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Editorial

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Relevance of molecular systematics in insect pest management

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Insects (Insecta, Arthropoda), undeniably represent the most triumphant group of living organisms, in terms of evolutionary achievement, existing on earth. With over one million described species, they account for more than 75 percent of all known species, and it is estimated that at least 4-5 million insect species still remain undiscovered and undescribed (Stork, 2018). They represent one of the largest components of biodiversity in the world, closely associated with human's wellbeing in different forms like pests, natural enemies, producers of economic products and facilitators of pollination. In contemporary times, despite notable progress in agricultural output and economic prosperity in many regions, the problem of food insecurity persists as a significant concern affecting substantial segments of the global population (Palli, 2022). To cater the food demand of the fast expanding global population, intensive agricultural practices like extensive use of chemical fertilizers and insecticides, greater tillage and irrigation, as well as heavy mechanization are followed. The result is frequent outbreak of phytophagous insect pests along with a rapid decline in the biodiversity of beneficial insects including natural enemies and pollinators. It is estimated that crop losses caused by insects are a major problem in both developed and developing countries, destroying 18 to 20 per cent of the annual crop production globally, having worth over US$ 470 billion (Srivastava and Chakravarty, 2021).

Initially, when pesticides were used to control or prevent insect pest outbreaks, the chemicals were often applied as soon as a problem was perceived, without accurate identification of the insect's identity or discovery of why the problem had developed in the first place. This lack of understanding of the cause of outbreak meant that the same problem could reoccur. Sustainable pest management requires a more scientific approach. The first step in this direction is the correct identification of the insect species. Accurate species identification, whether of the pest or its associated natural enemy along with their biological systematic studies provide backbone information for the success of any integrated pest management programme (Chakravarty *et al.,* 2022). Traditional systematics or taxonomy was primarily reliant on morphology-based taxon identification systems. However, the process of morphological identification poses significant challenges in numerous insect taxa, mostly attributable to the absence of dependable diagnostic traits or the presence of cryptic species complexes (Shashank *et al.*, 2022). Moreover, due to a decrease in the number of proficient morpho-taxonomists, specifically those specializing in lesser-known insect groups, there is a need for alternate approaches to species identification. Presently, entomologists are leveraging a wide array of molecular techniques that were previously untapped, while also embracing novel technologies under the paradigm of a "technology-driven revolution" in the field of systematics (Srivastava *et al.*, 2019).

Molecular techniques present a highly advantageous strategy for the identification and classification of insects, offering distinct benefits when compared to traditional morphological methods. Over the past twenty years, DNA barcoding has emerged as a swift and dependable technique for the identification of species, thereby revitalizing the field of taxonomic study. It refers to the technique, where short fragment of the conserved mitochondrial cytochrome c oxidase subunit I (COI) gene, the “DNA barcode,” is sequenced from a taxonomically undesignated specimen and comparisons are made with the DNA sequence of species of known origin for establishing a species level identification (Hebert *et al.*, 2003). This approach has been frequently employed in various studies focusing on insects (and other arthropods in general), leading to the identification of previously unknown or cryptic species. Additionally, it has helped identify species complexes and evolutionary significant units, thereby establishing a basis for further comprehensive integrative taxonomic research (Firake and Behere, 2021). DNA barcoding considerably facilitates the monitoring of invasive species, vectors, and economically important endangered and/or endemic arthropod species. Furthermore, the utilization of DNA metabarcoding in ecological and surveillance initiatives has become increasingly prevalent. This approach enables the rapid evaluation of biodiversity in certain geographical regions, as well as the study of arthropod biosystems and communities that would otherwise be inaccessible.

In recent times, entomologists in India have efficiently identified various invasive insect pest species, such as the elephant beetle, tomato pinworm, rugose spiralling whitefly, coconut case caterpillar, fall armyworm, and cassava mealy bug, by incorporating molecular systematics either as the sole method or in conjunction with traditional taxonomical tools (Srivastava and Chakravarty, 2021). In addition, there have been endeavours to offer extensive data through molecular characterization and/or DNA barcoding of indigenous organisms that serve as natural enemies and pollinators within diverse agricultural systems of India (Srivastava *et al.*, 2019). A good number of insect genomes, particularly the mitochondrial genome have also been wholly sequenced in the country, including both crop pests and beneficial insects (Firake and Behere, 2021). However, our nation renowned for its exceptional biodiversity, exhibits a mere 3.73% coverage of DNA barcodes for its documented insect species. Notably, the orders Lepidoptera and Hemiptera are the most extensively represented in this limited dataset (Shashank *et al.*, 2022). Such a delay in developing DNA barcode reference libraries for insects will set us back in our efforts to effectively document and preserve our rich biodiversity.

The introduction of molecular systematics has also precipitated a revolution in our understanding of intraspecific genetic diversity and population genetic structure of several key insect pest species of agricultural importance in the country, helpful to detect the changes they adapt to overcome hurdles of various selection pressures including insecticides (Chakravarty *et al.,* 2020). A necessity for the development of effective and safe management techniques for a target pest is the acquisition of comprehensive knowledge pertaining to its population structure and dynamics. Despite the emergence of inconsistencies between morphological and molecular phylogenies, as well as conflicting results from different molecular research, the utilization of phylogenomic analysis has proved helpful in resolving numerous controversial connections within insects. Over the past decade, our working group has devoted its research efforts entirely to this particular issue. Based on the molecular characterization with RAPD markers (Deepa and Srivastava, 2011) and COI gene (Chakravarty *et al*., 2021), phenotyping of immature and adult stages (Chakravarty and Srivastava, 2020; Chakravarty *et al*., 2023b), and other biological traits (Chakravarty *et al.*, 2019 and 2023a), existence of sub-specific level variations among *Helicoverpa armigera* populations from diverse agro-ecologies of India has been deciphered. Similar studies for *Leucinodes orbonalis* (Padwal *et al*., 2022), *Spodoptera litura* (Ganguly *et al.,* 2023) and *Maruca vitrata* (Mahalle *et al.*, 2022) revealed genetic homogeneity for these pest species in the country. Further, Mahalle *et al*. (2023) have also screened publically accessible expressed sequence tag resources to identify microsatellites and evaluate their suitability as DNA markers for investigating gene flow patterns among populations of *M. vitrata* from pigeonpea fields throughout India.

Molecular systematics has also proven to be a valuable tool in the identification of convergent evolution phenomena, such as the emergence of eusocial behaviours and caste systems among Hymenoptera (Berens *et al*., 2015); comprehending predator-prey dynamics within trophic food web investigations (Novotny and Miller, 2014), as well as resolving challenges associated with limited specimen availability or local species populations (Deng *et al.,* 2019). Nevertheless, it is important to note that relying solely on molecular analyses to determine the identity of a species or assess population diversity can be precarious. This is due to potential biases introduced by the improper utilization of neighbor-joining trees, fixed distance thresholds, bootstrap resampling, interpretation of the barcoding gap, as well as limitations associated with DNA barcode repositories such as the Barcode of Life Data Systems (BOLD) and the National Centre for Biotechnology Information (NCBI). For instance, in a study conducted by Kvist (2013), it was found that 42% of invasive insects were not included in the BOLD database. Furthermore, the outcomes of phylogenetic analyses can be affected by various factors, such as the occurrence of recent speciation events, the presence of paraphyly, inadequate taxonomy, interspecific hybridization, and the high prevalence of endosymbiotic bacteria like *Wolbachia*, that hinders the replication or detection of the target sequence from insect specimens during the polymerase chain reaction, as highlighted by Shashank *et al.* (2022). Therefore, it is recommended that molecular methodologies should be utilized in conjunction with, rather than in lieu of, morphological identification in order to achieve optimal outcomes (Chakravarty *et al.*, 2023b).

Last but not the least, a note of appreciation for the "*Journal of Environmental Biology*" is also appropriate at this juncture. We are pleased to share our research experience and expertise through this editorial in the aforementioned journal, with which we have been affiliated for several years in various roles such as author, reviewer, and editor. This open access journal is notable for its comparatively modest processing charges, which enable researchers to publish their original work at an affordable cost. The enduring anticipation for highly critical reviews has contributed to the continued prominence of this journal within the realm of environmental science and related disciplines. We appreciate the visions of late Professor R.C. Dalela and his dedicated team, who have worked tirelessly over the years to make this journal a valuable resource for the global environmental outlook, with the ultimate aim of promoting societal well-being. Currently, the responsibility of overseeing this journal rests with Dr. Divakar Dalela, the Executive Editor, and Dr. Sumati Gaumat, the Editor, together with their dedicated publication team. They are diligently working towards upholding the international standards of this esteemed journal. We extend our best wishes for the continued success of the journal in the years to come.

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