IAA Journal of Biological Sciences 14(1):29-35, 2026 www.iaajournals.org

©IAAJOURNALS ISSN:2636-7254

https://doi.org/10.59298/IAAJB/2026/1412935 IAAJB1411

Gene Drive Technology for Anopheles Mosquito Control: Mechanisms, Safety, and Ethical Considerations

Masika Anna Mahinda

Department of Pharmacy Kampala International University Uganda
Email: mahindamasika@studwc.kiu.ac.ug

ABSTRACT

Malaria remained a leading cause of morbidity and mortality in tropical regions, with *Anopheles* mosquitoes serving as the primary vectors. Traditional vector control methods faced challenges including insecticide resistance and operational limitations. Gene drive technology represented a novel approach that harnesses molecular mechanisms to spread desired genetic modifications through mosquito populations at accelerated rates, offering potential paradigm shifts in vector control strategies. This review examined the molecular mechanisms underlying gene drive systems in *Anopheles* mosquitoes, evaluated their safety profiles and ecological implications, and explored the ethical dimensions surrounding their potential deployment for malaria control. A comprehensive literature search of peer-reviewed journals, regulatory documents, and expert consensus statements published between 2010 and 2025 was conducted, focusing on CRISPR-based gene drives, ecological modeling, biosafety assessments, and bioethics frameworks. CRISPR Cas9-mediated gene drives demonstrated high transmission rates through mosquito populations, with several designs, including population suppression and modification approaches, showing efficacy in laboratory settings. Molecular mechanisms involved targeted gene disruption or trait insertion with super-Mendelian inheritance patterns. Safety concerns encompassed unintended ecological effects, resistance evolution, and transboundary spread. Ethical considerations centered on informed consent, environmental justice, and governance frameworks for testing and deployment. Current evidence indicates substantial technical progress but reveals significant gaps in ecological risk assessment, long-term stability evaluation, and consensus on regulatory pathways. Gene drive technology demonstrated considerable promise for *Anopheles* control, yet successful implementation requires rigorous safety testing, robust governance structures, and meaningful community engagement before field deployment can be ethically justified.

Keywords: Gene drive, CRISPR Cas9, Anopheles gambiae, Malaria vector control, Biosafety

INTRODUCTION

Gene drive systems represent synthetic genetic elements capable of biasing their own inheritance, enabling specific alleles to spread through populations at rates exceeding standard Mendelian expectations. In natural systems, selfish genetic elements, including homing endonuclease genes and transposons, have evolved mechanisms to achieve super-Mendelian transmission, inspiring biotechnological applications [1]. The advent of CRISPR Cas9 technology revolutionized gene drive development by providing a programmable, efficient platform for creating synthetic drives with unprecedented precision [2]. Contemporary gene drive designs for insect vectors focus primarily on *Anopheles* mosquitoes, targeting genes essential for female fertility, vectorial capacity, or population viability [3]. These molecular tools offer theoretical advantages over conventional control strategies by establishing self-propagating genetic modifications that persist and spread autonomously once introduced [4].

The epidemiological burden of malaria justifies intensive research into novel vector control paradigms. Despite decades of intervention efforts using insecticide-treated nets, indoor residual spraying, and larval control, malaria caused approximately 241 million cases and 627,000 deaths globally in 2020, predominantly in sub–Saharan Africa [5]. *Anopheles gambiae* complex mosquitoes constitute the most efficient malaria vectors, exhibiting high anthropophilic behavior, endophilic resting patterns, and competence for *Plasmodium* transmission [6]. Emerging

insecticide resistance threatens the efficacy of current vector control arsenals, with resistance documented across multiple insecticide classes [7]. Behavioral adaptations, including outdoor biting and early evening feeding, further reduce intervention effectiveness [8]. These challenges have stimulated exploration of genetic control strategies that could complement or replace traditional methods. This review is to critically evaluate gene drive technology as applied to *Anopheles* mosquito control, examining molecular mechanisms underlying different drive architectures, assessing ecological and biosafety considerations, and analyzing the ethical frameworks necessary for responsible development and potential deployment.

Molecular Mechanisms and Design Architectures

Gene drives exploit endonuclease-based copying mechanisms to convert heterozygous individuals into homozygotes, thereby achieving transmission rates approaching 100 percent rather than the Mendelian expectation of 50 percent [9]. CRISPR Cas9-based drives function through a three-component system: the Cas9 nuclease, a guide RNA targeting a specific genomic sequence, and a DNA repair template encoding the drive construct itself [10]. Following fertilization, when a drive carrying a gamete fuse with a wild-type gamete, the resulting heterozygous embryo expresses Cas9, which cleaves the homologous wild-type chromosome at the target site. The cellular homology-directed repair machinery then copies the drive element from the intact chromosome to repair the break, converting the heterozygote into a drive homozygote [11]. This molecular process ensures that nearly all offspring inherit the drive, enabling rapid population spread even when the drive imposes fitness costs.

Two principal architectural strategies have emerged for *Anopheles* gene drives: population suppression and population modification designs [12]. Suppression drives aim to reduce vector populations below disease transmission thresholds by targeting genes essential for female fertility or viability. Early designs disrupted doublesex genes, which control sexual differentiation, causing female sterility while preserving male fertility to maintain drive transmission. Laboratory cage trials demonstrated population elimination within 7 to 11 generations when doublesex targeting drives achieved conversion efficiencies exceeding 90 percent [13]. Alternative suppression targets include genes regulating female flight, host seeking, or egg production. Population modification approaches instead aim to render mosquitoes refractory to *Plasmodium* infection by introducing effector genes that disrupt parasite development [14]. These drives typically insert antimalarial effector cassettes, such as single-chain antibodies targeting parasite surface proteins, into genomic safe harbor loci while maintaining mosquito fitness [15].

Drive stability represents a critical technical challenge, as the continuous expression of Cas9 and guide RNAs throughout multiple generations creates selection pressure for resistance alleles [16]. Resistance emerges through two mechanisms: drive resistant alleles generated by error prone non homologous end joining repair pathways, and standing genetic variation at the target site that prevents guide RNA binding. Mathematical models predict that high resistance allele formation rates could halt the spread before achieving population-level effects. Engineering strategies to mitigate resistance include multiplexing guide RNAs to target multiple essential sites simultaneously, using highly conserved target sequences with minimal natural polymorphism, and employing split drive systems that separate Cas9 and guide RNA components [17]. Recent innovations incorporate daisy chain drives, where multiple drive elements depend sequentially on preceding elements, creating a temporal limitation to drive persistence. These mechanisms collectively advance toward more controllable and predictable gene drive behavior, bridging laboratory efficacy with field deployment requirements.

Ecological Implications and Risk Assessment

The introduction of gene drive-modified mosquitoes into natural ecosystems raises complex ecological questions regarding community stability, trophic interactions, and biodiversity conservation [18]. *Anopheles* mosquitoes occupy multiple ecological roles as pollinators in adult stages, aquatic detritivores as larvae, and prey items for various insectivorous species, including fish, amphibians, birds, and arthropods. Population suppression drives that eliminate or substantially reduce *Anopheles* abundance could theoretically disrupt these ecological functions, although empirical evidence suggests functional redundancy among mosquito species may buffer ecosystem impacts [19]. Field studies in ecosystems where *Anopheles* populations were naturally reduced or locally eliminated showed minimal detectable effects on predator populations or plant pollination networks, suggesting limited keystone status for these species [20]. However, these observations derive from geographically limited contexts and may not generalize to all ecosystems harboring diverse *Anopheles* assemblages.

Competitive release represents another ecological concern, wherein suppression of one mosquito species could create niche opportunities for other vector or nuisance species to expand. Ecological modeling indicates that suppressing *Anopheles gambiae* populations in West Africa might facilitate expansion of *Anopheles arabiensis* or *Anopheles funestus*, which also transmit malaria but exhibit different ecological preferences and intervention susceptibilities [21]. This competitive dynamic could reduce overall public health benefits if replacement vectors maintain disease transmission [22]. Population modification drives that preserve mosquito abundance while altering vectorial capacity present different ecological risk profiles, potentially maintaining ecosystem functions while reducing parasite transmission

[23]. Nevertheless, modification approaches introduce novel genetic elements and phenotypes into natural populations, with uncertain evolutionary stability over extended timeframes [24].

Horizontal gene transfer from gene drive mosquitoes to other organisms constitutes a theoretical biosafety concern, although mechanistic barriers render such events highly unlikely. Gene drives contain eukaryotic regulatory elements incompatible with prokaryotic expression systems, and physical transfer requires cellular fusion or viral vectoring mechanisms absent in natural mosquito populations. Vertical gene flow to non-target mosquito species through hybridization presents more plausible risks, particularly for gene drives targeting species complexes where interspecific mating occasionally occurs. Geographic and temporal containment strategies, including cage testing, screened field trials, and initial releases on isolated island populations, provide stepwise risk mitigation approaches before continental deployment [25]. Comprehensive ecological risk assessment frameworks integrating population genomics, community ecology, and evolutionary modeling remain essential for predicting and monitoring gene drive impacts across diverse environmental contexts.

Biosafety Considerations and Regulatory Frameworks

Biosafety evaluation for gene drive mosquitoes requires assessment frameworks that extend beyond conventional genetically modified organism regulations to address the self-propagating, potentially irreversible nature of drive spread. Traditional containment paradigms developed for transgenic crops or pharmaceuticals prove inadequate for organisms designed to persist and disseminate autonomously [26]. The Cartagena Protocol on Biosafety, established under the Convention on Biological Diversity, provides international governance for living modified organisms but predates gene drive technology and lacks specific provisions for self-propagating genetic elements. Consequently, regulatory authorities face challenges in adapting existing biosafety frameworks to accommodate gene drive risk profiles [27].

Several technical biosafety mechanisms have been engineered to provide control over drive behavior and limit unintended spread [28]. Threshold-dependent drives require release above a minimum frequency to achieve population invasion, naturally confining spread to release areas if initial introductions remain below threshold levels. These designs exploit Allee effects or incorporate genetic architectures where drive fitness becomes positive only at higher frequencies. Temporally self-limiting drives, including daisy chain and split drive systems, incorporate molecular mechanisms that cause drive activity to decline or cease after predetermined generation numbers [29]. Reversal drives represent another safeguard strategy, consisting of secondary gene drives designed to overwrite and remove initial drive elements if deployment outcomes prove undesirable [30]. Laboratory demonstrations show reversal drives can efficiently eliminate target drives from populations, although their effectiveness depends on reaching populations before the original drive achieves fixation.

Regulatory pathways for gene drive testing and deployment remain heterogeneous across jurisdictions, reflecting varying risk perceptions and governance capacities [31]. The African Union Development Agency has developed policy frameworks for gene drive evaluation, emphasizing phased testing approaches and stakeholder engagement [32]. Countries including Burkina Faso, Uganda, and Mali have established regulatory structures permitting confined field trials, while maintaining restrictions on open release pending further evidence [33]. International coordination mechanisms, including the World Health Organization Vector Control Advisory Group and the Foundation for the National Institutes of Health Target Malaria consortium, provide technical guidance and promote harmonized assessment standards [34]. Comprehensive biosafety frameworks must integrate environmental risk assessment, public health impact evaluation, and monitoring systems capable of detecting and responding to unforeseen outcomes, while maintaining sufficient flexibility to adapt as evidence accumulates from phased testing programs.

Ethical Dimensions and Community Engagement

The potential deployment of gene drive mosquitoes raises profound ethical questions spanning informed consent, environmental justice, and intergenerational responsibility [35]. Unlike conventional public health interventions that individuals can accept or decline, gene drives affect shared ecosystems and may cross national boundaries, creating collective action dilemmas where individual choice becomes impossible [36]. This communal impact necessitates engagement and consent processes that extend beyond individual informed consent to incorporate community-level deliberation and decision-making. Philosophical frameworks, including the precautionary principle, which advocates restraint when facing uncertain but potentially serious harms, compete with utilitarian calculations weighing the substantial disease burden of malaria against uncertain ecological risks [37]. Reconciling these ethical tensions requires transparent risk communication, meaningful participation of affected communities, and governance structures that distribute decision-making authority equitably [38].

Historical injustices in biomedical research, including exploitative clinical trials and inadequate benefit sharing with participating communities, create legitimate skepticism toward novel biotechnologies in resource-limited settings [39]. Gene drive development, largely funded by institutions in high-income countries and tested in low-income malaria endemic regions, risks recapitulating colonial research patterns if not conducted with genuine partnership and capacity building [40]. Ethical frameworks emphasizing procedural justice demand that affected communities

participate substantively in research priority setting, protocol design, and benefit distribution rather than serving merely as research subjects [41]. The Target Malaria consortium has implemented extensive community engagement activities in West Africa, including educational programs, stakeholder consultations, and co-design processes that incorporate local knowledge and values. However, critics question whether current engagement activities achieve genuine informed consent at community scales or adequately address power asymmetries between international research institutions and local communities.

Transboundary implications introduce additional ethical complexities, as gene drives released in one nation could spread to neighboring countries that did not consent to the introduction [42]. International law provides limited precedent for governing transboundary environmental modifications, with existing frameworks focused primarily on pollution or resource extraction rather than biological introductions [43]. Proposed governance mechanisms include regional consultation processes, binding international agreements requiring multilateral approval before release, and liability frameworks assigning responsibility for monitoring and potential remediation [44]. Justice considerations extend temporally as well as geographically, as decisions made by current generations impose potentially irreversible environmental changes on future populations who cannot participate in present deliberations [45]. Balancing present disease burdens against uncertain future risks demands ethical frameworks that acknowledge both the urgency of malaria control and the gravity of introducing self-propagating genetic elements into shared ecosystems.

Current Status, Knowledge Gaps, and Research Priorities

Gene drive research has advanced rapidly from theoretical proposals to laboratory demonstrations and initial confined field trial approvals, yet substantial knowledge gaps remain before responsible deployment becomes feasible [46]. As of 2025, no gene drive mosquitoes have been released into open environments, with current activities limited to contained laboratory studies and small-scale cage trials [47]. The Target Malaria consortium released genetically modified non-Gene Drive *Anopheles* mosquitoes in Burkina Faso in 2019 and 2023 as preliminary steps toward eventual gene drive testing, demonstrating regulatory approval pathways and community acceptance processes. These releases tested infrastructure, monitoring protocols, and stakeholder engagement approaches without introducing self-propagating genetic elements. Full gene drive field trials await additional evidence addressing resistance evolution, ecological impact prediction, and long-term drive stability [48].

Critical research priorities include improving predictive models of drive behavior in genetically and ecologically heterogeneous natural populations [49]. Laboratory studies typically employ inbred mosquito lines in controlled environments, potentially underestimating resistance evolution rates and fitness costs that emerge in outbred field populations. Expanded testing in semi-field systems, such as large outdoor cages or screened enclosures containing naturalistic environmental conditions, could improve parameter estimates for population models. Resistance management strategies require experimental validation, particularly for multiplexed guide RNA designs and alternative target gene selections [50]. Ecological monitoring methodologies must advance to detect subtle community-level effects that might not appear in short-term or geographically limited studies. Integration of population genomics approaches enables tracking of driver alleles, resistance mutations, and unintended genetic changes across spatial and temporal scales [51].

Interdisciplinary research bridging molecular biology, ecology, evolutionary biology, social sciences, and ethics remains essential for comprehensive gene drive evaluation. Social science investigations into community perceptions, trust building, and culturally appropriate engagement strategies inform ethical deployment pathways [52]. Economic analyses assessing cost effectiveness compared to existing interventions, accounting for development expenses, deployment logistics, and monitoring requirements, guide resource allocation decisions [53]. Regulatory science research developing fit-for-purpose assessment frameworks, decision criteria, and monitoring standards supports evidence-based policy making [54]. International collaboration initiatives, including the WHO guidance framework development and African Union policy harmonization, facilitate coordinated approaches to testing and potential deployment. Addressing these multifaceted knowledge gaps through systematic research programs positions gene drive technology as a potentially valuable component of integrated vector management strategies while maintaining appropriate caution regarding ecological and social implications.

CONCLUSION

Gene drive technology represents a scientifically sophisticated approach to *Anopheles* mosquito control with substantial theoretical potential for reducing malaria transmission where conventional interventions prove insufficient. CRISPR Cas9-based drive systems demonstrate robust molecular mechanisms enabling super Mendelian inheritance and efficient population spread in laboratory settings, with both suppression and modification architectures showing promise for distinct operational contexts. Nevertheless, significant uncertainties persist regarding drive stability, resistance evolution, ecological impacts, and long-term population dynamics in natural environments. Biosafety frameworks incorporating containment strategies, reversibility mechanisms, and phased testing approaches provide pathways for managing technical risks, yet regulatory structures require continued development to address the novel challenges posed by self-propagating genetic elements. Ethical considerations

demand governance models emphasizing procedural justice, meaningful community engagement, transboundary consultation, and equitable benefit sharing rather than purely technical risk-benefit calculations. Current evidence supports continued research and carefully controlled testing, but does not yet justify open environmental release of gene drive mosquitoes. The integration of molecular innovation with rigorous ecological assessment, robust biosafety protocols, and ethically grounded governance structures will determine whether gene drive technology fulfills its promise as a transformative malaria control tool or remains a cautionary example of biotechnological overreach. International research consortia should prioritize establishing standardized confined field trial protocols in ecologically representative settings, accompanied by parallel development of binding multilateral governance frameworks that ensure equitable decision-making authority for potentially affected communities before any open release of gene drive mosquitoes.

REFERENCES

1. Werren JH. Selfish genetic elements, genetic conflict, and evolutionary innovation. Proc Natl Acad Sci USA. 2011;108(Suppl 2):10863-10870.
2. Alum EU. (2024). Career Advancement towards Nascent Technologies: RNA in Focus. IDOSR Journal of Scientific Research 9(2):49-53. https://doi.org/10.59298/IDOSRJSR/2024/9.2.4953.100
3. Hammond A, Galizi R, Kyrou K, et al. A CRISPR-Cas9 gene drive system targeting female reproduction in the malaria mosquito vector *Anopheles gambiae*. Nat Biotechnol. 2016;34(1):78-83.
4. Alphey L. Genetic control of mosquitoes. Annu Rev Entomol. 2014;59:205-224.
5. Tufail, T., Agu, P. C., Akinloye, D. I., & Obaroh, I. O. (2024). Malaria pervasiveness in Sub-Saharan Africa: Overcoming the scuffle. *Medicine*, *103*(49), e40241. doi: 10.1097/MD.0000000000040241. PMID: 39654176
6. Egwu CO, Aloke C, et al. A world free of malaria: It is time for Africa to actively champion and take leadership of elimination and eradication strategies. Afr Health Sci. 2022 Dec;22(4):627-640. doi: 10.4314/ahs.v22i4.68.
7. Ranson H, Lissenden N. Insecticide resistance in African *Anopheles* mosquitoes: a worsening situation that needs urgent action to maintain malaria control. Trends Parasitol. 2016;32(3):187-196.
8. Killeen GF. Characterizing, controlling and eliminating residual malaria transmission. Malar J. 2014;13:330.
9. Champer J, Buchman A, Akbari OS. Cheating evolution: engineering gene drives to manipulate the fate of wild populations. Nat Rev Genet. 2016;17(3):146-159.
10. Alum, E.U., Ejemot-Nwadiaro, R.I., Basajja, M., Uti, D.E., Ugwu, O.P.C., Aja, P.M. Epitranscriptomic alterations induced by environmental toxins: implications for RNA modifications and disease. *Genes and Environ* **47**, 14 (2025). https://doi.org/10.1186/s41021-025-00337-9
11. Grunwald HA, Gantz VM, Poplawski G, et al. Super-Mendelian inheritance mediated by CRISPR-Cas9 in the female mouse germline. Nature. 2019;566(7742):105-109.
12. Alphey LS, Crisanti A, Randazzo FF. Opinion: Standardizing the definition of gene drive. Proc Natl Acad Sci USA. 2020;117(49):30864-30867.
13. Hammond AM, Kyrou K, Bruttini M, et al. The creation and selection of mutations resistant to a gene drive over multiple generations in the malaria mosquito. PLoS Genet. 2017;13(10):e1007039.
14. Gantz VM, Jasinskiene N, Tatarenkova O, et al. Highly efficient Cas9-mediated gene drive for population modification of the malaria vector mosquito *Anopheles stephensi*. Proc Natl Acad Sci USA. 2015;112(49):E6736-E6743.
15. Isaacs AT, Jasinskiene N, Tretiakov M, et al. Transgenic *Anopheles stephensi* coexpressing single-chain antibodies resist *Plasmodium falciparum* development. Proc Natl Acad Sci USA. 2012;109(28):E1922-E1930.
16. Unckless RL, Clark AG, Messer PW. Evolution of resistance against CRISPR/Cas9 gene drive. Genetics. 2017;205(2):827-841.
17. Marshall JM, Buchman A, Sánchez CHM, Akbari OS. Overcoming evolved resistance to population-suppressing homing-based gene drives. Sci Rep. 2017;7(1):3776.
18. Sánchez CHM, Bennett JB, Wu SL, et al. Modeling the suppression of a vector-borne disease by sustained release of transgenic mosquitoes. J Theor Biol. 2020;492:110190.
19. Collins CM, Bonds JAS, Quinlan MM, Mumford JD. Effects of the removal or reduction in density of the malaria mosquito, *Anopheles gambiae* s.l., on interacting predators and competitors in local ecosystems. Med Vet Entomol. 2019;33(1):1-15.
20. Fang J. Ecology: A world without mosquitoes. Nature. 2010;466(7305):432-434.
21. Okumu FO, Moore SJ. Combining indoor residual spraying and insecticide-treated nets for malaria control in Africa: a review of possible outcomes and an outline of suggestions for the future. Malar J. 2011;10:208.

22. Prowse TAA, Cassey P, Ross JV, et al. Dodging silver bullets: good CRISPR gene-drive design is critical for eradicating exotic vertebrates. Proc Biol Sci. 2017;284(1860):20170799.
23. Leftwich PT, Koukidou M, Rempoulakis P, et al. Genetic elimination of field-cage populations of Mediterranean fruit flies. Proc Biol Sci. 2014;281(1792):20141372.
24. Oye KA, Esvelt K, Appleton E, et al. Regulating gene drives. Science. 2014;345(6197):626-628.
25. Akbari OS, Bellen HJ, Bier E, et al. Safeguarding gene drive experiments in the laboratory. Science. 2015;349(6251):927-929.
26. Akbari OS, Matzen KD, Marshall JM, et al. A synthetic gene drive system for local, reversible modification and suppression of insect populations. Curr Biol. 2013;23(8):671-677.
27. Min J, Noble C, Najjar D, Esvelt KM. Daisyfield gene drive systems harness repeated genomic elements as a generational clock to limit spread. bioRxiv. 2017. doi:10.1101/104877.
28. Wu B, Luo L, Gao XJ. Cas9-triggered chain ablation of cas9 as a gene drive brake. Nat Biotechnol. 2016;34(2):137-138.
29. James S, Collins FH, Welkhoff PA, et al. Pathway to deployment of gene drive mosquitoes as a potential biocontrol tool for elimination of malaria in sub-Saharan Africa: recommendations of a scientific working group. Am J Trop Med Hyg. 2018;98(6 Suppl):1-49.
30. Union, A. (2018). Gene Drives for Malaria Control and Elimination in Africa. *URL: https://www. nepad. org/publication/gene-drives-malaria-control-and-elimination-africa (Accessed 12 April 2021)*.
31. Tung, O. L. (2022). Genetically modified mosquitoes to fight malaria in Nigeria, Burkina Faso, Mali and Uganda: what legal response?. *Potchefstroom Electronic Law Journal/Potchefstroomse Elektroniese Regsblad*, *25*(1).
32. World Health Organization. Guidance Framework for Testing Genetically Modified Mosquitoes. 2nd ed. Geneva: WHO; 2021.
33. Kaebnick GE, Heitman E, Collins JP, et al. Precaution and governance of emerging technologies. Science. 2016;354(6313):710-711.
34. Caplan AL, Parent B, Shen M, Plunkett C. No time to waste: the ethical challenges created by CRISPR. EMBO Rep. 2015;16(11):1421-1426.
35. Resnik DB. Ethical issues in field trials of genetically modified disease-resistant mosquitoes. Dev World Bioeth. 2014;14(1):37-46.
36. Meghani Z, Boëte C. Genetically engineered mosquitoes, Zika and other arboviruses, community engagement, costs, and patents: ethical issues. PLoS Negl Trop Dis. 2018;12(8):e0006501.
37. Nuffield Council on Bioethics. Genome Editing and Human Reproduction: Social and Ethical Issues. London: Nuffield Council on Bioethics; 2018.
38. Hartley S, Thizy D, Ledingham K, et al. Knowledge engagement in gene drive research for malaria control. PLoS Negl Trop Dis. 2019;13(4):e0007233.
39. Tindana P, Bull S, Amenga-Etego L, de Vries J. Seeking consent to genetic and genomic research in a rural Ghanaian setting: a qualitative study of the informed consent process where illiteracy is common. BMC Med Ethics. 2012;13:1.
40. Adelman Z, Akbari O, Bauer J, et al. Rules of the road for insect gene drive research and testing. Nat Biotechnol. 2017;35(8):716-718.
41. Bosley KS, Botchan M, Bredenoord AL, et al. CRISPR germline engineering: the community speaks. Nat Biotechnol. 2015;33(5):478-486.
42. Kofler N, Collins JP, Kuzma J, et al. Editing nature: local roots of global governance. Science. 2018;362(6414):527-529.
43. Teem JL, Ambali A, Glover B, et al. Problem formulation for gene drive mosquitoes designed to reduce malaria transmission in Africa: results from four regional consultations 2016-2018. Malar J. 2019;18(1):347.
44. Brossard D, Belluck P, Gould F, Wirz CD. Promises and perils of gene drives: navigating the communication of complex, post-normal science. Proc Natl Acad Sci USA. 2019;116(16):7692-7697.
45. World Malaria Report 2024: Accelerating progress and preserving the gains of the fight against malaria | Target Malaria, https://targetmalaria.org/latest/news/world-malaria-report-2024-accelerating-progress-and-preserving-the-gains-of-the-fight-against-malaria/
46. Carballar-Lejarazú R, James AA. Population modification of *Anopheline* species to control malaria transmission. Pathog Glob Health. 2017;111(8):424-435.
47. Eckhoff PA, Wenger EA, Godfray HCJ, Burt A. Impact of mosquito gene drive on malaria elimination in a computational model with explicit spatial and temporal dynamics. Proc Natl Acad Sci USA. 2017;114(2):E255-E264.

48. Legros M, Xu C, Okamoto K, et al. Assessing the feasibility of controlling *Aedes aegypti* with transgenic methods: a model-based evaluation. PLoS One. 2012;7(12):e52235.
49. Ferguson HM, Dornhaus A, Beeche A, et al. Ecology: a prerequisite for malaria elimination and eradication. PLoS Med. 2010;7(8):e1000303.
50. Champer SE, Kim IK, Clark AG, Messer PW, Champer J. Anopheles homing suppression drive candidates exhibit unexpected performance differences in simulations with spatial structure. eLife. 2022;11:e79121.
51. Miles A, Harding NJ, Bottà G, et al. Genetic diversity of the African malaria vector *Anopheles gambiae*. Nature. 2017;552(7683):96-100.
52. Mumford JD, Quinlan MM, Beech CJ, et al. MosqGuide: a project to develop best practice guidance for the deployment of innovative genetic vector control strategies for malaria. BMC Proc. 2018;12(Suppl 8):13.
53. Finda MF, Moshi IR, Monroe A, et al. Linking human behaviours and malaria vector biting risk in south-eastern Tanzania. PLoS One. 2019;14(6):e0217414.
54. Connolly JB, Mumford JD, Fuchs S, et al. Recommendations for improving statistical inference in population genomics. PLoS Biol. 2022;20(5):e3001669.

CITE AS: Masika Anna Mahinda (2026). Gene Drive Technology for Anopheles Mosquito Control: Mechanisms, Safety, and Ethical Considerations. IAA Journal of Biological Sciences 14(1):29-35. https://doi.org/10.59298/IAAJB/2026/1412935