

Poster Communication 80

SNaPshot in forensic entomology: Molecular identification of Calliphoridae (Diptera) species

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Abstract

Background: Forensic entomology enables estimation of the minimum post-mortem interval (minPMI) by analysing the sequence and age of insects colonising decomposing remains. Traditionally based on morphological/morphometric methods, insect identification is constrained when distinguishing closely related taxa. In these cases, relying solely on morphological characteristics is insufficient, making it challenging to accurately identify the insect species present. To surpass this limitation, molecular identification methods have been developed to support daily practice and identify insect species, such as cytochrome c oxidase subunit I (COI), which is considered the most successful gene sequence for insect identification. However, gene sequencing has its disadvantages, such as being time-consuming and expensive. Other techniques, such as SNaPshot - a minisequencing technique based on single nucleotide polymorphism (SNP) that allows species differentiation - have been proposed to improve the precision of identification of forensically important species [1,2]. **Objective:** This study aims to identify gaps in the use of SNaPshot-based analysis for the molecular identification of forensically relevant insect species, particularly closely related taxa and immature stages. **Methods:** A systematic literature review was conducted in accordance with PRISMA guidelines using Google Scholar, Web of Science, ScienceDirect, and PubMed databases. Studies published between 2020 and 2025 addressing the molecular identification of *Calliphora* spp., *Lucilia* spp., and *Chrysomya* spp. (Diptera: Calliphoridae) using SNaPshot. **Results:** Systematic research clarified grey areas in molecular identification using SNaPshot, highlighting its value for forensic important blowfly species (2020–2025). Only one addressed the distinction between *Calliphora* spp. and *Lucilia* spp., and there were no reports of *Chrysomya* spp. This gap is an opportunity to broaden knowledge and explore new techniques for successful identification [3]. **Conclusions:** The findings highlight a significant gap in the use of SNP-based techniques, such as SNaPshot, to identify forensically relevant blowfly species. Expanding molecular approaches may improve species-level identification, particularly for closely related taxa and immature stages, strengthening forensic entomology in medico-legal investigations.

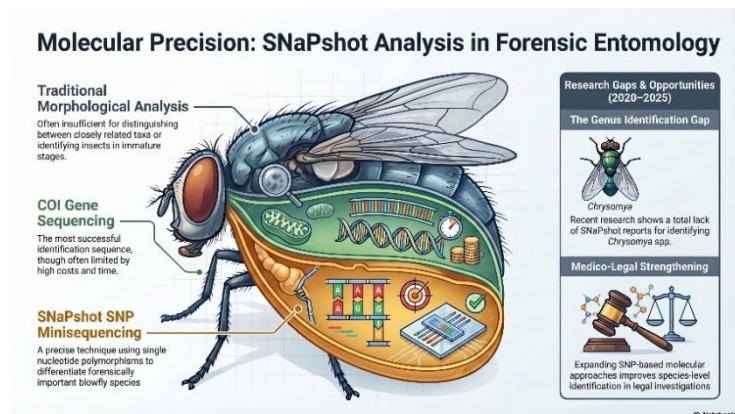


Figure 1. Systematic representation of inclusion and exclusion based on research of manuscripts across public access databases

Keywords: Calliphoridae; Diptera; molecular identification; SNaPshot; forensic entomology

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References

1. Scieuzo, C. et al. The contribution of molecular biology to forensic entomology. *Insects* **2025**, *16*, 694, doi: 10.3390/insects16070694.
2. Oliveira, M. et al. Feasibility of mitochondrial single nucleotide polymorphisms to detect and identify *Aspergillus fumigatus* in clinical samples. *Diagn Microbiol Infect Dis* **2014**, *80*, 53–58, doi: 10.1016/j.diagmicrobio.2014.05.007.
3. Godfrey, H. et al. IdentiFLY: The development and validation of a 15-plex SNP assay for forensic identification of UK blowfly species (Calliphoridae). *Taxonomy* **2024**, *4*, 680–695, doi: 10.3390/taxonomy4040035.



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