Wigyan Varta www.vigyanvarta.com www.vigyanvarta.in

Vol. 5, Issue 11

Review on Cutting-Edge Genetic Markers in Insect Science: Current Trends and Applications

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Keywords

Molecular markers, Insect Science, Trends, Application

How to cite this article:

Warghat, A. N., Singh, K.P., Tayde, A. R. and Bawane, A. S., 2024. Review on Cutting-Edge Genetic Markers in Insect Science: Current Trends and Applications. *Vigyan Varta* 5(11): 24-29.

ABSTRACT

Molecular markers are pivotal in modern entomology, enabling the identification and differentiation of insect species, populations, and individuals. This review highlights the significance of molecular techniques such as DNA barcoding, microsatellites, and single nucleotide polymorphisms (SNPs) in enhancing our understanding of genetic diversity, evolutionary processes, and ecological interactions among insects. These markers facilitate reliable species identification, particularly in cases of cryptic species, and provide insights into population structure and gene flow, which are crucial for conservation efforts. Additionally, molecular markers contribute to elucidating evolutionary relationships, aiding in the reconstruction of phylogenies and understanding adaptation. Furthermore, they play a vital role in studying ecological interactions, including insect-plant relationships and ecosystem dynamics. As molecular technologies continue to evolve, their applications in entomology will expand, offering deeper insights into insect biology and their roles in ecosystems, with implications for biodiversity conservation and environmental management.

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INTRODUCTION

olecular markers are specific sequences in the genome that can be used to identify and differentiate between individuals, populations, and species of insects. These markers play a crucial role in modern entomology, enhancing our understanding genetic of diversity, evolutionary processes, and ecological interactions. Molecular markers are specific sequences of DNA or RNA that serve as identifiable features within the genome of an organism. In entomology, these markers are instrumental in differentiating between individuals, populations, and species of insects. Their application has transformed various aspects of insect research, providing insights into genetic diversity, evolutionary dynamics, and ecological interactions that are critical for understanding insect biology and behavior. Identification and Differentiation of Species as one of the primary uses of molecular markers in entomology is species identification. Traditional morphological methods can be limited, particularly when dealing with cryptic species-organisms that are morphologically similar but genetically distinct. Molecular techniques, such as DNA barcoding, utilize short, standardized genetic sequences (often from mitochondrial genes like cytochrome c oxidase I) to provide reliable species identification. This method has greatly enhanced our ability to catalogue biodiversity, detect invasive species, and monitor ecosystem health (Hebert et al., 2003).

Understanding Genetic Diversity as a genetic diversity is vital for the adaptability and resilience of populations. Molecular markers, such as microsatellites and single nucleotide polymorphisms (SNPs), allow researchers to assess levels of genetic variation within and among populations. By analysing this diversity, scientists can infer historical patterns of gene flow, population structure, and inbreeding levels, which are crucial for understanding how populations respond to environmental changes and pressures (Hughes *et al.*, 2000). Such insights are essential for the conservation of endangered insect species, enabling the development of strategies that maintain or enhance genetic diversity.

In Insights into Evolutionary Processes molecular markers also play a significant role elucidating evolutionary relationships in among insect species. Phylogenetic analyses based on molecular data can reveal the evolutionary history of species, helping to resolve complex relationships that morphological studies may fail to clarify. By constructing phylogenetic trees, researchers can identify common ancestors, understand speciation events, and track evolutionary adaptations to various ecological niches (Kress understanding et al.. 2005). This of evolutionary processes is fundamental for predicting how species might respond to future environmental changes, including climate change.

As per the Ecological Interactions the application of molecular markers extends beyond taxonomy and population genetics; they are also invaluable in studying ecological interactions among species. For instance, molecular techniques can be used to assess host plant associations and feeding behaviors in herbivorous insects, revealing the dynamics of insect-plant interactions. Additionally, understanding the genetic structure of insect populations can shed light on their roles in ecosystems, such as pollination, nutrient cycling, and as prey or predators in food webs (Sweeney et al., 2011). In this review the molecular markers are essential tools in modern entomology that enhance our understanding of insect biodiversity, genetic variation, evolutionary history, and ecological



interactions. As molecular technologies continue to advance, their applications will expand, providing even deeper insights into the complex lives of insects and their roles in ecosystems. This knowledge is crucial not only for academic research but also for practical applications in agriculture, conservation, and public health.

1.1 Types of Molecular Markers

1.2.1. DNA Barcoding

- Description: DNA barcoding involves sequencing a short, standardized region of the genome, typically mitochondrial genes like cytochrome c oxidase I (COI). This technique allows for rapid species identification and has become a cornerstone in taxonomic studies.
- Application: It is particularly useful for identifying cryptic species and assessing biodiversity in various habitats (Hebert *et al.*, 2003).

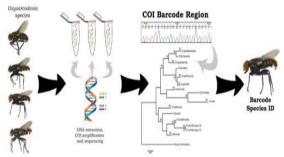


Fig 1 Typical DNA barcoding in insect species

1.2.2. Microsatellites

- Description: Also known as simple sequence repeats (SSRs), microsatellites are short, repetitive DNA sequences that exhibit high variability among individuals. They are co-dominant markers, allowing for the detection of heterozygosity.
- Application: Commonly used in studies of population structure, gene flow, and genetic diversity (Zane *et al.*, 2002).

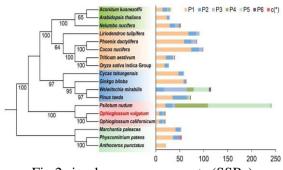


Fig 2 simple sequence repeats (SSRs)

1.2.3. Single Nucleotide Polymorphisms (SNPs)

- Description: SNPs are variations at a single nucleotide position in the genome. They are abundant and can be used to study genetic variation at a fine scale.
- -Application: Useful in phylogenetic studies, population genetics, and mapping traits related to adaptation (Elshire *et al.*, 2011).

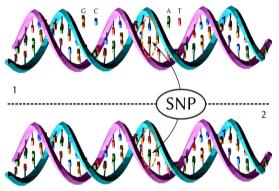


Fig 3 Single Nucleotide Polymorphisms (SNPs)

1.2 Amplified Fragment Length Polymorphism (AFLP)

- Description: AFLP involves the selective amplification of specific DNA fragments using restriction enzymes, followed by gel electrophoresis. This method allows for the analysis of multiple loci simultaneously.
- Application: AFLP is valuable for assessing genetic diversity and relationships among populations (Vos *et al.*, 1995).



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1.3 Restriction Fragment Length Polymorphism (RFLP)

- Description: RFLP involves digesting DNA with restriction enzymes and analysing the resulting fragment lengths. Variations in fragment length are used to distinguish between different genotypes.
- Application: RFLP is utilized in genetic mapping, population studies, and the identification of species (Pflieger *et al.*, 1999).

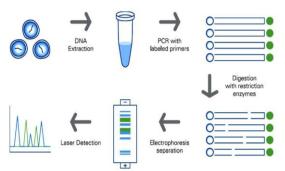


Fig 4 Restriction Fragment Length Polymorphism (RFLP)

1.4 Applications in Entomology

1.4.1 Taxonomy and Systematics

- Molecular markers have revolutionized insect taxonomy by providing objective criteria for species identification and resolving complex phylogenetic relationships (Kress *et al.*, 2005). For example, DNA barcoding has facilitated the identification of many previously unrecognized species.

1.4.2 Population Genetics

- By analysing genetic diversity within and between populations, researchers can assess levels of inbreeding, gene flow, and evolutionary pressures (Hughes *et al.*, 2000). This information is critical for understanding how populations adapt to changing environments.

1.4.3 Ecological Studies

- Molecular markers help track dispersal patterns and host associations in insects, which are essential for understanding ecological interactions and the dynamics of ecosystems (Sweeney *et al.*, 2011).

1.4.4 Conservation Biology

- Genetic studies are vital for conservation efforts, allowing scientists to identify genetically distinct populations and assess their viability (Frankham *et al.*, 2002). This information aids in the development of effective conservation strategies for endangered insect species.

1.4.5 Disease Vector Studies

Molecular markers are crucial in identifying and monitoring disease vectors. Understanding the genetic diversity of vector populations can inform control strategies for vector-borne diseases (Lindsay *et al.*, 2016).

1.4.6 Forensic Entomology

Molecular techniques can assist in identifying insect species involved in decomposition, providing valuable information in criminal investigations (Benecke, 2001).

2.1 Case Study and Review of Drosophila melanogaster



2.1.1 Introduction

Drosophila melanogaster, commonly known as the fruit fly, is a pivotal model organism in genetics and molecular biology. Its ease of cultivation, short life cycle, and well-mapped



genome make it an invaluable resource for scientific research.

2.1.2 Biology and Life Cycle

Drosophila melanogaster undergoes complete metamorphosis, with four distinct life stages: egg, larva, pupa, and adult.

- 1. **Egg Stage**: The female lays eggs on fermenting fruit. These eggs hatch within 24 hours.
- 2. Larval Stage: The larvae go through three instar stages, feeding on yeast and bacteria in the fruit. This stage lasts about 4-5 days.
- 3. **Pupal Stage**: The larvae form pupae, within which they undergo metamorphosis. This stage lasts about 4 days.
- 4. **Adult Stage**: The adult emerges from the pupa. Adults are sexually mature within 8-12 hours and can live for several weeks.

2.1.3 Use as a Genetic Resource

Drosophila melanogaster has been instrumental in numerous genetic discoveries due to its genetic simplicity and the availability of sophisticated genetic tools. Key reasons for its use include:

- 1. **Short Generation Time**: A complete life cycle in about 10 days allows for rapid generation turnover.
- 2. Large Number of Offspring: Females can lay hundreds of eggs, providing ample material for genetic studies.
- 3. Well-Characterized Genome: The genome of *D. melanogaster* is fully sequenced, with many genetic tools available for manipulation.
- 4. **Ease of Maintenance**: They can be easily cultured in the laboratory on simple media.

2.1.4 Key Studies and Results

- 1. **Genetic Mapping**: Early work by Thomas Hunt Morgan and colleagues used *D*. *melanogaster* to establish the chromosomal theory of inheritance. They mapped genes to specific chromosomes, demonstrating that genes are arranged linearly on chromosomes (Morgan, 1910).
- 2. **Developmental Biology**: Studies on *D. melanogaster* have elucidated key aspects of developmental biology, including the discovery of homeotic genes, which control the body plan of the embryo (Lewis, 1978).
- 3. **Behavioral Genetics**: Research has also explored the genetic basis of behavior, such as circadian rhythms and mating behaviors (Konopka & Benzer, 1971).

2.1.5 Recent Advances

Recent studies have leveraged advanced genetic tools like CRISPR/Cas9 to edit the *Drosophila* genome, allowing for precise manipulation of genes to study their functions (Gratz *et al.*, 2013). Additionally, *D. melanogaster* is used in studies of human disease models, including neurodegenerative diseases and cancer, due to the conservation of many genetic pathways between flies and humans (Pandey & Nichols, 2011).

The *Drosophila melanogaster* remains a cornerstone of genetic research, providing insights into fundamental biological processes and human diseases. Its continued use in research promises to yield further significant discoveries.

CONCLUSION:

Advancements in genomic technologies, such as next-generation sequencing (NGS), are likely to enhance the resolution and scope of molecular marker studies in entomology. The integration of genomic data with ecological



and behavioral studies will provide a more comprehensive understanding of insect biology, facilitating studies on biodiversity, conservation, and the impacts of climate change. More research in application of these could be a fascinating way to discover an unimaginable life of insect and its biology.

REFERENCES:

- Benecke, M. (2001). A brief history of forensic entomology. *Forensic Science International*, 120(1-2), 2-14.
- Elshire, R. J., Glaubitz, J. C., Sun, Q., Poland, J. A., Kawamoto, K., & Buckler, E. S. (2011). A robust, simple, and costeffective method for genotyping SNPs in a large number of samples. PLoS ONE, 6(5), e19379.
- Frankham, R., Ballou, J. D., & Briscoe, D. A. (2002). Introduction to Conservation Genetics. *Cambridge University Press*.
- Gratz, S. J., Rubinstein, C. D., Harrison, M. M., Wildonger, J., & O'Connor-Giles, K. M. (2013). CRISPR-Cas9 genome editing in Drosophila. Current Protocols in Molecular Biology, 107(1), 31-36.
- Hebert, P. D. N., Cywinska, A., Ball, S. L., & deWaard, J. R. (2003). Biological identifications through DNA barcodes. Proceedings of the Royal Society B: *Biological Sciences*, 270(1512), 313-321.
- Hughes, C. R., Stoeckel, J. L., & Weller, S. J. (2000). Genetic diversity and population structure in the yellow fever mosquito, *Aedes aegypti*. Genetics, 155(1), 91-104.
- Konopka, R. J., & Benzer, S. (1971). Clock mutants of Drosophila melanogaster. Proceedings of the National Academy of Sciences, 68(9), 2112-2116.

- Kress, W. J., Garcia-Robledo, C., Uriarte, M., & Erickson, D. L. (2005). DNA barcodes for the identification of plant species. *Proceedings of the National Academy of Sciences*, 102(23), 8369-8374.
- Lewis, E. B. (1978). A gene complex controlling segmentation in *Drosophila*. *Nature*, 276(5688), 565-570.
- Lindsay, S. W., Emerson, P. M., & Charlwood, J. D. (2016). Mosquitoes and malaria: Insect vectors of the malaria parasite. *Nature Reviews Microbiology*, 14(8), 577-586.
- Morgan, T. H. (1910). Sex limited inheritance in *Drosophila. Science*, 32(812), 120-122.
- Pandey, U. B., & Nichols, C. D. (2011). Human disease models in *Drosophila melanogaster* and the role of the fly in therapeutic drug discovery. *Pharmacological Reviews*, 63(2), 411-436.
- Pflieger, W. L., & O'Leary, S. J. (1999). Restriction fragment length polymorphism in fish genetics. In Fish Molecular Genetics and Biotechnology (pp. 101-112). *Kluwer Academic Publishers*.
- Sweeney, B. W., Ahn, C., & Newbold, J. D. (2011). DNA barcoding for environmental monitoring and biodiversity assessment. *BioScience*, 61(1), 46-57.
- Vos, P., Hogers, R., Bleeker, M., Reijans, M., van de Lee, T., & Hornes, M. (1995). AFLP: a new technique for DNA fingerprinting. *Nucleic Acids Research*, 23(21), 4407-4414.
- Zane, L., Pemberton, J. M., & Hartl, D. L. (2002). Population genetics of microsatellite markers in natural populations of insects. *Heredity*, 88(5), 383-390.