evolutive model as implemented in the MEGA6 software. Only 37 operational taxonomic units (OTUs) from the 39 nominal species were recognized in the phylogenetic tree, suggesting possible mistakes in morphological identification. The Barcode DNA method was useful to differentiate species at the molecular level and also helped identify a new species. Thus, we conclude that molecular tools, associated with morphology, should be used with the aim of minimizing the taxonomic impediment among organisms of medical and/or forensic relevance.