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Portable Genomics at the Frontline: Principles, Adoption, Applications and Future Prospects of Oxford Nanopore Minion Technology in Africa – A Narrative Review

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Abstract

Background: Genomic sequencing has become increasingly important for infectious disease surveillance, outbreak investigation, and antimicrobial resistance monitoring. Conventional next-generation sequencing platforms are often centralized, costly, and infrastructure-intensive, thereby limiting their accessibility in many African settings. Oxford Nanopore Technologies, particularly the MinION sequencer, offer a potentially more deployable approach because of their portability, real-time sequencing capability, long-read output, and suitability for field-based workflows.

Results: This narrative review describes the principles of MinION Nanopore sequencing and critically examines its applications in public health and infectious disease genomics across Africa, with emphasis on epidemic response, infectious disease genomic surveillance, antimicrobial resistance monitoring, and One Health investigations. The review discusses key African use cases, highlights the advantages of decentralized genomic technologies, and examines implementation challenges related to use such as the cost, bioinformatics capacity, quality assurance, and sustainability. The review further considers future prospects including integration into routine diagnostics, surveillance, and pandemic preparedness.

Conclusion: Overall, MinION technology has contributed to the expansion of genomic surveillance capacity in Africa and has considerable potential to strengthen public health preparedness and response across the continent.

Keywords
Nanopore sequencing; MinION; genomic surveillance; infectious diseases; antimicrobial resistance; Africa

Introduction

Genomic sequencing represents a central strategy for infectious disease surveillance, outbreak investigation, antimicrobial resistance monitoring, and pathogen evolution studies. By enabling whole-genome analysis of pathogens, sequencing supports transmission mapping, variant detection, source attribution, and identification of resistance determinants[1,2].

Although genomic sequencing has become integrated into routine public health practice in many high-income settings, access remains limited in many low- and middle-income countries, including several African countries, because of cost, infrastructure, workforce, and logistics constraints.[1,2]Conventional next-generation sequencing platforms often rely on centralised laboratories, expensive equipment, and complex workflows, which restrict their use in resource-limited environments. [2–6]

Conceptual and experimental advances in nanopore-based single-molecule detection during the 1990s and early 2000s laid the foundation for commercially available nanopore sequencing platforms.[7] The large-scale commercialisation of nanopore sequencing by Oxford Nanopore Technologies (ONT) in the 2010s expanded access to long-read sequencing. [8] Compared with many conventional sequencing platforms, the MinION has a low initial instrument cost, small physical footprint, USB-powered operation, and capacity for real-time sequencing.[9] However, implementation still requires reliable sample preparation workflows, consumables, trained personnel, bioinformatics capacity, and quality assurance systems. [9]

Many African countries experience a high burden of infectious diseases, including malaria, tuberculosis, viral haemorrhagic fevers, emerging zoonotic infections, and antimicrobial-resistant bacterial pathogens.[3,4] These threats increase the need for timely, locally generated genomic data to support surveillance, outbreak response, and public health decision-making.[11] Historically, genomic analyses of African pathogens were often performed outside the continent, resulting in delayed data generation and limited local ownership of genomic information.[10]These challenges emphasise the need for accessible, decentralised sequencing platforms capable of operating in resource-constrained environments. [10]

Because pathogen genomes vary widely in size and complexity, sequencing platforms differ in their suitability for pathogen detection, genome assembly, and resistance characterisation.[3] Nanopore sequencing does not rely on sequencing by synthesis and can generate long reads, often reaching tens of kilobases depending on sample quality, library preparation, and run conditions. Sequencing single molecules bypasses the need for PCR amplification and its associated biases, which can be advantageous for applications such as structural variant detection and resolution of repeat-rich regions. [6]

Although MinION sequencing has been applied in several African settings, there remains a need for a focused synthesis of its technical principles, implementation patterns, public health applications, challenges, and prospects across the continent.

Accordingly, this narrative review aimed to synthesise available literature on Oxford Nanopore MinION sequencing in Africa and to summarise the principles of the technology. Other aims of the review include examining the adoption of Oxford Nanopore MinION sequencing and its applications in infectious disease surveillance, outbreak investigation, antimicrobial resistance monitoring, and One Health research, and discussing implementation challenges and prospects for strengthening genomic surveillance and public health preparedness.

Methods

Review Design

The current study is a narrative review, which uses a structured literature search and thematic synthesis of published literature and institutional reports related to the application of Oxford Nanopore Technologies (ONT) MinION sequencing in Africa.

Information Sources and Search Strategy

Relevant sources were identified via searches of the bibliographic databases PubMed and Web of Science, the scholarly search engine Google Scholar, and reports from the World Health Organisation (WHO) and Africa Centres for Disease Control and Prevention (Africa CDC). Relevant literature published in English between January 2014 and March 2025 was included. This period was selected because portable nanopore sequencing technologies, particularly the MinION platform, became increasingly available and adopted for applied genomic surveillance during this time.

The following search terms were used in combination with Boolean operators: "Oxford Nanopore," "MinION," "nanopore sequencing," “portable sequencing,” “genomic surveillance,” "pathogen genomics," "infectious disease," "outbreak," "antimicrobial resistance," "AMR," "One Health," "Africa," and "sub-Saharan Africa". The names of individual African countries were used where relevant.

The search strategy used in PubMed was:

("Oxford Nanopore" OR MinION OR "nanopore sequencing" OR "portable sequencing") AND (Africa OR "sub-Saharan Africa" OR names of individual African countries) AND ("genomic surveillance" OR "infectious disease" OR outbreak OR "antimicrobial resistance" OR AMR OR "One Health").

Additional relevant publications were identified via backward citations through manual screening of the reference lists of the selected articles and reports.

Inclusion criteria:

Sources which described either the application, evaluation, implementation, or public health use of Oxford Nanopore MinION sequencing;

Sources which focused on African settings or provided essential technical background with transferable relevance to Africa;

Sources which addressed either infectious disease surveillance, outbreak investigation, antimicrobial resistance monitoring, or One Health investigations.

Exclusion criteria:

Sources which did not discuss Oxford Nanopore or MinION sequencing, were unrelated to infectious disease or public health applications, or focused exclusively on non-African settings without transferable technical relevance were excluded. Other sources excluded include those which lacked sufficient methodological or contextual detail, duplicates, and non-English publications (as translation resources were not available). Preprints were excluded unless they provided unique data not available in peer-reviewed form.

Study Selection and Data Extraction

Titles and abstracts were screened for relevance to the review objectives. Full-text articles were then assessed to determine whether they described technical principles, implementation experience, or applications of MinION sequencing relevant to African infectious disease surveillance, antimicrobial resistance monitoring, outbreak response, or One Health. Key information was extracted narratively, including country or region, pathogen or disease area, sequencing application, reported benefits, implementation challenges, and public health relevance. Screening and synthesis were conducted by the lead author.

The information extracted included publication year, country or region, and pathogen or disease focus. Others are the type of MinION application, setting of use, reported advantages, implementation barriers, bioinformatics requirements, quality assurance issues, and relevance to public health decision-making.

Data Synthesis

The findings were synthesised narratively and organised thematically. The themes include the principles of MinION sequencing, adoption of nanopore sequencing in Africa, infectious disease surveillance and outbreak response. Others are antimicrobial resistance monitoring, One Health applications, implementation challenges, and prospects for genomic surveillance on the continent.

Literature Selection Process

A flow diagram was used to summarise the literature identification, screening, eligibility assessment, and inclusion process (Figure 1).

PRISMA flow diagram

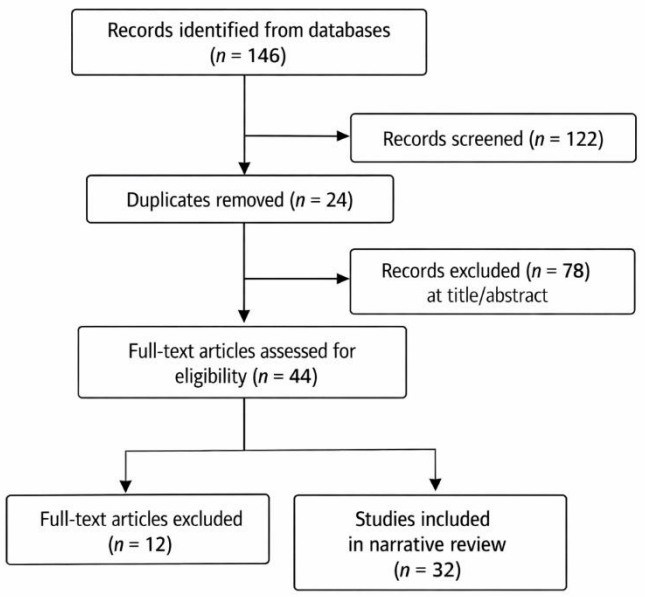

Figure 1: PRISMA flow diagram illustrating the literature search strategy and study selection process used in this review

Narrative Synthesis

Genetics and genomic principles

Genomic analysis allows identification of pathogens, as well as characterisation of the patterns of transmission, evolution, and genetic determinants of antimicrobial resistance. [8] For infectious disease surveillance, whole-genome sequencing can provide higher-resolution information than conventional diagnostic methods, particularly during outbreaks and for monitoring emerging variants.[3,4]

Principles of Oxford nanopore MinION sequencing

Nanopore sequencing works on the principle that nucleic acid molecules passing through biological nanopores embedded within an electrically resistant membrane generate characteristic disruptions in ionic current, producing electrical signals that can be measured and interpreted [14]

Nanopore sequencing measures changes in ionic current as DNA or RNA molecules pass through protein nanopores embedded in a membrane. Multiple nanopores are fixed within the membrane, while electrodes positioned on either side generate a stable electric field that drives nucleic acid molecules through the nanopores.[16] Motor proteins regulate strand translocation and possess helicase activity that unwinds double-stranded DNA into single-stranded molecules before passage through the nanopore. As nucleotides traverse the nanopore, they produce characteristic disruptions in ionic current. These signal patterns are detected and converted into nucleotide sequence data through computational basecalling algorithms.[14,16] [Figures 2 and 3]

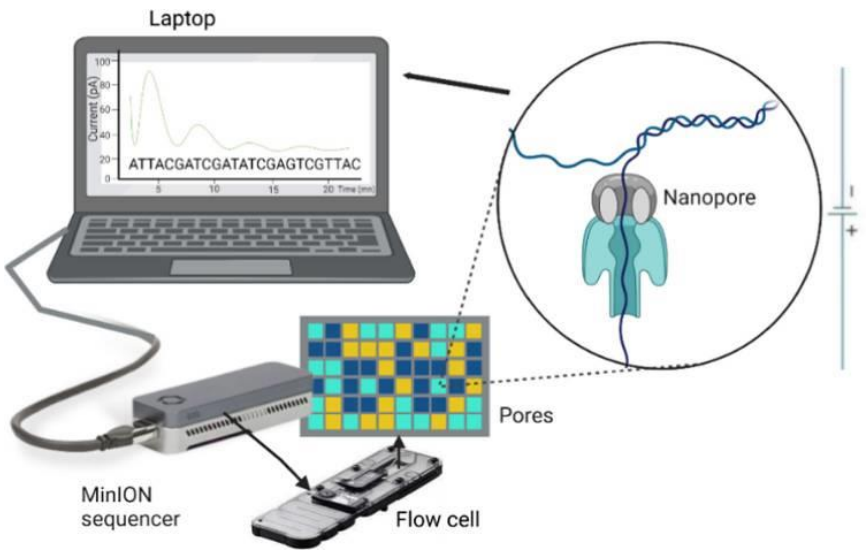

Figure 2. Schematic diagram indicating the composition of the MinION device, flow cell, nanopore, real-time computer access, and process management. Green is active, blue is inactive, and yellow is recovery pores on the Nanopore membrane. The figure was designed using BioRender [14].

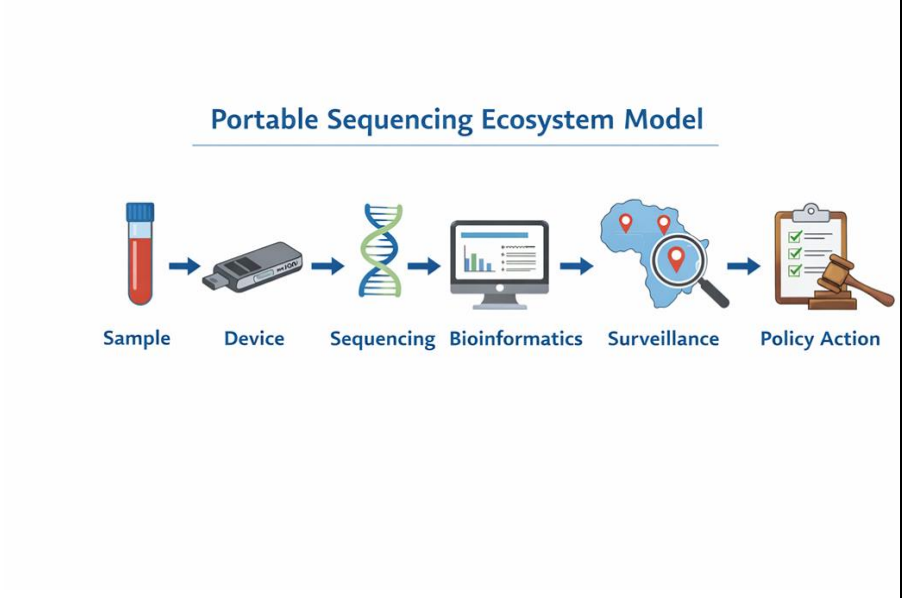

Figure 3: Portable Sequencing Ecosystem Model illustrating the pathway from device deployment to policy action. Source: Author's conceptual framework [2026].

The Oxford Nanopore MinION sequencing platform offers several distinctive features, including long-read sequencing, real-time data acquisition, and portability [9]. Long reads facilitate de novo genome assembly, resolution of repetitive genomic regions, and detection of structural variants. [9] Earlier MinION chemistries were associated with higher raw-read error rates than short-read sequencing platforms; however, advances in pore chemistry, flow-cell design, duplex sequencing approaches, and basecalling algorithms have substantially improved sequencing accuracy. [15]For many public health applications, consensus sequencing and adequate genome coverage can effectively mitigate raw-read errors. However, applications requiring high-confidence single-nucleotide variant detection still require careful validation. The platform has been successfully used in investigations of bacterial outbreaks and other public health emergencies.[15]

The real-time sequencing capability of the Oxford Nanopore platform enables rapid data analysis, thereby supporting timely public health decision-making during outbreaks [14,17]

MinION devices operate through a direct connection to a laptop computer [Figure 2] and can be deployed in field laboratories, mobile units, and other resource-limited settings.[9]Advances in sequencing chemistry, flow-cell design, and basecalling accuracy have progressively improved data quality, making MinION increasingly competitive with conventional sequencing platforms while maintaining its unique advantages in portability and rapid deployment. [9]

Rationale for adoption in African public health systems

The introduction of genomic technologies into many African clinical and public health settings has historically been constrained by infrastructural, logistical, and financial challenges, despite the growing need for genomic surveillance and pathogen characterisation across the continent.[14] In disease epidemiology, locally generated sequencing data provide opportunities for real-time surveillance, monitoring of emerging pathogens, tracking of circulating strains, and detection of drug resistance during outbreaks. [14]

In resource-limited African settings, characterised by delayed referral of samples, rapid local sequencing may be particularly valuable in enabling timely outbreak response and public health decision-making.[14] Furthermore, sequencing technologies must be affordable, accessible, and adaptable to local contexts to achieve sustainable implementation.[14]

Conventional next-generation sequencing (NGS) platforms have several limitations relevant to resource-limited African settings. For example, the platforms often require centralised laboratory infrastructure, stable power supplies, climate-controlled environments, and substantial capital investment. [3] Also, access to high-throughput sequencing facilities remains uneven across many African countries because of geographical disparities and slow referral systems, resulting in prolonged turnaround times for pathogen characterisation and outbreak investigations.[4]These limitations are particularly important in a region that experiences a high burden of infectious diseases and recurrent outbreaks requiring rapid genomic responses. [17–19]

The Oxford Nanopore Technologies MinION sequencing platform possesses technical and operational characteristics that address several of these challenges. As a compact USB-powered device, the MinION can operate using a standard laptop computer, thereby reducing the need for specialised infrastructure. [9] Its small physical footprint and minimal power requirements allow deployment in regional hospitals, field laboratories, and outbreak settings. [14] This portability represents a major departure from conventional centralised sequencing paradigms and aligns well with the decentralised diagnostic and surveillance needs of many African health systems [9].

MinION sequencing has proven particularly valuable during infectious disease outbreaks, where timely genomic information can inform public health decision-making, guide containment strategies, and support molecular epidemiology, a notable demonstration occurred during the West African Ebola virus disease outbreak, where MinION sequencing was successfully deployed in field settings to generate near-real-time genomic data, demonstrating the feasibility of decentralized sequencing in resource-limited environments this experience provided an important proof of concept for the use of portable sequencing technologies in African outbreak response.[3,4]

Furthermore, practical applications of MinION sequencing across the continent have reinforced its relevance for public health genomics; the platform has been extensively used for SARS-CoV-2 genomic surveillance in many African countries, enabling local generation of viral genome data and contributing to regional and global variant-tracking efforts.[4,11] MinION sequencing has also been applied to pathogens such as Mycobacterium tuberculosis, Lassa virus, arboviruses including yellow fever virus, mpox virus, and Vibrio cholerae, supporting outbreak investigation, genomic surveillance, and pathogen characterisation.[4,]

These studies collectively demonstrate that MinION technology can function effectively within African laboratory systems when supported by appropriate infrastructure, training, and bioinformatics capacity.[16,22] The ability to perform sequencing locally reduces dependence on overseas laboratories, minimises delays associated with sample export, and promotes locally generated genomic data.[16,22]This decentralisation is particularly relevant in the African context, where ethical, legal, and logistical challenges associated with cross-border sample shipment may hinder timely genomic investigations.[16,22]

Regional and international investments in genomic surveillance have supported training programmes, laboratory networking, and bioinformatics capacity development across several African settings, contributing to workforce development and strengthening local expertise in genomics and bioinformatics.[23]

Although MinION can support rapid local sequencing and decentralised genomic surveillance, its public health value depends on sample quality, validated protocols, trained personnel, sustainable financing, data interpretation capacity, and integration with broader epidemiological response systems.[9,10,24]

Incorporating MinION technology into national and regional surveillance systems aligns with global health priorities that emphasise early outbreak detection, rapid response, and equitable access to genomic technologies.[26]

MinION sequencing has been applied across Africa for real-time Ebola virus lineage tracking in Guinea, continental SARS-CoV-2 variant surveillance through Africa CDC, Lassa fever metagenomics in Nigeria, mpox genome completion in the Central African Republic, T12 Vibrio cholerae O1 tracking in West Africa, and same-day drug-resistance profiling of Mycobacterium tuberculosis in Zambia.[17,27] These applications, alongside One Health AMR characterisation in Nigerian livestock, align with the Africa CDC Pathogen Genomic Surveillance Policy Framework and WHO's 2022 global genomic surveillance strategy endorsing portable sequencing for outbreak response.[28] [Table 1]

Table 1: Selected Applications of MinION Technology in Africa

Application Area	Country Example	Impact	Public Health Relevance
Ebola outbreak sequencing	West Africa	Rapid lineage tracking	Real-time outbreak response
SARS-CoV-2 surveillance	Nigeria, South Africa	Variant detection	Pandemic monitoring
AMR gene detection	Kenya, Nigeria	Identification of resistance determinants	Stewardship programs
TB genomic surveillance	South Africa	Drug resistance profiling	National TB control
Zoonotic pathogen surveillance	Uganda	One Health integration	Emerging disease prevention

Applications in routine infectious disease surveillance

A major early demonstration of MinION technology in Africa occurred during the 2014–2016 Ebola virus disease outbreak in West Africa.[26]Mobile sequencing laboratories equipped with MinION devices were deployed in Guinea and Sierra Leone, enabling real-time sequencing of Ebola virus genomes.[28] These efforts provided significant insights into viral transmission chains and outbreak dynamics.[27,28]

Furthermore, MinION sequencing has been used in Africa for genomic investigations of Lassa fever in Nigeria, surveillance of arboviruses including yellow fever virus, mpox virus investigations in the Central African Republic, and other viral haemorrhagic fevers.[4,26]

The COVID-19 pandemic marked a significant milestone in the expansion of genomic sequencing capacity across Africa by stimulating widespread adoption of genomic technologies, development of policy frameworks, and establishment of national and regional genomic surveillance systems [28,29]. MinION sequencing supported the detection and monitoring of SARS-CoV-2 variants of concern and contributed to public health interventions across multiple countries. [5]

Tuberculosis remains a major public health challenge in Africa, particularly because of the emergence of drug-resistant strains [28]. This has driven the application of MinION sequencing technology for whole-genome sequencing of Mycobacterium tuberculosis, enabling drug-resistance profiling and transmission analysis [30].

Across the African literature, MinION use appears most established in outbreak response and viral genomic surveillance, particularly for Ebola virus disease, SARS-CoV-2, Lassa fever, and other viral pathogens. [17,22,28] Applications in bacterial genomics, tuberculosis drug-resistance profiling, antimicrobial resistance surveillance, and One Health investigations are increasingly reported but remain less consistently implemented across the continent.[28–31]Current evidence suggests that MinION is most effective when integrated within trained laboratory networks, reliable sample-processing workflows, and bioinformatics support systems rather than being deployed as a stand-alone technology. [9,10]

The generation of locally generated genomic data has contributed substantially to global surveillance efforts and underscored the importance of decentralised sequencing capacity.–[17,28] The ability to generate genomic information directly within outbreak settings has strengthened epidemic preparedness and response capabilities across the continent.[17,26]

Antimicrobial resistance applications

MinION sequencing has considerable potential for antimicrobial resistance (AMR) surveillance because long-read sequencing can resolve plasmids, resistance gene contexts, and mobile genetic elements that are often difficult to reconstruct using short-read sequencing technologies.[8] The technology enables the identification and characterisation of antimicrobial resistance genes from clinical, veterinary, food, and environmental samples, supporting genomic epidemiological investigations of multidrug-resistant pathogens.[31]

In African settings, MinION sequencing may contribute to surveillance of healthcare-associated outbreaks caused by multidrug-resistant organisms and facilitate investigation of resistance transmission pathways across human, animal, and environmental reservoirs within a One Health framework. [31]The long-read capability of MinION provides advantages for linking resistance genes to their bacterial hosts and characterising the genomic architecture of plasmids and other mobile genetic elements that drive the dissemination of antimicrobial resistance.[29,34,35]

However, genotype-based prediction of antimicrobial resistance should be interpreted with caution. Expression of the resistance genes may be influenced by gene regulation, genomic context, sequencing depth, database completeness, and bioinformatics pipeline selection. [32] Therefore, the presence of resistance genes does not always correlate with phenotypic resistance. Accordingly, genomic findings should ideally be interpreted alongside phenotypic antimicrobial susceptibility testing, epidemiological investigations, and validated analytical workflows to ensure accurate public health and clinical decision-making.[31,32]

One health and environmental applications

MinION sequencing is important in supporting integrated surveillance at the human-animal-environment interface. Potential applications in One Health contexts include genomic characterisation of zoonotic pathogens, detection and monitoring of antimicrobial resistance genes in animal and environmental reservoirs. Others are wastewater-based surveillance and field-adapted metagenomic investigations.[31,32]

The MinION platform is quite portable, a feature which allows its deployment in remote locations where laboratory infrastructure may be limited. This facilitates real-time genomic investigations during zoonotic disease outbreaks and environmental surveillance activities[9,32] [14,31]. These capabilities may also support monitoring of livestock-associated pathogens, wildlife reservoirs, foodborne pathogens, and environmental microbial communities that contribute to disease emergence and transmission[29,30]

In African settings, wastewater surveillance and environmental metagenomics are emerging applications with potential utility for

early outbreak detection, monitoring pathogen circulation, and tracking antimicrobial resistance determinants in communities.[18,29–31] However, standardised sampling strategies, contamination control measures, and validated bioinformatics pipelines are needed for successful implementation of the MinION technology. Other requirements include quality assurance systems and effective data-sharing frameworks involving public health, veterinary, agricultural, and environmental sectors.[31,32]

Implementation challenges

Several operational challenges exist to the widespread implementation of MinION technology in African settings. Top on the list is power instability, a significant concern in many resource-limited environments, which may affect sequencing runs, reagent storage conditions, and data processing activities.[14] Earlier nanopore sequencing chemistries were associated with higher raw-read error rates than short-read sequencing platforms; however, substantial improvements in sequencing chemistry, flow-cell design, duplex sequencing approaches, and basecalling algorithms have significantly improved accuracy. [14] Nevertheless, applications requiring ultra-high analytical precision, such as single-nucleotide variant detection in complex genomes, may require additional validation.[14]

Additional challenges include limited bioinformatics expertise, inadequate computational infrastructure, internet connectivity constraints, data storage requirements, and recurring costs associated with consumables and reagent procurement [9,10]. Furthermore, shipping reagents to some African settings may be complicated by cold-chain requirements, potentially affecting reagent performance and sequencing quality [5]. Quality assurance and standardisation across laboratories also remain critical considerations for ensuring reliable and reproducible genomic data. [14]

The major implementation challenges and potential mitigation strategies relevant to African settings are summarised in Table 2.

Table 2. Key Challenges and Potential Mitigation Strategies for MinION Implementation in African Settings

Challenge	Why it Matters	Potential Mitigation Strategies
Consumable costs	Flow cells and library preparation kits may limit routine implementation in underfunded laboratories.	Sustainable financing mechanisms, pooled procurement, regional sequencing hubs, negotiated pricing agreements.
Cold-chain logistics	Reagent degradation during transport may compromise sequencing performance	Local stock management systems, validated transportation procedures, temperature monitoring systems
Bioinformatics capacity	Data analysis requires specialised expertise and computing resources	Structured training programmes, regional bioinformatics support networks, development of user-friendly offline analysis tools
Power instability	Power interruptions can disrupt sequencing runs and data processing	UPS systems, solar backup systems, portable power stations, local data storage
Internet connectivity	Cloud-based analyses may be difficult in remote settings	Offline basecalling tools, local computational infrastructure, hybrid analysis workflows
Data storage and computing resources	Large sequencing datasets require adequate storage and processing capacity	Institutional servers, cloud-storage partnerships, regional data centres
Quality assurance	Reliable results are essential for surveillance and public health action	Standard operating procedures, external quality assessment schemes, proficiency testing programmes
Supply-chain disruptions	Delays in obtaining reagents and consumables can interrupt surveillance activities.	Regional procurement networks, local distributors, inventory management systems
Workforce limitations	Skilled personnel remain insufficient in some settings	Continuous professional development, mentorship programmes, incorporation of genomics into training curricula
Sequencing accuracy considerations	Some applications require very high analytical precision	Improved chemistries, consensus sequencing, validation against established laboratory methods

Capacity building and sustainability

The MicroGEM PDQeX (Pretty Darn Quick Extraction) technology developed by MicroGEM, which enables DNA extraction and purification within a single closed-tube system, may provide practical advantages in settings where conventional molecular laboratory infrastructure is limited [14]. Development of offline MinION whole-genome sequencing analysis tools could further improve accessibility in remote settings with limited internet connectivity and unreliable power supplies.[27,34,35]

Training remains a critical requirement for successful implementation of nanopore sequencing programmes; structured training modules incorporating DNA/RNA extraction, library

preparation, sequencing workflows, bioinformatics analysis, software tutorials, and hands-on practical exercises can strengthen local capacity and facilitate sustainable adoption of the technology in African settings. [14]

Sustainable implementation of MinION technology requires long-term investment in workforce development, laboratory infrastructure, institutional support, and government commitment. Regional sequencing hubs, mentorship programmes, collaborative networks, and integration into national surveillance frameworks will be essential to maximise the long-term public health impact of genomic sequencing technologies in Africa. [14]

Future prospects

Future applications of MinION technology in Africa include expanded integration into public health surveillance systems, wastewater-based epidemiology, antimicrobial resistance monitoring, outbreak preparedness, and pandemic response activities. Continued advances in sequencing chemistry, flow-cell technology, analytical software, and bioinformatics pipelines are expected to further improve sequencing accuracy, accessibility, and usability. As genomic capacity continues to expand across the continent, MinION sequencing may play an increasingly important complementary role in strengthening infectious disease surveillance, outbreak response, antimicrobial resistance monitoring, and One Health initiatives in African settings.

Recent efforts to scale antimicrobial resistance (AMR) genomic surveillance in Africa under a One Health approach have leveraged Nanopore Technologies' MinION platform for its low start-up cost, portability, and minimal infrastructural demand.[19]

Limitations of the review approach

No formal quality or risk-of-bias assessment of the included studies was used in the current review. Also, Google Scholar screening was restricted to the first 200 hits, which may have omitted some relevant sources.

Conclusion

Portable nanopore sequencing has expanded opportunities for decentralised genomic surveillance and infectious disease research across Africa by enabling portable, real-time sequencing in resource-limited settings. However, its long-term public health value will depend on sustained investment in workforce development, laboratory infrastructure, supply chains, bioinformatics capacity, quality assurance, and integration into national and regional surveillance systems. When strategically utilised, MinION technology provides a scalable and resilient model for strengthening genomic sovereignty, including local data generation, analysis, interpretation, and use for public health decision-making—and pandemic preparedness. Future efforts should prioritise validated workflows, sustainable financing, regional training networks, and mechanisms for translating sequencing data into timely public health action.

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