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Genomic Surveillance of Infectious Diseases in West Africa: Lessons from ACEGID and Emerging GeneDrive Technologies

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Abstract

In recent times, West Africa has emerged as both a critical frontline and experimental ground for global infectious disease surveillance. This study examines the evolution of genomic surveillance in the region, with a focus on the African Centre of Excellence for Genomics of Infectious Diseases (ACEGID) as a continental leader in outbreak response and capacity building. Drawing on case studies of Ebola, COVID-19, and Lassa fever, we explore how ACEGID's strategic innovations, spanning logistics, data sharing, and human resource development have shaped a resilient regional framework. We interrogate the ethical and political dimensions of genomic data sovereignty, highlighting tensions between local benefits and global collaboration. The review also evaluates emerging gene-drive technologies, particularly CRISPR-based approaches targeting vector-borne diseases, assessing their scientific potential, governance challenges, and socio-political implications within West Africa. Finally, we propose a conceptual model integrating real-time pathogen genomics with adaptive gene-drive interventions, while outlining policy recommendations for sustainable, African-led genomic stewardship. By synthesizing lessons from ACEGID's operational model, we argue for a genomic sovereignty paradigm that balances innovation with equity, and technology with public trust.

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1. Introduction

Genomics is an interdisciplinary field within molecular biology, which focuses on the composition, evolution, mapping, editing, and structure of genomes. The entirety of an organism's DNA, including all of its genes and its three-dimensional, hierarchical structural arrangement, is called its genome [1, 2, 3, 4].

Genomic surveillance, a critical application of genome, involves the monitoring of genetic variations in pathogen, such as bacteria and viruses. Enabled by next-generation sequencing (NGS)-which is now faster and more affordable due to technological advancements, the entire genome of a pathogen can be swiftly and accurately sequenced and analyzed. The surveillance systems in Sub-Saharan Africa in the past were based on microbiology and serology, which were good at detecting pathogens but lacked the precision required for tracking outbreaks and monitoring mutations in real time. The COVID-19 pandemic exposed these limitations very clearly, underscoring Africa's urgent need for more advanced surveillance systems.

Today, more than half [5, 6] of African Member States have established in-country genomic sequencing capabilities, mostly centered on next-generation sequencing (NGS) [7]. A notable contributor to this progress is the African Center of Excellence for Genomics of Infectious Diseases (ACEGID), based at Redeemer's University in Mowe, Nigeria, and supported by World Bank.

The ACEGID aims to identify pathogens causing febrile illness, investigate fevers of unknown origins using metagenomics, and empower African scientists to conduct impactful, locally relevant research. During the 2014 Ebola outbreak, ACEGID played a critical role by diagnosing Ebola cases in Nigeria and Sierra Leone and tracing the virus's origin and evolution in West Africa [8].

Beyond research, ACEGID focuses on long-term capacity building through education and training. Its objectives include developing a skilled workforce in genomics, creating relevant curricula, and promoting public health engagement. Africa’s growing contribution to global platforms such as GISAID (Global Initiative on Sharing All Influenza Data) initiatives reflects the success of such [9].

In parallel, Gene-drive technologies have emerged as a powerful tool for vector control. Gene drives are genetic mechanisms that are intended to suppress or alter populations of disease vectors, such as Anopheles mosquitoes, by spreading particular genes through populations at rates faster than those of regular Mendelian inheritance [10]. When integrated with genomic surveillance, gene drives enable real-time monitoring of vector population and pathogen evolution facilitating the evaluation of the ecological impacts and effectiveness [11].

This integration holds promise for eliminating vector-borne diseases like malaria and dengue. For instance, gene drives targeting reproductive genes have led to complete population collapse in confirmed *Anopheles gambiae* [12]. Coupled with genomic surveillance, these tools can be precisely monitored for ecological impact, mutation rates, and unintended gene spread, ensuring greater safety and effectiveness.

However, the peril of the deployment of gene drives in surveillance programs carries significant risks that must not be overlooked. Their irreversible nature and unprecedented ecological effects raise concerns about unintended outcomes, such as the loss of beneficial insects, emergence of resistant vectors, and disruption of ecosystems [13]. The cross-border spread of gene-drive organisms further complicates regulation, especially in areas with limited public engagement and biosafety capacity [14].

Thus, while genomic surveillance can serve as a critical oversight mechanism, the responsible application of gene-drive technologies requires transparent international collaboration, robust risk assessment protocols, and sustained stakeholder involvement. These tools represent a double-edged sword—offering transformative health benefits while demanding careful ethical and ecological navigation.

2. The Rise of Genomic Surveillance in West Africa

2.1 From Outbreaks to Action: How Ebola and COVID-19 Shaped Genomic Surveillance in West Africa

A number of significant pandemics have struck the world since the early 20th century, including the 1918 "Spanish" flu brought on by the influenza A (H1N1) virus, the 1957 and 1968 influenza A (H2N2) and H3N2 outbreaks, the 2002 Severe Acute Respiratory Syndrome (SARS) outbreak brought on by the SARS coronavirus, and the 2009 Swine Flu associated with influenza A (H1N1) [15, 16]. The West African Ebola Virus Disease (EVD) outbreak from 2013 to 2016 had a significant regional impact and was believed to have killed 11,300 people, while not being formally categorized as a pandemic [17].

The COVID-19 virus, which is caused by an infection with the Severe Acute Respiratory Syndrome Coronavirus 2 (SARS-CoV-2), first appeared in Wuhan, China, in December 2019. Since then, there has been a spread of the disease to pandemic level throughout the world. On February 14, 2020, Egypt reported the first COVID-19 case in Africa. Algeria followed on February 25, 2020, and Nigeria on February 27, 2020[18]. The first confirmed case of COVID-19 in Nigeria involved an Italian national who arrived in Lagos from Milan. On March 11, 2020, the World Health Organization (WHO) officially declared the outbreak a global pandemic [19]. It is now widely known that the virus spreads through respiratory droplets and through close or prolonged contact with infected individuals or contaminated surfaces [20]. As of July 5, 2021, more than 183 million cases had been reported globally, with close to four million deaths. Africa accounted for approximately 2.3% of all confirmed cases and around 2.5% of the global death toll [21].

Many of the disease threats we face today—including new epidemics and pandemics—have been traced back to animals, making zoonotic origins a recurring pattern [22]. While the exact timing of epidemic threats may be unpredictable, their emergence is inevitable. Consequently, response plans must be robust and readily deployable. Sub-Saharan Africa has taken important steps to strengthen its preparedness, particularly through advancements in genomic surveillance. Institutions such as the African Centre of Excellence for Genomics of Infectious Diseases (ACEGID) and the Africa Pathogen Genomics Initiative (PGI), led by the Africa Centre for Disease Control and Prevention (Africa CDC), have significantly enhanced the region’s capacity to monitor and respond to public health emergencies of international concern [23].

Beyond surveillance, however, there is a growing recognition of the need for comprehensive policy frameworks—especially in areas such as biobanking and biosecurity. In Lagos State of Nigeria for example, gaps in legal guidelines became evident. Biobanking—the systematic collection and storage of biological samples with associated data—was essential for the understanding of an emerging disease and the pathogens responsible [24, 25].

2.2 Infrastructure Gap and Strategic Innovation

Infectious diseases such as Ebola, cholera, meningitis, malaria, and other viral hemorrhagic fevers are prevalent in Sub-Saharan Africa [26]. However, the Ebola virus outbreaks in 2014–2016 revealed the limitations of traditional diagnostic techniques and led to investment in genomic surveillance infrastructure throughout West African nations [27]. The African Centre of Excellence for Genomics of Infectious Diseases (ACEGID), based at Redeemer’s University in Mowe, Nigeria, and supported by the World Bank has revolutionized the genomic surveillance of infectious diseases in Nigeria and across West Africa. They achieved this by establishing ACEGID as a regional genomics hub, educating local scientists, and facilitating real-time sequencing and data sharing during outbreaks [28].

The growth of genomic surveillance capabilities in West Africa was further accelerated by the COVID-19 pandemic. This development has contributed to strengthening public health in West Africa in the right direction as more than 170,000 SARS-CoV-2 genomes from 53 African countries had been shared by the middle of 2022, with major contributions from West African countries like Senegal, Ghana, and Nigeria [29]. Collaborations with international platforms such as GISAID and the Africa Pathogen

Genomics Initiative (PGI), The Africa CDC's coordination played a key role in supporting these efforts. Rapid detection of variants like Delta and Omicron was made possible by these platforms, which also helped to guide public health actions by facilitating the prompt sharing of genomic data.

Today, beyond the COVID-19 pandemic, surveillance programs are being developed using genomic tools and technologies. For example, genomics has been used to track the evolution and patterns of transmission of the Lassa fever virus in Nigeria and Sierra Leone, which has aided with vaccine development and improved knowledge of zoonotic reservoirs [30]. To further guide treatment policies and sustain progress toward elimination goals, the use of genomic techniques in malaria surveillance has aided the detection of drug-resistant strains of Plasmodium falciparum [31].

2.3 ACEGID's Mandate and Model

The mission of the ACEGID is to:

1. Build a critical mass of highly qualified scientists to advance African genomics research capacity
2. Empower African researchers to use genomics knowledge and tools to control and eradicate infectious diseases
3. Develop a genomics curriculum to support and promote cutting-edge genomics-based research for health advancement
4. Establish a formal postdoctoral training program in infectious disease translational research in Africa
5. Create a dynamic academic and research environment free from external influences that transcends national boundaries and ensures the conduct of pertinent, responsive, ethical, and high-quality translational genomics-based research on health in Africa.

3. Case Studies in Pathogen Tracking: Lessons from ACEGID

3.1 Ebola: Mapping the Invisible Highways of Viral Spread

Ebola virus disease (EVD), also known as Ebola hemorrhagic fever (EHF), is a viral hemorrhagic fever that is caused by Ebola virus that affects humans and other primates. It was first recognized in 1976 during two concurrent outbreaks: one in Nzara, South Sudan, and the other in Yambuku, a community near the Ebola River in the Democratic Republic of the Congo-after which the disease was named. In the tropical regions of sub-Saharan Africa, Ebola epidemics occur sporadically [32]. Between 1976 and 2012, World Health Organization reports that there were 24 Ebola outbreaks, resulting in 2,387 cases and 1,590 fatalities. The largest outbreak of Ebola in West Africa occurred between December 2014 to January 2016, with a total recorded case of 28,646 and 11,323 deaths [33].

Traditional epidemiological methods often struggled to track Ebola's complex transmission dynamics. These methods, which primarily rely on clinical reporting and contact tracking, provided limited insight to hidden pathway of spread. The advent of genomic surveillance has revolutionized this process by allowing researchers reconstruct the lineage and evolutionary changes of viral genomes by molecular epidemiology, specifically genomic sequencing, which reveals patterns of transmission that reflect socio-political links and population mobility [34], significantly enhanced our understanding by revealing previously unseen routes of viral spread.

Although Ebola is not transmitted via persistent networks like HIV, its spread follows less visible pathways—such as migration routes, socio-political connections, and porous borders—that genomic tools help uncover. Direct contact with bodily fluids from an infected person or animal will spread the Ebola virus. Contact with blood, vomit, feces, sweat, saliva, semen, breast milk, and other fluids are included in this. Additionally, coming into contact with contaminated bedding and needles can also transmit it.

The African Centre of Excellence for Genomics of Infectious Diseases (ACEGID) in Nigeria has played a pivotal role during the 2014 Ebola outbreak by rapid sequencing viral genomes and sharing vital genomic data to international partners [28]. Their genomic surveillance efforts helped identify the origin, mutations, and spread dynamics across West Africa, enabling timely reconstruction of viral transmission networks [35]. The Center's capacity for real-time sequencing and open data sharing was a game-changer for Africa's response to epidemics and bolstered local scientific infrastructure.

Furthermore, genomic data have allowed researchers to been able to construct *phylogenetic trees* linking viral evolution to geographical transmission routes. These trees confirmed the correlation between genetic variation and geographic spread, thereby validating genomic surveillance as a critical tool in epidemic preparedness and response [8].

3.2 COVID-19: Building Regional Networks in Real Time

Sub-Saharan Africa has advanced significantly in genomic surveillance, with a number of noteworthy accomplishments made both during and after the pandemic.

Prior to and during the early stage of the COVID-19 pandemic, laboratories in underserved regions across Africa relied heavily on external facilities—often located overseas—for genomic analysis. Due to this dependence, there were fewer chances for local capacity building and delayed outbreak responses. The ability to perform genomic sequencing and submit genomes to the Global Initiative on Sharing All Influenza Data (GISAID) was limited to 7 of the 55 African Union (AU) Member States at the time [36].

Currently, regional sequencing hubs have been established as 53 of the 55 AU Member States in 2024 [7, 37] to carry out genetic sequencing in-country. Collaboration between African institutions, governments, international organizations, and business sector partners was the driving force behind this change. In order to expand genomic capacity in Africa, WHO and Africa CDC took the lead in offering support for public health laboratories throughout the continent as well as training in genomic sequencing methods, bioinformatics, variant tracking, and data sharing via platforms like the Integrated Genomic Surveillance and Data Sharing Platform (IGS) which has supported real-time response strategies to emerging health threats.

In West Africa, these advancements have significantly reduced turnaround times for genomic data generation in countries like Nigeria, Ghana, and Senegal, facilitating faster detection of variants and more coordinated outbreak control measures.

3.3 Lassa Fever: From Silent Endemic to Genomic Spotlight

In Western Africa, Lassa fever is a viral hemorrhagic disease that is prevalent and causes approximately 300,000 cases and 3,000 deaths annually [38]. According to the World Health

Organization (WHO) and the Coalition for Epidemic Preparedness Innovations (CEPI), it poses a serious risk to global health and requires immediate research attention [39, 40, 41] .Despite the prevalence of Lassa virus, there is presently no approved vaccine, and the only pharmacologic treatment is available, which is early intravenous administration of the antiviral ribavirin [42, 43, 44].

Nigeria saw a sharp rise in Lassa fever infections in early 2018; by early March, there were 394 confirmed cases, more than in any other year. 19 states in Nigeria reported confirmed cases, with an approximate case fatality rate of 25% [45]. Public health officials were concerned that something had changed fundamentally about this endemic disease because the mechanisms causing this surge were unknown.

In a presumed Lassa fever outbreak, genomic study of contemporaneous Lassa virus in samples from affected patients can complement traditional epidemiological data in a suspected Lassa fever epidemic by identifying whether modifications to the virus's inherent characteristics account for the rise in cases. Specifically, viral genomic analysis can quickly determine whether the case increase is related to a modified viral transmission pathway, a novel variant, or a particular viral lineage. The majorities of Lassa virus infections in humans are caused by contact with infected *Mastomys natalensis* or their feces, although human-to-human transmission has been observed in hospital environments and is the subject of public health surveillance [46, 47].

The African Center of Excellence for Genomics of Infectious Disease (ACEGID), located at Redeemer's University in Nigeria, conducted a near real-time genomic sequencing of Lassa virus from patients between January and March 2018. These findings further clarify the geographic distribution of the endemic Lassa virus population throughout Nigeria and offer crucial genetic background for the recent Lassa fever outbreak.

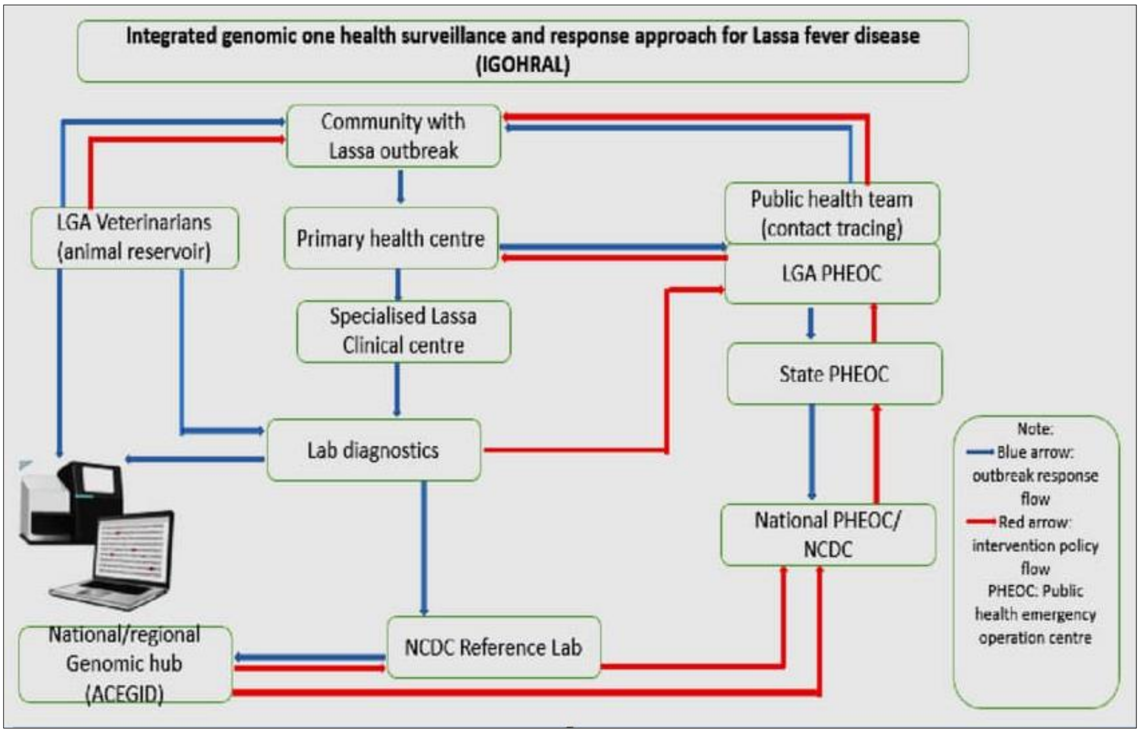

Fig 3.1: Integrated Genomic One Health surveillance and Response Approach for Lassa fever (IGOHRAL) flow chart [71].

Data Sovereignty and Equity in Genomic Surveillance

In Africa's public health landscape, genomic surveillance has emerged as a crucial tool that facilitates prompt epidemic response, variants tracking, and pathogen discovery. However, its growth has raised complicated questions about equity and data sovereignty. The right of countries to manage the storage, access, and use of genomic data produced inside their boundaries is known as data sovereignty. Concerns about external exploitation and the loss of local control over valuable biological and digital resources have increased in West Africa as a result of previous events, such as the unconsented export of Ebola samples during the 2013–2014 outbreaks [48].

The issue of equity, which is closely related to sovereignty, pertains to who plans, carries out, and gains from genomic research. Historically, African scientists have been mostly assigned to sample collection roles, and downstream analyses have been carried out overseas, which limit authorship, recognition, and capacity development [49]. Initiatives like H3Africa, the African Society of Human Genetics, and the Three Million African Genomes (3MAG) project seek to address historical imbalances by encouraging research led by Africans, establishing infrastructure, and guaranteeing representation in global genomic databases [50]. However, obstacles still exist, such as inadequate sequencing infrastructure, high equipment and reagent costs, limited bioinformatics capacity, and reliance on temporary donor funding [51]. Workforce retention is hindered by brain drain and limited career pathways, while governance frameworks remain fragmented, with inconsistent consent models, weak sample export controls, and limited protections for secondary data use [52].

The legacy of colonialism and extractive research, where Western-centric data-sharing frameworks predominate and frequently ignore African epistemologies and weaken local agency, exacerbates ethical issues [53]. Furthermore, data loss and underutilization result from a lack of sustainable data management, such as that outlined in the FAIR principles (Findable, Accessible, Interoperable, and Reusable [49]. With success stories like the establishment of in-country sequencing in Senegal and Nigeria's leadership in SARS-CoV-2 genomic surveillance, initiatives like the Africa Pathogen Genomics Initiative (Africa-PGI), the African Centre of Excellence for Genomics of Infectious Diseases (ACEGID), and the Centre for Epidemic Response and Innovation (CERI) show the potential of regional capacity-building [54].

In terms of ethics, open-domain repositories are less egalitarian than models such as GISAID's data-sharing approach, which preserves data-provider control [55]. Scholars increasingly advocate for human-rights-based approaches to genomic regulation, prioritizing participation rights, benefit-sharing, and alignment with African values such as Ubuntu, which emphasizes solidarity, reciprocity, and collective benefit [56]. Harmonized governance frameworks, long-term infrastructure investment, local reagent manufacturing, sustainable funding mechanisms, applied bioinformatics training, equitable authorship norms, and transparent and trust-based community engagement are all necessary to achieve sovereignty and equity

Table 4: Differences between global and local benefits of genomic data sharing, adapted and expanded from [54].

Benefit Type	Global Benefit	Local Benefit
Scientific Advancement	- Accelerates research leading to new discoveries and treatments for rare and common illnesses	- Improves research accuracy - Identifies genetic predispositions - Informs personalized medicine
Public Health Impact	- Supports global surveillance and response to outbreaks (e.g., COVID-19) - Informs vaccine development	- Enhances diagnostic accuracy - Identifies effective therapies - Optimizes medication choice
Cost Effectiveness	- Reduces research duplication - Accelerates drug development - Lowers healthcare costs via prevention	- Informs risk-benefit analyses - Reduces unnecessary or ineffective treatments
Ethical Considerations	- Promotes data sharing for the common good - Requires privacy and equity safeguards	- Informs public health policy - Strengthens collaboration - Builds trust in research
Challenges	- Risk of inequitable access, especially for low- and middle-income countries	- Privacy concerns, such as data breaches and misuse of genetic information

5. Emerging Gene-Drive Technologies: A Double-Edged Sword

5.1 The Science of Gene Drives: Beyond the Simplistic Narrative

Gene drives are self-replicating genetic entities that skew their transmission to facilitate more rapid dissemination within populations. In the 1960s, the idea of employing gene drives to stop pests from spreading was first conceived [57]. Because engineered gene drives can disseminate harmful features, like sterility, throughout a target population, they can be used to control pests or disease vectors [57]. When engineered gene drives can disseminate harmful features, like sterility, throughout a target population, they can be used to manage pests or disease vectors. Advances in CRISPR technology have propelled the development of gene drives, broadening their potential uses and enhancing their safety for practical application [57].

The CRISPR-Cas9 system has greatly expanded the capabilities of gene drive technologies. The promise of CRISPR gene drives to stop mosquitoes and other diseases from spreading diseases like malaria has drawn a lot of attention [57]. Although this is the most well-known use, CRISPR gene drives can be applied to address a number of practical problems.

Gene drives can be broadly classified into two categories: Transposable elements and homing endonuclease genes (HEGs) are examples of natural gene drives that take place in a range of organisms [57]. On the other hand, synthetic gene drives are created in a lab to provide the desired results [57].

In the CRISPR-Cas9 technology, desired variation and CRISPR components (guide RNA and Cas9) are both present in the "drive allele" of CRISPR-based gene drives [57]. When the wild-type chromosome is damaged, the cell replicates the drive into both chromosomes by employing the drive allele as a template for homology-directed repair [57].

CRISPR gene drives can generally be designed in two forms: modification drives, which disseminate an altered gene, and suppression drives, which decrease population size by propagating a harmful allele [57].

5.2 Current Trials and Global Concerns

Gene drives are scientifically promising for public-health goals like malaria control. This technology enables precise targeting of mosquito populations, helping to regulate their numbers and manage resistance, making it an important asset in the fight to eliminate malaria in Africa [58, 59]. By focusing specifically on malaria-carrying mosquitoes, this approach can lower transmission risks in certain regions and act as a supportive measure alongside current malaria control methods [60, 61].

Research and development on gene drive technology to reduce malaria-transmitting mosquitoes is underway in Burkina Faso, Uganda, Tanzania, and Mali [58, 62, 63]. The objective of these studies is to create long-lasting solutions to control mosquito populations, lower the incidence of malaria transmission, and lessen the disease's burden [62, 59, 54]. In laboratory tests, the technique has produced encouraging outcomes. To assess the efficacy and safety of genetically engineered mosquitoes using gene drive mechanisms in actual environments, field tests are being proposed [60, 63, 65].

5.3 Socio-Political Dimension in West Africa

The application of gene drive technology, especially in West Africa, is a question of governance, ethics, and public trust as much as it is of scientific innovation [11, 66]. While the technical ability to create and apply gene drives is developing quickly, the success or failure of these technologies can be influenced by the social, political, and cultural contexts in which they are used [67, 72].

Gene drive project must have strong governance as its foundation [58]. This technique has great promise for disease control in West Africa, for instance malaria [68]. However, the absence of clear governance frameworks exposes the system to dangers like abuse, inadequate supervision, and unjust implementation [69]. In order to avoid this, national regulators must collaborate with regional organizations such as the African Union Development Agency (AUDA-NEPAD) and the West African Health Organization (WAHO) to establish precise, workable guidelines for research, testing, and implementation [66].

The public consent is another key component to the legitimacy of gene drive initiatives (National Academies of Sciences, Engineering, and Medicine, 2016) [70]. Early interaction with affected communities is crucial in West Africa because previous experiences and cultural values influence public opinion. Transparent disclosure of risks and benefits, along with culturally sensitive and clear communication, ensure that consent is both informed and voluntary (African Union, 2018; Resnik, 2019) [58, 69].

6. The Convergence of Genomic Surveillance and Gene Drives

As evidenced by programs like ACEGID, genomic surveillance provides high-resolution tracking of pathogen evolution, geographic spread, and resistance patterns in near real-time, beyond the scope of traditional epidemiological functions to provide actionable intelligence that can inform the timing, location, and parameters of gene-drive interventions. In theory, genomic datasets could be employed to direct adaptive gene-drive deployment — for instance, by identifying shifts in vector populations, allelic frequencies associated with insecticide resistance, or gene flow dynamics across ecological zones [73, 75].

CRISPR-based gene drives function within naturally dynamic ecological and evolutionary systems, especially those that target Anopheles mosquitoes to prevent malaria. It is still challenging to forecast the permanence, dissemination, and unforeseen ecological effects of a released gene drive in the absence of ongoing genomic feedback. Iterative checkpoints for safety, efficacy, and reversibility may be provided by incorporating pathogen and vector genomic surveillance into the gene-drive trial's operating workflow. Although the participants in this model are wild populations with transboundary migration patterns, it is similar to adaptive clinical trials in pharmacology, where transitory genetic data guides mid-course modifications [76, 77].

Moreover, such integration may solve some of the governance and consent difficulties connected with gene drives in West Africa. Stakeholders, including governments, public health organizations, and impacted communities, can interact with tangible, locally sourced data instead of theoretical estimates by tying deployment decisions to regionally owned genetic evidence. By guaranteeing that the genomic intelligence directing interventions is produced, preserved, and interpreted within the continent's scientific infrastructure, this procedure may also strengthen the principles of data sovereignty [78]. In turn, this would decrease dependency on external laboratories, increase regional trust, and allow African institutions to negotiate from a position of informational strength in global health governance issues [79].

However, there are logistical and technical difficulties in operationalizing such a convergence. While pathogen genomic monitoring must continue to be responsive to new outbreak threats, vector genomic surveillance requires laboratory throughput and sample intensity that can keep up with the ecological spread of target species. Merging these procedures would require harmonised bioinformatic frameworks capable of handling various data types — from whole-genome assemblies of mosquito populations to metagenomic reads from human clinical samples. Long-term genomic studies in West Africa have historically been hampered by infrastructural breakdowns and funding variations, therefore these systems must likewise be robust against these events [80, 81].

Ultimately, the confluence of genomic surveillance and gene-drive technologies is less a solitary innovation than the steady development of an integrated biosecurity ecosystem. If properly implemented, such a framework could offer West Africa the capacity not only to respond to epidemics but to forecast and pre-empt them. In this case, genomic data would represent a strategic shift in the region's approach to infectious disease management by acting as both an early-warning system and a compass for precision vector control decision-making [82].

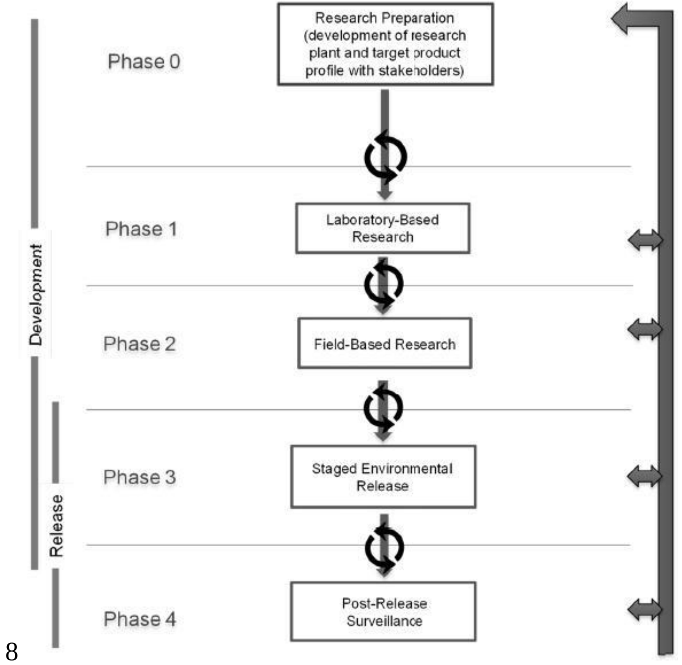

Figure 6.1: Phased testing pathway for gene drive research, illustrating sequential development from laboratory-based studies to post-release

surveillance, with advancement between phases determined by pre-defined milestones and decision points [74].

7. Lessons Learned: ACEGID's Template for Resilient Genomics in Africa

Beyond its scientific contributions, ACEGID has refined institutional strategies that address systemic weaknesses in health security infrastructures across West Africa, including capacity building, workforce retention, regional collaboration, and the integration of genomics into public health pipelines. The center's resilience can be attributed to its dedication to self-reliance, the strategic cultivation of partnerships, and the embedding of genomic science into real-world epidemic response systems. The operational trajectory of ACEGID offers a demonstrable model for how African-led genomic initiatives can evolve from nascent research hubs to continental reference points for outbreak outbreak preparedness and response.

7.1 Training the Next Generation of African Genomic Scientists

The development of capacity utilization is still one of ACEGID's most significant contributions to the genomic landscape in West Africa. Through postgraduate fellowships, short-course workshops, and targeted training programs, ACEGID has developed a cadre of African scientists who can generate, analyze, and interpret genomic data in local contexts [83, 84]. These efforts address a historical challenge in the region: outsourcing high-resolution genomic analyses to laboratories in the Global North, which frequently led to delayed feedback loops, loss of data sovereignty, and decreased local capacity to independently manage outbreaks [85].

Multidisciplinary training across bioinformatics, molecular biology, field epidemiology, and science communication is a key element of ACEGID's model, ensuring that graduates are not only technical operators but also scientific leaders capable of navigating both laboratory and policy environments [86]. Crucially, structured career pathways, competitive stipends, and collaborative research projects that promote long-term engagement rather than brain drain [87] are used to support the retention of trained scientists within African institutions, thereby reducing the chronic human capital flight that has historically hampered health innovation in the region.

7.2 Building Rapid Response Pipelines for Future Pandemics

During the COVID-19 pandemic, ACEGID's genomic surveillance outputs informed public health interventions and helped track global variants within weeks of initial case detections in the region [89]. The center has shown that the combination of field-deployable sequencing technologies, robust sample transport networks, and integrated bioinformatic platforms enables near real-time pathogen characterization during outbreaks [88]. This experience highlights the importance of pre-positioned genomic infrastructure that can pivot quickly in the face of emergent threats.

In order to ensure that sequence data is not isolated but rather actively informs diagnostic, clinical, and policy decisions, it is crucial that genomics be seamlessly integrated into existing public health surveillance systems. The model developed by ACEGID promotes a "surveillance-to-action" feedback loop in which laboratory outputs are immediately channeled into risk assessments, epidemiological modeling, and targeted interventions [90]. The model also emphasizes the importance of regional genomic networks that facilitate cross-border data sharing, allowing neighboring countries to benefit from each other's genomic intelligence in managing transboundary disease threats [91].

Looking forward, consistent funding, unified regulatory frameworks, and a dedication to genetic sovereignty across the continent will be necessary to scale this paradigm throughout Africa. The accomplishments of ACEGID demonstrate that, given the adequate resources, infrastructure, and governance frameworks, African-led genomic organizations are capable of meeting and even outperforming international conventions [92].

8. Unresolved Challenges and Controversies

The insights gained from ACEGID and other regional genomic initiatives highlight the significance of critically assessing these unresolved problems in order to ensure that technological advancement is matched by sustainability, inclusivity, and accountability. While genomic surveillance and emerging biotechnologies hold transformative potential for infectious disease control in West Africa, their deployment is accompanied by persistent and complex challenges, including ethical, socio-political, infrastructural, and financial dimensions.

8.1 Bioethical Quandaries of Editing Wild Populations

Despite the potential of CRISPR-based gene-drive technologies to reduce disease vectors like Anopheles gambiae is well established, concerns remain regarding unintended ecological cascades, horizontal gene transfer, and the ethical implications of making decisions that alter species that cross national boundaries [94, a95]. The development of CRISPR-based gene-drive technologies has heightened the debate over the moral legitimacy of editing wild populations. Gene drives, by design, alter the genetic makeup of entire species, often with irreversible ecological consequences [93].

A gene drive discharged in one country might propagate into states nearby without their explicit permission, which creates conflicts between national sovereignty and regional public health priorities [96]. Additionally, public acceptance cannot be presumed as perceptions of genetic manipulation in the region are shaped by cultural narratives, historical mistrust of externally driven interventions, and concerns about the commodification of biological resources [97]. These factors make it difficult to define legitimate decision-making authority from a governance standpoint.

International regulatory frameworks like the Cartagena Protocol on Biosafety and institutional ethics committees provide some guidance, but the pace at which gene-drive research is progressing has surpassed the capacity of current mechanisms to handle emerging hazards. Bypassing the difficulties of technocratic decision-making requires a proactive strategy that incorporates ethical review and community involvement into each phase of gene-drive research [98].

8.2 Surveillance Blind Spots: Rural vs. Urban Divide

West African genomic surveillance systems persist to suffer from uneven geographic coverage, with urban centers disproportionately benefiting from sequencing infrastructure and data integration [99]. Rural and peri-urban areas, which are frequently the frontlines for zoonotic spillover events and vector breeding, are underrepresented in surveillance datasets, creating blind spots that compromise both early detection and intervention strategies [100]. This disparity is partially logistical, as rural regions often lack high-throughput laboratories, reliable cold-chain transport, and broadband internet, which are necessary for real-time genomic data transmission. Additionally, sample collection in remote communities may be hampered by inadequate road networks, security issues, and low public health literacy [101]. Decentralizing genomic capacity is necessary to bridge this gap. This includes training staff in rural areas in biospecimen collection, genomic analysis, and secure data handling, in addition to distributing portable sequencing platforms such as Oxford Nanopore devices [103]. Incorporating community health workers into surveillance frameworks can also ensure that rural signals are not lost in the shuffle of urban-centric datasets by providing a human network that can quickly acquire samples and report on epidemics [104].

8.3 Funding Volatility and the Politics of Global Health

Instability in funding is undoubtedly the most significant threat to long-term genomic surveillance in West Africa. A significant portion of the existing infrastructure and capacity-building programs, such as those at ACEGID, are funded by project-based, donor-driven grants, frequently from charitable organizations or foreign governments [105]. Although essential for early capacity building, these financial sources are time-constrained and sometimes linked to illness priorities that may not be in line with local health requirements [106]. This dependence on outside funding makes genomic programs vulnerable to changes in the political landscape of global health. During the COVID-19 pandemic, donors prioritized SARS-CoV-2, diverting resources away from endemic threats like Lassa fever and yellow fever [107, 110].

9. Future Roadmap: Integrating Genomics with Public Health Policy

While West Africa is at a crossroads where advanced pathogen sequencing, real-time epidemiological intelligence, and molecular interventions like gene drives could converge to form a responsive, data-driven public health ecosystem, the integration of genomic surveillance into public health policy frameworks in the region is both a strategic imperative and a complex governance challenge. This integration will not happen naturally; it requires intentional policy design, intersectoral collaboration, and sustained political commitment [111].

Embedding genomic laboratories and bioinformatics units within ministries of health, with clearly defined roles in outbreak response, vaccine strain selection, antimicrobial resistance monitoring, and vector control planning, is at the core of this roadmap, which recognizes that genomic surveillance should be treated as an operational arm of national and regional health systems rather than as a separate research function [112]. The policy challenge is converting genomic data into actionable interventions within the frequently slow-moving bureaucratic machinery of public health governance.

In order to provide standardized genetic frameworks, continental and regional organizations like the African Union (AU) and the Economic Community of West African States (ECOWAS) play a crucial role. These organizations are in a unique position to create and implement standardized bioinformatics pipelines, cross-border data-sharing protocols, and reciprocal recognition of genetic certification and quality assurance systems [113]. Such alignment is particularly important in the West African environment, where disease propagation rarely respects country boundaries and disparate genetic strategies among neighboring states can compromise the ability to conduct collective surveillance [114]. Formalizing data sovereignty rules is another requirement for integrating genomics into public health policy. African-led legal frameworks that specify ownership, access rights, and benefit-sharing procedures ought to regulate genomic datasets produced in African labs. If this isn't accomplished, there's a likelihood that extractive research models may continue, where local scientists are restricted to gathering samples while foreign institutions handle downstream processing, publication, and intellectual property [115]. This necessitates the use of policy tools that guarantee genetic data directly supports technological transfer, capacity building, and national health planning [116].

Building capacity itself needs to be a top focus for policymakers. For laboratory scientists and bioinformaticians, governments should establish fellowship programs, genetic epidemiology courses, and ongoing professional development. Investments in digital infrastructure, such as redundant data pipelines, safe cloud storage for genomic datasets, and computational power to support extensive genomic studies, should be made in tandem with this workforce expansion [117].

Additionally, incorporating genetics into policy necessitates a change in the way choices are made on public health. Real-time genetic intelligence should guide decision-making so that adaptive therapies can react to changing epidemiological conditions. This is especially important for vaccination campaigns, vector control programs, and the use of novel molecular tools like gene drives [118]. According to this concept, genomic monitoring would act as a continuous feedback mechanism that links pathogen evolution, intervention impact, and policy recalibration, rather than as a passive diagnostic role [119]. If properly implemented, such a roadmap might spark a paradigm change in West African health security, where evidence-based policymaking, regional cooperation, and genetic sovereignty combine collectively to prevent epidemics rather than just respond to them. [120].

10. Conclusion: Toward a Genomic Sovereignty Revolution in West Africa

With its operational model that combines high-throughput sequencing, real-time epidemiological intelligence, and capacity building, the African Centre of Excellence for Genomics of Infectious Diseases (ACEGID) has become more than just a technical hub; it is a living proof-of-concept of what can be achieved when African institutions take the lead in the genomic domain. The trajectory of genomic surveillance in West Africa highlights the transformative potential of regionally driven scientific initiatives in reshaping the landscape of global health security [121].

In the West African context, the effectiveness of gene drives will be maximized only if they are integrated into a framework that includes ecological monitoring, pathogen genomic surveillance, and strong community engagement. Without these interconnected components, gene drives run the risk of becoming isolated technological interventions with limited sustainability or public legitimacy [122]. Gene-drive technologies hold promise in their ability to address persistent vector-borne disease burdens, but they must be approached as components of an integrated health security system rather than as single solutions.

Therefore, the demand for African-led oversight in the genomic age is not merely idealistic; rather, it is a realistic requirement to guarantee fair health results. Enforceable governance frameworks that specify ownership, control, and benefit-sharing of genetic resources are necessary to transform the idea of "genomic sovereignty" from policy language. This vision places African countries at the center of decision-making processes that have traditionally been dominated by external influences by employing genomic data generated in West Africa to inform not only local outbreak responses but also strategic policy decisions, intellectual property development, and research agenda setting [123].

West Africa might lead a genomic revolution that combines technical innovation and self-determination if the insights gathered from ACEGID are used throughout the continent. In order to do this, it would be necessary to reinforce international networks, harmonize regulatory frameworks, and integrate genetic knowledge into national health systems in a manner that goes beyond one-off initiatives and becomes an ongoing aspect of public health governance [124]. West Africa can transform its role from a passive beneficiary of global health interventions to an active builder of the genomic future by fostering domestic knowledge, protecting data sovereignty, and incorporating technology into policy.

11. References

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