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Population structure and genetic connectivity of *Aedes aegypti* (Diptera: Culicidae): A Review

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ABSTRACT

***Aedes aegypti* is the primary vector for many important arboviral diseases such as dengue, chikungunya, Zika, and yellow fever. Urbanisation, climate change, globalisation, and the increased mobility of populations around the world have driven its rapid global spread. Assessing the population structure of *Ae. aegypti* is vital in the understanding of dispersal, gene flow, adaptation to the environment, insecticide resistance, and vector-borne diseases. This review aims to provide a perspective on the population structure of *Ae. aegypti* and the biological, ecological, and anthropogenic influences on it. The important factors include container breeding, limited dispersal coupled with transport by man, urban adaptation, and seasonal climate variation. The review discusses the role of molecular markers in the population genetics of *Ae. aegypti*. Initial studies used allozymes and RAPD markers. More recently, studies have included mitochondrial DNA with a focus on the cytochrome c oxidase subunit I (*COI*) and nuclear microsatellite markers. *COI* markers have been beneficial in studying the phylogeography and the demography of *Ae. aegypti*, while microsatellites have been shown to provide better resolution for contemporary gene flow. Studies that combine both mitochondrial and genomic DNA have shown complex patterns of historical connectivity and contemporary population structures. The studies reviewed have shown that climate, urbanisation, transport, and ecological adaptation affect the population genetics of *Ae. aegypti*. The development of genomic-based and multidisciplinary approaches may enhance our understanding of the population structure of *Ae. aegypti* and may help develop better vector control measures.**

Introduction

Aedes aegypti is a mosquito that carries a number of arboviral diseases. Ae. aegypti transmits dengue, chikungunya, Zika, and yellow fever (Powell & Tabachnick, 2013) (Kraemer *et al*. 2015) and has become a mosquito vector of concern for public health globally. Over the past decades, the incidence of these diseases has risen rapidly due to many factors. These factors include climate change, globalisation, rapid urbanisation, and increased human mobility (Gubler, 2011) (Weaver & Reisen, 2010). Of the mosquito-borne diseases, dengue virus infection is one of the arboviral diseases that are spreading rapidly and are frequently occurring, especially in tropical and subtropical regions (Bhatt *et al*., 2013). The exceptional adaptation of Ae. aegypti,as noted by (Kraemer *et al*., 2015), explains the ease of its association with the human environment. *Ae. aegypt*i is believed to have emerged in Africa and subsequently spread to other locations along trade routes and through the transport network (Powell *et al*., 2018). *Ae. aegypti* is well adapted to urban and peri-urban habitats. *Ae. aegypti* distributes and breeds within artificial containers of water used by humans (Getachew *et al*. 2015) (Kweka *et al*. 2018). Other factors that facilitate the dispersal of *Ae. aegypti* include resistance to dehydration, attraction to humans, resting indoors, and the use of altered human environments (Christophers, 1960) (Guagliardo *et al*., 2019). Urbanisation and climate change have created many locations across the globe that are suitable for habitation by *Ae. aegypti* (Mordecai *et al*., 2019). Understanding the population structure of *Ae. aegypti* informs dispersal, gene flow, adaptation, and disease transmission (Gloria-Soria *et al*., 2016). The population structure shows how ecological, evolutionary, and anthropogenic processes and climate affect the distribution of genetic diversity in mosquito populations (Maffey *et al*., 2022). Genetic divergence within a species is influenced by its ecology, limited ability to move, passive transport, selection of heterogeneous environments, and the environment itself (Harrington *et al*., 2005) (Powell *et al*., 2018). Understanding population structures

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aids in predicting the dispersion of adaptive characteristics, such as insecticide resistance, and in assessing the potential for invasion (Hemingway & Ranson, 2000). Over the years, the development of molecular genetics has provided new insights into the population dynamics of mosquitoes. Previous studies primarily focused on low-level markers using allozymes and RAPDs (Randomly Amplified Polymorphic DNA). Since the population dynamics of mosquitoes have been focused on the utilisation of markers such as mitochondrial DNA, microsatellites, and markers on a genomic scale (Avise, 1995) (Williams *et al*., 1990). In mitochondrial DNA, the COI (cytochrome c oxidase subunit I) has been used for the most part in studies of demography and phylogeography, and in nuclear DNA, microsatellites have been used to study population structure and, among populations, gene flow (Gloria-Soria *et al*., 2016). The use of both mitochondrial and nuclear markers has contributed to the study of both ancient and modern evolutionary changes in *Ae. aegypti* populations (Liu *et al*., 2019) (Maynard *et al*., 2023). There may be numerous studies on the ecology and genetics of *Ae. aegypti*, but results may vary in different places due to the results being impacted by different climates, levels of urbanisation, sampling, and methods of molecular analysis. The information on the biology, ecology, and climate of *Ae. aegypti*, as well as the factors that determine its population structure, must be documented. This review aims to identify the main factors influencing the population structure of *Ae. aegypti* and to evaluate the molecular markers and genetic tools developed to study the population structure and connectivity of *Ae. aegypti*.

Breeding ecology and container adaptation

Specialisation can enhance the population success and resilience of a species, as demonstrated by the breeding behaviour of *Ae. aegypti*. Most mosquito species prefer natural habitats when selecting a location to deposit their eggs. For *Ae. aegypti*, preferred oviposition sites are artificial and smaller and contain man-made habitats (Kweka *et al*., 2018). Examples of container habitats include water tanks, discarded tyres, plastic containers, flowerpots, and elevated water tanks (Getachew *et al*., 2015). Container breeding allows *Ae. aegypti* to dissociate the reproductive and/or breeding process from the presence of natural water bodies. Spatial distribution of water can be found in places where humans are active. *Ae. aegypti* lays its eggs singularly, and this pattern maximises the oviposition site resistance of the eggs, ensuring that they will hatch (Prasad *et al*., 2023). Particle eggs can remain dormant in hostile environments. The eggs will hatch when the environment becomes more favourable, such as when the container fills with water after a rain (Chakraborty *et al*., 2025). The same breeding sites help the population survive and spread. *Ae. Aegypti's* breeding behaviour fosters local population stability and covers unused breeding sites. Container breeding can create clusters of breeding sites for larvae. Microspatial clusters lead to concentrations of breeding sites that give rise to new generations of related insects (Carvajal *et al*., 2020). Nevertheless, dispersal at larger scales often negates the effects of clustering at smaller scales (Wu *et al*., 2025).

Dispersal and human-mediated movement

Dispersal has implications for the structuring and dynamics of populations, as well as the distribution of genes across them (Wu *et al*., 2025). *Ae. aegypti* mosquitoes are generally thought to actively disperse poorly. Mark-release-recapture studies suggest that most mosquitoes do not move more than 50 m to 200 m from the site of their emergence, but female mosquitoes prefer to remain around humans and where they lay eggs (Harrington *et al*., 2005). Studies in semi-arid and temperate regions show that mosquitoes in these areas disperse more than expected. (Marcantonio *et al*., 2019) utilised stable isotope mark-release-recapture studies in Central California, finding mean dispersal distances of 224 m to 240 m, with variation based on local conditions and wind. *Ae. aegypti* mosquitoes are recent colonisers of temperate regions and can disperse more widely depending on environmental conditions. While dispersal is generally limited, this species shows extensive interconnectedness around the world due to human-mediated transport. Passive dispersal occurs when cargo, people, and containers carrying water accidentally transport eggs, larvae, and adult mosquitoes (Powell & Tabachnick, 2013). This form of dispersal can connect populations separated by large distances, can introduce new genetic variations, and can lead to decreased differentiation between regions and countries (Louise *et al*., 2015). This type of dispersal is characterised by two contradictory phenomena: sparse local dispersal but frequent long-distance dispersal, and usually the genetic population structure is heterogeneous but is connected on a large scale (Gao *et al*., 2021). This type of dispersal, if observed in urban or semi-urban areas which have a high density of roads and commercial activity, means that the city is the source of gene flow, and from there mosquitoes and their genes are distributed to the peripheral areas. Isolated populations that are far away from the city and more remote and a typical will have decreased connectivity. This will cause differentiation due to genetic drift and local adaptation (Maffey *et al*., 2022). Urban adaptation and anthropophily: A strong relationship between humans and the population of *Ae. Aegypti* also has a role in structuring this population (Guagliardo *et al*., 2019). The species has evolved over millions of years and developed a preference for feeding on

human blood, resting indoors, and breeding in human-associated containers (Khan *et al*., 2022). Urban adaptations of this nature have genetic and ecological ramifications. Firstly, urban environments exhibit a high degree of heterogeneity regarding various housing types, water storage and waste disposal practices, and insecticide application (Kolimenakis *et al*., 2021). This heterogeneity leads to the development of different selective pressures across the urban space, which in turn promotes adaptive changes. For example, the different levels of exposure to insecticides across cities and even different neighbourhoods can create spatial differentiation in the allele frequency of various genes associated with insecticide resistance (Hemingway & Ranson, 2000). Additionally, urbanisation can lead to changes in the temperature and, consequently, in the population dynamics of mosquitoes. The increased temperatures as a result of urbanisation may lead to an increase in the generation turnover rate in mosquitoes, which can create new selective pressures on the available genetic diversity in the urban environment (Grech *et al*., 2015). Moreover, urbanised areas may shield mosquitoes from extreme weather conditions and, thus, support year-round survival and sustained breeding during the warm months. This may lead to an overlap of generations and mask seasonal changes in the associated genetic variability. Furthermore, the practices associated with urbanisation may facilitate breeding and, subsequently, high population density. The practice of water storage in water supply scarcity zones also promotes breeding (Caprara *et al*., 2009). Conversely, the effective control of mosquito breeding sites may reduce the population density of mosquitoes and increase genetic drift (Forsyth *et al*., 2020). Seasonal changes and temperature, among other climatic parameters, may influence the population dynamics of Ae. aegypti. Temperature, humidity, and precipitation have all been noted to affect the reproduction rate, longevity, and rate of development of mosquitoes (Alto *et al*., 2008) (Sharma *et al*., 2025). (Clements, 1992) argues that the peak breeding population tends to occur after and during the rainy season due to the creation of new water-filled breeding sites. As variations in climate occur, the population of mosquitoes can exhibit periodic cycles of population growth and subsequent crashes due to seasonal variations in the environment that directly and adversely affect it. During the dry season, the population bottleneck effect can occur due to adverse effects on the mosquito population from larvae and adult mortality. Rapid population growth is observed once the adverse effect from the dry season subsides, and the effect of the population bottleneck and reduced size of the genetic pool is observed (Weaver *et al*., 2021). However, there can be continuous reproduction during favourable conditions, and stagnant population growth can also occur during this time. Nevertheless, year-round breeding is possible, and a slight change in climate (temperature or precipitation) can have an effect on the rate of mosquitoes, biting rate, and generation time (Prasad *et al*., 2024). The varying seasonal patterns in different climate zones result in geographic differences in the demographics of mosquitoes. It is possible to distinguish between different weather interactions through human behaviour, such as saving water in reservoirs or increasing the time spent outdoors during particular seasons (Clements, 1992). Breeding, flying, adapting, and seasonality create a hierarchical population structure for the urban mosquito, *Ae. aegypti*. Breeding in some rainy-season water containers can lead to the formation of a group of individuals that are related to each other (McCormack *et al*., 2019). The urban environment is heterogeneous and at a mid-range geographical level, leading to either separation between neighbourhoods or cities or slow dispersal (Maffey *et al*., 2022). Transport and climates at a large range of geographical levels lead to the retention of gene flow between populations that are distinct from one another (Huber *et al*., 2004). The hierarchical population structure of the mosquito is important for pathogen transmission and for understanding the management of the mosquito as a vector. The structure of a population at the local level makes mosquito control at that level possible. The interconnected nature of the population allows the mosquito population to re-colonise the area. Within the field of evolution, the interaction between the flow of genes and adaptation to a local environment determines the rapid spread of changes among the population, such as resistance to insecticides and vector competency. The importance of this work is that it provides the foundation for a proper understanding of the field of population genetics. Typically, there is a combination of high and low gene flow in a population, which demonstrates the particular nature of a species' life cycle. Genetic analysis, in combination with social, ecological, and biological aspects, constitutes a more comprehensive way to understand how mosquito populations are organised genetically.

Consequences for population genetic investigations

The ecology of *Ae. aegypti* extends the implications for population genetics beyond the urban milieu and emphasises the environmental dimensions of population genetics that include the role of human agency. Population genetic studies must consider the large-scale population distribution and the small -scale variance of population sampling. The differences in climate and the gradients of urbanisation and human migration must be considered as population structuring factors along with the external factors. This is particularly evident

in the countries of the world that have diverse climate conditions and where the process of urbanisation is intensive. Because of the ecological plasticity of *Ae. aegypti*, combined with human migration, it is flexible, adaptive, and active. Thus, it can rapidly evolve new traits and characteristics. The studies show that the evolution and distribution of *Ae. aegypti*, as well as the sustained exchange of genes with mosquito populations, was influenced by international commerce and other logistic activities performed by humans (Powell & Tabachnick, 2013).

Genetic techniques in Ae. aegypti population research

Historically, genetic markers in *Ae. aegypti* studies

Genetic studies of *Ae. aegypti* employed biochemical and PCR-based markers, as well as allozymes and RAPD, before the advanced automated DNA sequencing. Enzymatic electrophoresis of allozymes, which are distinct alleles of an enzyme, was among the early molecular techniques to analyse population genetics and geography of mosquitoes (Avise, 1995). Using multilocus allozyme electrophoresis, (Powell & Tabachnick, 2013) described the extensive geographical segregation of the world's populations of *Ae. aegypti*. Most early studies focusing on the African populations of *Ae. aegypti*, the African native subspecies, and domesticated non-African subspecies pointed to the occurrence of small genetic differences. A more viable option at the time was RAPD markers – a PCR technique developed to be a quicker and more efficient way of detecting unknown changes to a genome without needing to have a sequence beforehand (Williams *et a*l., 1990). RAPD analysis was useful to show genetic distinction and the isolation-by-distance phenomenon among mosquito populations. This revealed the presence of limited dispersal and localised mating activity within a population (Gorrochotegui-Escalante *et al*., 2000). Allozymes and RAPD markers were widely used to assess the genetic population structure of *Ae. aegypti*, but their drawbacks, such as low resolution and unreliability, meant that other markers were needed to provide the missing information on fine-scale population genetic structure. These included mitochondrial DNA and microsatellites.

Mitochondrial DNA markers and the COI gene

Mitochondrial DNA (mtDNA) is a popular genetic marker in insect population genetics and phylogeography (Mandal *et al*., 2014). The exclusive maternal inheritance and uniparental haploidy of mtDNA make them an interesting marker for studying demographic changes in a population (Avise, 1991). Among the many genes of the mitochondrion, researchers of Ae. aegypti pay special attention to the gene for the cytochrome c oxidase subunit I (COI) (Gandhi *et al*., 2020). This gene is relatively mutable and can therefore be used to study genetic variability within and among mosquito species. The widespread use of COI can be attributed to the development of universal primers and the adoption of COI as the official DNA barcode for animals (Ferri *et al*., 2009). Mosquito researchers find COI a great tool to study mosquito taxonomy and genetics (Chaiphongpachara *et al*., 2022). Many COI studies around the world have shown different levels of the genetic structure of *Ae. aegypti*, typically illustrating historical colonisation and the current dispersal of the species (Maynard *et al*., 2023). The study that analysed the COI data of mosquitoes across Asia, the Indo-Pacific, and Australasia, along with the nuclear microsatellites, found different levels of genetic structure throughout the region. This included genetic separation that had never been documented before between regions of Australia and between other regions of Malaysia, Indonesia, and the Torres Strait and Queensland Islands. This study used historical data to theorise that the current structure of the mosquito populations could be the result of both historical migrations and the ongoing human-caused isolation of the regions (Maynard *et al*., 2023). In comparison to other regions, African populations of *Ae. aegypti* may also be the most diverse when looking at COI haplotypes and nucleotides, and this diversity is likely the result of long-term stability of the populations and persistence of the subspecies. The mosquito population in the Sudanese section of the Sahel was diverse and had distinct haplotypes, and there was strong separation between the different subspecies of mosquitoes. This supports that Africa is the location of the origin of the genetically diverse *Ae. aegypt*i (Avise, 1991). Populations of *Ae. aegypti* from the Americas and portions of Asia typically have lower levels of mitochondrial diversity. They have shallow phylogenetic divergence and a smaller number of haplotypes. In Honduras, a study detected low diversity in COI haplotypes and low levels of nucleotide variation. This is likely due to founder effects, population bottlenecks, and a history of repeated introductions (Escobar *et al*., 2022). In Asia, COI studies found haplotypes to be widely shared but still showed regional differentiation, indicating some local population structuring and gene flow due to human activities (Md Naim *et al*., 2020). Similarly, studies in India have found low COI diversity with little to no phylogeographic structuring at the local and regional levels. For example, in a study by (Gandhi *et al*., 2020), COI analyses of *Ae. aegypti* populations from nine villages in Maharashtra, India, showed low diversity, with many populations forming only two closely related haplotypes. Additionally, the COI of field populations of *Ae. aegypti* showed low variation, and many formed closely related haplotypes, indicating gene flow and a lack of structure, which has been

attributed to the high human population. Laboratory and transgenic strains exhibited greater haplotypic diversity and phylogenetic divergence and therefore structure due to their unique origins. There are benefits and drawbacks to using the COI gene. One drawback is that due to the maternal nature of mtDNA, only female gene flow can be traced, which is less desirable because the majority of the *Ae. aegypti* dispersers are male. Mitochondrial DNA can also represent a smaller effective population size than diploid nuclear genes, as mtDNA can be much more prone to genetic drift (Ballard & Whitlock, 2004). Mitochondrial pseudogenes of the nucleus (numts) can also be bothersome while analysing data if they aren't sufficiently filtered. Either way, COI can be a potential genetic marker for illustrating past population structures and recognising ancient lineages as well as genetic differentiation among populations. The efficacy of the COI is also enhanced with the addition of nuclear genes due to biparental gene flow.

Nuclear microsatellite markers

Microsatellites, which are also called 'simple sequence repeats' (SSRs), are found within the nuclear genome as short repetitive sequences of DNA (Vieira *et al*., 2016). Microsatellites are highly mutable and show codominance and polymorphism and thus are among the best markers for conducting population genetics of *Ae. aegypti* (Ravel *et al*., 2002). Compared to mitochondrial markers, microsatellites provide better insights into the genetic differentiation and the structure of population interconnectivity due to their biparental inheritance and polymorphic nature at many loci. For instance, (Teske *et al*., 2018) highlighted in their review article that it is not uncommon for mitochondrial DNA to show no isolation-by-distance (IBD) when populations are broken down and analysed separately as opposed to in a large regional grouping. However, in those instances when mitochondrial tests showed no isolation-by-distance, microsatellites and SNPs had been employed to successfully identify such patterns. The variation of results between tests performed on mitochondrial and nuclear DNA was found in almost 50% of the studies assessed and was likely due to the loss of genetic diversity of mtDNA that is due to selection and the fact that mtDNA is composed of a single locus, in contrast with the high resolution exhibited by microsatellites. Many worldwide studies on *Ae. aegypti* mosquitoes have been used with microsatellites to study population genetics and invasiveness. One of the most notable ones is (Gloria-Soria *et al*., 2016), which used data from 12 microsatellite loci across 79 populations in 30 countries across all continents. The study concluded that the population structuring due to the historical invasions and current dispersals of *Ae. aegypti* mosquitoes was considerable. The research found notable genetic differences between the subspecies of the mosquitoes, *Ae. aegypti* formosus and *Ae. aegypti aegypti*. It also concluded that the populations that are not in Africa were the result of human-mediated, transoceanic migrations from the populations in Africa. While there were low levels of structuring in the ancestral population of Africa, there was a notable structuring in the populations outside Africa, which was caused by founder effects, habitat fragmentation, and low gene flow. This study was global and used microsatellites to describe the invasions of *Ae. aegypti* mosquitoes and is a great contribution to world literature. The use of microsatellites in studying the population genetics of *Ae. Aegypti* mosquitoes have also been successfully used in India. Studies with 10 to 15 microsatellite loci have reported that there is a large effective population and gene flow and have attributed this to the reported moderate-to-high levels of genetic diversity in populations of mosquitoes (Kumar *et al*., 2021) (Sumitha *et al*., 2023). Other studies have reported significant genetic differentiation of mosquitoes from different urban populations and climatic zones. Microsatellite genotyping combined with several Bayesian methods has allowed for the study of population structure using analyses such as STRUCTURE, AMOVA, and principal coordinate analyses. The findings of these analyses often suggest the formation of genetic clusters corresponding with geographical or urban locations (Slotman *et al*., 2007). Although the use of microsatellites offers many benefits, it also has some drawbacks. The phenomenon of homoplasy arises when alleles converge and produce a similar phenotype. Also, the presence of null alleles, scoring deviations, and Hardy-Weinberg equilibrium deviations often raises questions about microsatellite analysis. Nevertheless, the effectiveness of microsatellites for population genetic studies is unstinting.

Integration of mitochondrial and nuclear markers

The combination of mtDNA and nuclear DNA offers population geneticists a view of population structure that is more informative than the use of one system alone. Geneticists have become increasingly interested in integrated analyses of mtDNA and nuclear DNA in the study of the disease vector *Ae. aegypti*, particularly the integration of nuclear DNA with a focus on microsatellite systems (Tabachnick *et al*., 1979) (Liu *et al*., 2019). Mitochondrial loci and, in particular, COI, are often used to determine historical phylogeography and matriline extent, while nuclear microsatellites are more likely to be influenced by spatial demography, recent developments in population size, and contemporary flow of genes. Thus, the timing and order of population separation and reproductive isolation can be inferred from the agreement or disparity between

the two datasets. There is an observable situation with an increasing number of citations that include an analysis of mtDNA and nuclear DNA, where a distinction in nuclear population structures has been accompanied by a lack of mtDNA, particularly for populations that have undergone recent population growth. As an example, in (Liu *et al*., 2019), while analysing mosquito samples collected from Yunnan, China, the mtDNA and nuclear DNA datasets of microsatellites revealed that although the populations had a uniform mtDNA structure, there was a geographic separation of the populations, which was reflective of the population expansion when analysed in terms of nuclear DNA. In contrast, recent gene flow in the context of nuclear DNA has contributed to the structure of nuclear DNA and has resulted in significant differences in mtDNA. Integrative marker systems are beneficial for studying the population structure of mosquitoes and the effects of dispersal by humans. (Maynard *et al*., 2023) carried out an analysis on both mitochondrial COI and multilocus microsatellite markers across the Indo-Pacific and found that geographically segregated populations of *Ae. Aegypti* often had identical mitochondrial haplotypes and showed higher levels of microsatellite divergence at a much smaller geographic scale. This divergence was indicative of a phenomenon of global colonisation of populations coupled with limited dispersal and recent regional isolation. The integration of mitochondrial and nuclear markers creates opportunities for vector control and management of disease. The multimarker approach will enhance the assessment of the colonisation and invasion processes, including the spread of adaptive traits, such as the spread of insecticide resistance. Along with these adaptive traits, genetic markers can be used to predict the invasion dynamics of Wolbachia and the potential success of genetic control measures. In regions with climatic and geographic variability, multi-locus systems will differentiate between historical events and present-day gene flow.

Conclusion and future perspectives

Being aware of *Ae. aegypti's* population biology will aid in epidemiological projections and the development of appropriate vector control strategies. This review highlights that the life cycle of *Ae. aegypti* is modulated by complex interactions of many factors, including biology, ecology, climate change, urbanisation, and dispersal. These factors, coupled with the mosquito's ability to make use of both artificial and natural water storage, resistance to dehydration, and its adaptability to varying climatic conditions, have facilitated the establishment of different populations of *Ae. aegypti* that are genetically distinct, yet correspondingly differentiated. The study of the evolution and population dynamics of *Ae. aegypti* has benefited from the combination of both mitochondrial and nuclear DNA markers. In this context, the COI gene and other mitochondrial DNA markers have been critical in phylogeny and research of *Ae. aegypti* mosquito dispersal. On the other hand, DNA microsatellites have been useful in identifying genetic variations in urban populations and have highlighted recent gene flow in the *Ae. aedes aegypti* mosquito. Coupled analysis of both mitochondrial and nuclear DNA markers has shown that populations of mosquitoes, and perhaps other organisms, can be historically connected yet spatially separated. The reviewed studies collectively indicate that factors like urbanisation, climatic variation, transport routes, and environmental conditions of the local areas are significant determinants of the structure of the mosquito population. Although there is likely to be extensive gene flow between widely distributed populations via passive dispersal, local environmental conditions, which include exposure to insecticides, urban climates, and availability of breeding sites, might contribute to adaptation on smaller spatial scales. However, there still exists a significant lack of knowledge on this issue. Many areas, especially those in less developed countries and possessing varying climates, are understudied for large-scale genetic population analyses. Furthermore, several previous studies have used small marker sets and a narrow area sampling scope, which might have underestimated the complexities involved in mosquito population structuring. For future research, there is a need to increasingly use advanced genomic analysis methods such as SNP genotyping, sequencing reduction, and whole-genome sequencing. Genomic information should be combined with information from ecology, climate, epidemiology, and human movements. Thus, the gradual integration of ecology and molecular biology is revolutionising the way we understand *Ae. aegypti* population biology. It is necessary to develop sustainable and adaptive methods for vector control, considering such factors as urbanisation, global warming, globalisation, and the increase in the spread of mosquito-transmitted diseases across the world.

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Ethical Statement

The study does not require any ethical approval.

Use of Artificial Intelligence (AI) Tools

The authors confirm that they did not use any artificial intelligence (AI) tools in the preparation, analysis, or writing of this manuscript.

Conflict of Interest

The authors declare that they have no conflicts of interest.

Data Availability Statement

The data that support the findings of this study are available from the corresponding author upon reasonable request.

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