Functional Genomics of Mosquito Vector Competence and Pathogen Transmission

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Abstract The primary objective of this study is to provide an in-depth overview of the functional genomics that underlie mosquito vector competence and the transmission of pathogens. The study integrates recent advancements and systematic analyses to elucidate the complex genetic and biochemical interactions that define how mosquitoes interact with and transmit pathogens. We highlight key genetic determinants of vector competence, demonstrating how specific genes and genomic configurations influence the ability of mosquitoes to acquire, sustain, and transmit a range of pathogens. The interactions between mosquito vectors and pathogens are explored, with an emphasis on how these relationships are mediated by genetic factors and influenced by external environmental conditions. Additionally, the study discusses the role of advanced genomic technologies, such as CRISPR/Cas9, RNA interference (RNAi), and high-throughput sequencing, which have been pivotal in dissecting these interactions and developing potential vector control strategies. Overall, the findings presented in this study enhance our understanding of the genetic mechanisms underpinning pathogen transmission by mosquitoes and lay the groundwork for future research aimed at disrupting these processes to reduce the prevalence of mosquito-borne diseases.

Keywords Mosquito vector competence; Pathogen transmission; Functional genomics; Genetic determinants; Genomic technologies

Mosquito-borne diseases represent a significant global health challenge, affecting millions of people annually. Diseases such as dengue, yellow fever, Zika, and Chikungunya are transmitted by mosquitoes, particularly species like *Aedes aegypti* and *Anopheles* spp. These pathogens impose a growing burden on public health systems worldwide, leading to substantial morbidity and mortality (Baldon et al., 2022). The ability of mosquitoes to transmit these pathogens is a critical factor in the epidemiology of these diseases, making the study of mosquito vector competence essential.

Vector competence refers to the intrinsic ability of a mosquito to acquire, maintain, and transmit a pathogen. This concept is crucial for understanding disease transmission dynamics, as it influences the efficiency and rate at which diseases spread within populations. Factors affecting vector competence include genetic variations, environmental conditions, and interactions between the mosquito and the pathogen (Baldon et al., 2022; Collins et al., 2022). For instance, the development of immunocompromised animal models, such as the AG129 mouse, has provided valuable insights into the transmission cycles of arboviruses, highlighting the importance of vector competence in disease propagation (Baldon et al., 2022).

This study aims to explore the functional genomics of mosquito vector competence and pathogen transmission. By focusing on genomic approaches, we seek to understand the genetic determinants that influence vector competence and identify potential targets for intervention. The study will cover recent advancements in genome sequencing technologies, such as targeted amplicon sequencing, which have facilitated the identification of mutations associated with insecticide resistance in mosquito populations (Collins et al., 2022). Through this comprehensive analysis, we expect to provide a deeper understanding of the molecular mechanisms underlying vector competence and offer insights into novel strategies for controlling mosquito-borne diseases.
1 Genetic Bases of Mosquito Vector Competence

1.1 Genetic traits
Genetic traits play a crucial role in determining mosquito susceptibility to pathogen infection and their subsequent transmission capabilities. For instance, the study by Raddi et al. (2020) highlights the importance of hemocytes in mosquito immunity, identifying a new hemocyte type, the megacyte, which is involved in immune response and differentiation during immune priming. This suggests that specific genetic traits related to immune cell function can influence vector competence. Additionally, the genomic amplification of carboxylesterase genes in Aedes aegypti, as described by Cattel et al. (2020), confers resistance to organophosphate insecticides, which indirectly affects vector competence by enabling mosquitoes to survive in environments with high insecticide use.

1.2 Molecular genetics
Molecular genetics studies have explored various genetic modifications in mosquitoes that affect vector competence. The development of gene-drive systems, such as the Cas9/gRNA-mediated gene-drive rescue system in Anopheles stephensi, has shown promise in population modification to reduce vector competence (Adolfi et al., 2020) (Figure 1). This system effectively integrates into the mosquito genome and eliminates non-functional resistant alleles, ensuring a high prevalence of the gene-drive in the population. Furthermore, the study on DNA methylation in Anopheles albimanus by Gómez-Diaz et al. (2020) demonstrates that epigenetic modifications can modulate the immune response against Plasmodium berghei, suggesting that targeted epigenetic interventions could be a potential strategy for controlling vector competence.

1.3 Genomic approaches
Genomic tools such as CRISPR/Cas9, RNA interference (RNAi), and transgenic technologies have been instrumental in studying and manipulating mosquito genetics. The CRISPR/Cas9 system has been utilized to create gene-drive mechanisms that can spread desired genetic traits through mosquito populations, as demonstrated in Anopheles stephensi (Adolfi et al., 2020). RNAi has also shown potential in vector control, with advances in oral RNAi delivery systems enabling the functional characterization of mosquito genes and the development of RNAi-based pesticides. Additionally, the optimization of physical genome mapping techniques, as described by Masri et al. (2021), has improved our ability to create high-quality genome assemblies, facilitating the identification of genes responsible for vector competence and other epidemiological traits.

In conclusion, the integration of genetic traits, molecular genetics, and advanced genomic approaches provides a comprehensive understanding of mosquito vector competence and pathogen transmission. These insights are crucial for developing innovative strategies to control mosquito populations and reduce the transmission of vector-borne diseases.

2 Biochemical and Physiological Mechanisms of Pathogen Transmission

2.1 Pathogen lifecycle
The lifecycle of pathogens within mosquito vectors involves several critical stages where genomic factors play a significant role. For instance, the malaria parasite Plasmodium falciparum undergoes a complex lifecycle that includes the development of gametocytes, which are taken up by the mosquito during a blood meal. Within the mosquito midgut, male gametogenesis is crucial for the release of male gametes, a process regulated by the calcium-dependent protein kinase 4 (PfCDPK4). This kinase is essential for the phosphorylation of proteins necessary for male gamete emergence, DNA replication, mRNA translation, and cell motility, thereby facilitating the parasite's transmission to the mosquito vector (Kumar et al., 2021). Additionally, single-cell transcriptomics has revealed the transcriptional signatures and developmental trajectories of P. falciparum as it colonizes the mosquito midgut and salivary glands, highlighting the gene usage across different transmission stages (Real et al., 2020).
Figure 1 Effects of lethal/sterile mosaicism on the Reckh gene-drive system (Adopted from Adolfi et al., 2020)

Image caption: a A female heterozygous for the drive can produce eggs carrying a copy of the drive (green circle, khRec+) or eggs carrying an EJ-induced nonfunctional resistant allele (white circle, kh−). Both types of eggs carry maternally deposited cytoplasmic Cas9/gRNA complexes (light blue filling) that can act on the incoming WT paternal allele (black circle, kh+). b The soma of individuals inheriting a copy of the drive from their mothers is a mosaic of cells with varying proportions of genotypes khRec+/kh−, khRec+/kh+, and khRec+/khRec+. Reckh individuals emerging from such embryos have at least one functional copy of kh provided by the drive system (khRec+), therefore have GFP+/black eyes and females are fit for reproduction. c The soma of individuals inheriting an EJ nonfunctional mutation from their drive mothers is a mosaic of cells with genotypes kh−/kh− or kh−/kh+. The ability of females emerging from such embryos to survive and reproduce depends on the proportion of somatic cells with genotype kh−/kh−. These individuals may display mosaic or white-eye phenotype if mutations affect the cells forming the eyes. Diploid cells in (b) and (c) that become germline progenitors also may be affected by mosaicism, which can affect drive capabilities (Adopted from Adolfi et al., 2020)

The findings of Adolfi et al. (2020) indicate the potential of gene drive technology in manipulating genetic traits in populations. The visual data illustrate the process of gene drive propagation, showing how genetically modified alleles can be spread through a population. This involves the use of CRISPR/Cas9 systems to ensure the inheritance of specific genetic traits, significantly increasing their presence in subsequent generations. The graphical representation emphasizes the efficiency of gene drive mechanisms in altering genetic compositions, which can have profound implications for controlling pest populations or eliminating disease vectors. This study underscores the transformative potential of gene editing technologies in ecological management and genetic research, highlighting both the opportunities and challenges associated with their use.

2.2 Host-pathogen interactions
The interactions between mosquito hosts and their pathogens are mediated by complex biochemical and genetic
mechanisms. For example, the genome of Anopheles stephensi, a vector of urban malaria, contains numerous transposable elements (TEs) that play a widespread role in genome evolution and phenotypic variation. These TEs include insecticide resistance genes and male-linked gene candidates, which are critical for the mosquito's ability to transmit malaria (Chakraborty et al., 2022) (Figure 2). Furthermore, the genetic basis of vectorial capacity and the development of genetic control strategies are often impeded by limitations in genome assembly quality. High-quality genome assemblies, such as those achieved through long-read sequencing technologies, enable the identification of genes responsible for vector competence and insecticide resistance, thereby enhancing our understanding of mosquito-pathogen interactions (Masri et al., 2021).

Figure 2 Gene expression changes in adult female mosquitoes after a blood meal (Adopted from Chakraborty et al., 2022)

Image caption: a Transcript abundance of genes that are in the top 1% (> ~ 64-fold) of the PBM transcript abundance changes. As evident here, more genes show upregulation than downregulation, although expression changes of some genes may not be due to the blood meal. b GO gene enrichment analysis of the genes from panel a. Consistent with the role of the blood meal in mosquito biology, the genes involved in cell division, DNA replication, amino acid metabolism, and cell signaling are enriched among the differentially expressed genes. c Protein sequence identity between the An. stephensi genes showing PBM upregulation and their An. gambiae orthologs. d Despite being a common genetic marker, the sequence of the PBM upregulated white gene was fragmented in the draft assembly of An. stephensi. e Transcript abundance of four yellow genes (yellow, yellow-b, yellow-e, yellow-g) before and after a blood meal. All genes show a similar transcript profile until 6 h PBM, after which yellow-g transcripts become more abundant. f A Cyp450 orthologous to D. melanogaster Cyp305a1 shows PBM upregulation (Adopted from Chakraborty et al., 2022)

The findings of Chakraborty et al. (2022) indicate significant changes in gene expression following blood feeding in mosquitoes. The visual data show dynamic patterns in read counts over time, reflecting the upregulation and downregulation of various genes. Functional enrichment analysis highlights key biological processes and pathways that are significantly affected, providing insights into cellular responses post-feeding. The distribution of protein identity percentages among identified genes suggests a high degree of conservation for certain proteins. Comparative genomic analyses reveal differences between old and new genome assemblies, emphasizing the
importance of updated genomic data for accurate interpretation. These findings underscore the complexity of mosquito physiology and the intricate molecular mechanisms involved in their response to blood feeding, which can inform strategies for disease vector control and management.

2.3 Manipulation of transmission pathways
Genetic engineering has been employed to alter biochemical pathways in mosquitoes to reduce or block pathogen transmission. For instance, the development of high-quality genome assemblies and physical genome mapping techniques has facilitated the identification and manipulation of genes involved in vector competence and insecticide resistance. By using gene-based physical mapping approaches, researchers can create and validate chromosome-scale genome assemblies, which are essential for designing novel genome-based control strategies (Masri et al., 2021). Additionally, targeting specific kinases such as PjCDPK4 in P. falciparum can disrupt critical processes in the parasite's lifecycle, providing insights into effective malaria transmission-blocking strategies (Kumar et al., 2021).

Collectively, these studies underscore the importance of understanding the genomic and biochemical mechanisms underlying pathogen transmission in mosquito vectors. By leveraging advanced genomic technologies and genetic engineering, researchers can develop innovative strategies to control mosquito-borne diseases and reduce the global burden of these infections.

3 Case Studies
3.1 Genetically modified mosquitoes
Genetically modified mosquitoes have been developed to reduce the transmission of diseases such as dengue, Zika, and malaria. One notable case study involves the use of a Cas9/guide RNA-based gene drive system in Anopheles gambiae, a primary vector for malaria. This system, known as AgNosCd-1, was designed to deliver antiparasite effector molecules, achieving a high efficacy rate of 98–100% in both sexes during small cage trials. The gene drive system successfully introduced the desired genetic modifications within 6 to 10 generations following a single release of gene-drive males, demonstrating its potential for stable and sustainable malaria control (Carballar-Lejarazú et al., 2020). Another case study highlights the development of a gene-drive rescue system in Anopheles stephensi, which targets the kynurenine hydroxylase gene. This system effectively modified the mosquito population, with over 95% of mosquitoes carrying the drive within 5-11 generations (Adolfi et al., 2020).

3.2 Field trials
Field trials involving genetically modified mosquitoes have shown both successes and challenges. The AgNosCd-1 gene drive system in Anopheles gambiae demonstrated promising results in small cage trials, achieving full introduction of the gene drive within a few generations without significant genetic load impairing performance (Carballar-Lejarazú et al., 2020). However, field trials also face challenges such as the potential emergence of drive-resistant alleles, although these were observed at a frequency of less than 0.1% in the AgNosCd-1 system (Carballar-Lejarazú et al., 2020) (Figure 3). Another field trial involving the gene-drive rescue system in Anopheles stephensi showed efficient population modification, but the success of such trials depends on various factors including initial release ratios and environmental conditions (Adolfi et al., 2020). These trials underscore the importance of continuous monitoring and adaptation to address potential resistance and ensure long-term efficacy.

The findings of Carballar-Lejarazú et al. (2020) indicate the successful implementation of gene editing techniques to study gene function in mosquitoes. The visual data compare wild-type mosquitoes with genetically modified AgNosCd-1 mosquitoes, highlighting distinct physical and developmental differences. The gene editing process, which involves the insertion of specific genetic constructs, demonstrates how targeted modifications can result in observable phenotypic changes. These findings illustrate the potential of CRISPR/Cas9 technology in advancing our understanding of genetic roles and mechanisms in mosquitoes. The differences observed in various
developmental stages emphasize the significance of precise genetic manipulations in studying insect biology, potentially contributing to innovative approaches in vector control and disease prevention. This research underscores the importance of genetic tools in unraveling complex biological processes and improving public health strategies.

Figure 3 Aged gene, pCO37 gene-drive construct, and resulting phenotypes (Adopted from Carballar-Lejarazú et al., 2020)

Image caption: (A) Aged gene: maroon blocks, exons (E1-4); empty blocks, 3′ - and 5′ -untranslated regions (UTR); thick black line, introns and intergenic DNA. pCO37 plasmid: maroon blocks, homology arms from the Aged gene; blue blocks, dominant marker gene components (3XP3 and CFP); tan blocks, drive components (nanos promoter and SpCas9 protein-encoding sequences); green blocks, guide RNA components (U6 promoter and gRNA sequence); dark gray block, ϕC31 attP “docking” site. Genes and features of pCO37 are not to scale and approximate sizes of components in kilobases are listed in the Materials and Methods. Recombination resulting from HDR initiated at the SpCas9/gRNA-mediated cut site (broken-line arrow) occurring within the pink-shaded regions results in integration of the gene-drive construct. (B) CFP+ (blue arrow) and homozygous Aged-mutant (red arrow) phenotypes in larvae and (C) Aged-mutant (red arrow) phenotype in pupae. (D) Homozygous Aged mutant phenotype “red eye” (red arrows) in adults. Approximate image magnifications for B, C, and D are 20, 10, and 20×, respectively (Adopted from Carballar-Lejarazú et al., 2020)

3.3 Successful modifications
Several case studies have demonstrated successful genetic and biochemical modifications that altered mosquito
vector competence. The AgNosCd-1 gene drive system in Anopheles gambiae is a prime example, where the integration of antiparasite effector molecules led to a significant reduction in malaria transmission potential (Carballar-Lejarazú et al., 2020). Similarly, the gene-drive rescue system in Anopheles stephensi successfully relieved the genetic load in females and achieved efficient population modification, highlighting the potential of such systems for large-scale implementation (Adolfi et al., 2020). Additionally, the use of targeted amplicon sequencing to identify insecticide resistance mutations in Aedes aegypti populations has provided valuable insights for developing more effective vector control strategies. This approach revealed the presence of resistance-associated mutations, such as the 296S rdl mutation, which can inform future genetic modifications to enhance vector control (Collins et al., 2022).

By leveraging these genetic and biochemical modifications, researchers are making significant strides in reducing the transmission of mosquito-borne diseases, paving the way for more effective and sustainable vector control strategies.

4 Challenges and Ethical Considerations

4.1 Technical limitations

The study of mosquito vectors through functional genomics faces several technical challenges. One significant limitation is the complexity of mosquito genomes, which are often large and enriched with repetitive DNA sequences. This complexity can lead to potential misassemblies, making it difficult to create accurate genome maps. For instance, the development of a gene-based physical mapping approach for the Aedes albopictus genome highlighted the difficulties in avoiding amplification of repetitive DNA and ensuring unambiguous mapping of genomic scaffolds to chromosome regions (Masri et al., 2021).

Moreover, while long-read sequencing technologies and new genome mapping techniques like Hi-C scaffolding and optical mapping have improved genome quality, they still fall short in connecting genomic scaffolds to specific chromosomes. Cytogenetic mapping using fluorescence in situ hybridization (FISH) remains essential for creating and validating chromosome-scale genome assemblies, but it is labor-intensive and technically demanding (Masri et al., 2021). Another technical challenge is the incomplete and draft-quality genome assemblies of many mosquito species, which contain numerous sequence gaps. These gaps can obscure important genetic elements crucial for understanding vectorial capacity and developing genetic interventions. For example, the genome assembly of Anopheles stephensi revealed previously hidden transposable elements and insecticide resistance genes, underscoring the need for high-quality reference genomes to facilitate genetic control strategies (Chakraborty et al., 2022).

4.2 Ethical and ecological impacts

The release of genetically modified mosquitoes into natural environments raises significant ethical and ecological concerns. One of the primary ethical considerations is the potential unintended consequences of gene-drive systems, which are designed to spread genetic modifications rapidly through mosquito populations. These systems, such as the Cas9/gRNA-mediated gene-drive rescue system developed for Anopheles stephensi, have shown promise in population modification and suppression. However, the long-term ecological impacts of such interventions are not fully understood, and there is a risk of disrupting local ecosystems and non-target species (Adolfi et al., 2020).

Additionally, the ethical implications of releasing genetically modified organisms (GMOs) into the wild must be carefully considered. There is a need for robust regulatory frameworks and public engagement to address concerns about the safety and acceptability of these technologies. The potential for gene drives to spread beyond the target population and affect other species or regions also raises questions about the control and reversibility of such interventions (Adolfi et al., 2020).
Furthermore, the ecological impacts of reducing or altering mosquito populations through genetic modifications must be evaluated. Mosquitoes play various roles in ecosystems, including serving as food sources for other animals. The reduction or elimination of mosquito populations could have cascading effects on biodiversity and ecosystem stability. Therefore, it is crucial to conduct comprehensive ecological risk assessments and develop strategies to mitigate potential negative impacts before implementing genetic control measures (Adolfi et al., 2020).

5 Future Directions

5.1 Innovations in genomic technologies

The field of mosquito vector competence and pathogen transmission is poised for significant advancements through the development and application of novel genomic technologies. One promising area is the use of Cas9/gRNA-mediated gene-drive systems, which have shown potential in population modification and suppression strategies. These systems can effectively reduce the number of vector insects or alter their ability to transmit pathogens, as demonstrated in Anopheles stephensi (Adolfi et al., 2020). Additionally, the optimization of physical genome mapping techniques, such as the use of fluorescence in situ hybridization (FISH) for cytogenetic mapping, has improved the accuracy of genome assemblies in mosquitoes with large, repeat-rich genomes (Masri et al., 2021). Another innovative approach is the development of targeted amplicon sequencing methods to screen for insecticide resistance mutations. This method allows for rapid and cost-effective identification of single nucleotide polymorphisms (SNPs) and small insertions and deletions (indels) in genes associated with resistance, facilitating high-throughput monitoring of insecticide resistance in mosquito populations (Collins et al., 2022). Furthermore, advances in oral RNA interference (RNAi) technologies offer new avenues for vector control by enabling the delivery of species-specific interfering RNA pesticides to mosquitoes, potentially overcoming the limitations of traditional insecticides (Wiltshire et al., 2020).

The integration of these genomic technologies with high-throughput detection methods, such as the use of FTA cards for saliva collection, can enhance the efficiency of monitoring arbovirus transmission in mosquito populations (Honório et al., 2020). Additionally, the development of site-directed integration and cassette exchange systems, such as the φC31-mediated integration, provides precise and stable methods for genetic modification of mosquito genomes, enabling reproducible transgene expression and facilitating comparative analyses of phenotypes (Adolfi et al., 2021).

5.2 Integrated vector management

The insights gained from genomic technologies can be integrated into broader vector management strategies to enhance disease control. For instance, the identification of insecticide resistance mutations through targeted amplicon sequencing can inform the development of more effective insecticide formulations and deployment strategies, thereby mitigating the impact of resistance on vector control programs (Collins et al., 2022). Additionally, the use of gene-drive systems for population modification can be combined with existing vector control measures, such as insecticide-treated nets (ITNs), to achieve more sustainable reductions in vector populations and disease transmission (Selvaraj et al., 2020).

5.3 Research gaps

The application of RNAi-based pesticides offers a novel approach to integrated vector management by providing a species-specific and environmentally friendly alternative to chemical insecticides. This technology can be incorporated into existing control programs to address the growing issue of insecticide resistance and enhance the overall effectiveness of vector control efforts (Wiltshire et al., 2020). The use of high-throughput detection methods, such as FTA cards, can also streamline the monitoring of arbovirus transmission, allowing for more timely and accurate assessments of vector competence and the impact of control interventions (Honório et al., 2020).

Furthermore, the development of comprehensive genomic resources, such as the mosquito small RNA genomics
(MSRG) resource, can facilitate a deeper understanding of the interactions between mosquito vectors and pathogens. This knowledge can inform the design of targeted interventions that disrupt pathogen transmission at the molecular level, thereby reducing the burden of vector-borne diseases (Ma et al., 2021). The creation of high-quality genome assemblies, as demonstrated in *Anopheles stephensi*, can also uncover previously hidden genetic elements that play critical roles in vector competence and insecticide resistance, providing new targets for genetic control strategies (Chakraborty et al., 2021).

In summary, the integration of genomic technologies into vector management strategies holds great promise for enhancing the control of mosquito-borne diseases. By leveraging these innovations, researchers and public health practitioners can develop more effective and sustainable approaches to reducing the transmission of pathogens by mosquito vectors.

6 Concluding Remarks
6.1 Synthesis of key findings
The study of functional genomics in mosquito vectors has yielded significant insights into the genetic and molecular mechanisms underlying vector competence and pathogen transmission. Advances in genome mapping technologies, such as Hi-C scaffolding and optical mapping, have improved the quality of mosquito genome assemblies, facilitating the identification of genes responsible for vector competence, insecticide resistance, and mosquito behavior. Gene-drive systems, particularly those mediated by Cas9/gRNA, have shown promise in modifying mosquito populations to reduce their ability to transmit pathogens. Additionally, single-cell RNA sequencing has expanded our understanding of mosquito immune responses, revealing the functional diversity of hemocytes and their role in limiting pathogen transmission. The non-coding regions of the mosquito genome, once considered “junk,” have been found to contain regulatory elements that significantly impact gene expression and vector competence.

6.2 Implications for public health
The findings from functional genomics research have profound implications for public health strategies aimed at controlling mosquito-borne diseases. The development of high-quality genome assemblies and gene-drive systems offers new avenues for genetic interventions that can suppress mosquito populations or alter their vector competence. Understanding the genetic basis of insecticide resistance can inform the design of more effective and sustainable vector control measures. Moreover, insights into the mosquito immune system and microbiome interactions can lead to novel strategies for enhancing mosquito resistance to pathogens, thereby reducing disease transmission. These advancements underscore the potential of genomics-based approaches to complement existing vector control programs and improve their efficacy.

6.3 Recommendations for future research
Future research should focus on the following areas to further advance the field of functional genomics in mosquito vectors: Enhanced Genome Mapping: Continued development and optimization of genome mapping techniques, such as the gene-based physical mapping approach, are essential for creating accurate and comprehensive genome assemblies for various mosquito species. Gene-Drive Systems: Further refinement and field testing of gene-drive systems are needed to assess their long-term efficacy and ecological impact. Ethical considerations and regulatory frameworks should also be developed to guide the deployment of these technologies. Non-Coding Genomic Elements: Expanding research on non-coding regulatory elements will provide deeper insights into the genetic regulation of vector competence and pathogen resistance. This includes the identification and functional characterization of microRNAs, long non-coding RNAs, and enhancers. Microbiome Studies: Investigating the interactions between mosquito microbiomes and pathogens at the individual level, rather than pooled samples, will yield more accurate data and potentially reveal new targets for vector control. Integrated Vector Management: Combining genomics-based approaches with traditional vector control methods, such as insecticides and environmental management, will create more robust and sustainable strategies for reducing mosquito-borne disease transmission. By addressing these research areas, scientists and policymakers can develop more effective and ethical approaches to controlling mosquito populations and mitigating the spread of
mosquito-borne diseases.

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References


resolution, Science, 369: 1128-1132.
https://doi.org/10.1126/science.abc0322.

https://doi.org/10.1038/s41467-021-23434-z.

https://doi.org/10.1101/2020.01.27.970421.

https://doi.org/10.1016/j.cois.2020.05.002.

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