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Harnessing Genomics for One Health: A Blueprint for Equity, Access, and Action

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ABSTRACT: Recent epidemics of new infectious illnesses emphasize the importance of real-time genomics. The causative microorganisms' augmented growth rates, potent ability to spread, propensity for medication resistance, and diagnosis turnaround times of hours are important. The discovery of viruses during pandemics has greatly influenced the implementation of genome sequencing and molecular epidemiology in public health. By meticulously describing the genetic deterioration of species that plunge into an extinction vortex, real-time genomic tools evaluate the effects of environmental change on ecosystem composition and functioning, potentially resolving negative consequences. Omics methodologies are utilized for diagnosing infectious illnesses, novel computational algorithms for evaluating biomarkers, and unique systems for integrating omics and electronic medical record data for the clinical treatment of developing infectious diseases. Species identification, the creation of genetic data for cryptic and endangered species, quick census reporting, hybridization zone monitoring, and invasive species detection are all accomplished by nanopore sequencing. Traditional genetic approaches, like the sequencing of particular genetic markers or mitochondrial DNA, have turned into standard tools in animal forensics. Portable sequencing methods provide long reads to improve taxonomic precision and accuracy for establishing the provenance of a seized material. The genomic analysis aids in monitoring and maintaining the biodiversity of the environment through local research and education.

KEYWORDS: Long reads, Nanopore Sequencing, Omics Method, Portable Sequencing, Real-time Genomics.

I. INTRODUCTION

In recent years, the interconnections between human health, animal welfare, and environmental sustainability have become increasingly apparent, giving rise to the need for integrated approaches to global health challenges. Recent global health events have highlighted the importance of rapid genomic analysis.

A. *Pathogen identification and surveillance*

The presence of viruses in sewage and wastewater, in addition to presumably frozen food that is packaged, constitutes substantial pools of infectious agents and raises a risk for contracting illness due to the emergence of more transmissible viral variations [1]. Phylodynamic analysis from comprehensive sequencing efforts during the Ebola epidemic between 2013 and 2016 demonstrated that the outbreak was sustained by spread from person to person rather than by repeated zoonotic introduction. Genome sequencing played a key role in identifying the first case [2].

B. *Outbreak investigation and response*

As SARS-CoV-2 continues to gain genetic mutations, faster identification of genome sequences in the present pandemic has been vital for tracking and confirming the expected sensitivity of multiple diagnostic procedures, even within a locality [3].
To facilitate coordinated worldwide responses to cross-border risks from infectious illnesses and AMR, it is essential to harmonize genomic surveillance methodologies and nomenclature internationally and to allow prompt data sharing [4].

C. *Environment and wildlife impacts*

As the pandemic propagated, it became evident that a large number of other organisms, particularly mammals, were the disease's secondary targets [1].
Though the relationship between the spread of zoonotic diseases, the destruction of natural habitats, and the decline in biodiversity is still unclear [5] [6]. There is little doubt that anticipated environmental changes will put more strain on human and environmental health [6].

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D. *Technological advancement*

Several approaches to target amplification-free CRISPR/Cas-based detection have been developed to detect non-nucleic acid targets, offset sensitivity loss resulting from the lack of pre-amplification, and facilitate integration into portable devices [7].

It is crucial to achieve diagnosis turnaround times of hours rather than days or weeks because of the causative pathogens' exponential growth rates, high potential for transmission, and frequent incidences of medication resistance. This makes it impossible to ship samples to major international locations [6] [8].

The development of the genomic method presents possible answers to these problems. Many frontline techniques often ignore molecular biology, even though it may offer valuable solutions to environmental issues [9]. Regarding the future of our relationship with planetary health, society is currently at a crossroads, and the window of opportunity for action is quickly closing.

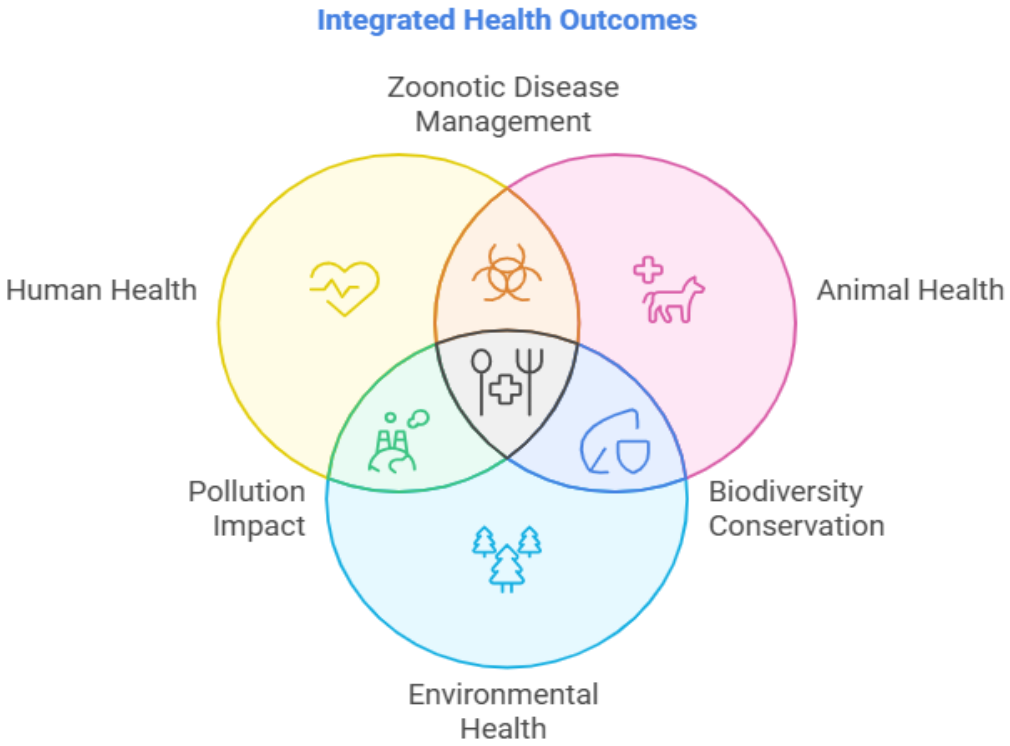

Fig1. A schematic diagram illustrating the "One Health" approach and the interconnections between human health, animal welfare, and environmental sustainability.

This research delves into the uses of real-time genomics within One Health, emphasizing its importance for monitoring infectious diseases, identifying pathogens, investigating outbreaks, and monitoring antimicrobial resistance.

II. REAL-TIME GENOMICS

Whole-genome sequencing (WGS) has become an essential instrument in viral epidemiology research, especially for investigating pathogen outbreaks, by utilizing next-generation sequencing (NGS) technology. When searching for tightly clustered infections caused by a specific pathogen in space and time that differ by less than 10 alleles using core genome multi-locus sequence typing (cgMLST) analysis or less than 10 single-nucleotide polymorphisms (SNPs), public health experts typically use WGS to identify outbreaks. [10]. In order to facilitate quick pathogen identification, antibiotic susceptibility testing, outbreak investigation, and surveillance, WGS can also be used on cultivated isolates of bacteria and fungus [11].

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A. *Real-Time Genomics in Infectious Disease Surveillance*

One of the most important uses of real-time genomics is in the field of infectious disease surveillance. It is possible to rapidly identify the pathogenic agent and determine its genetic characteristics by directly sequencing the genomes of pathogens from clinical samples. This information can be used to guide public health initiatives such as contact tracing, isolation, and the prescription of appropriate antimicrobial medications.

Foodborne pathogens frequently produce outbreaks across international borders, and as more laboratories include WGS into their regular surveillance, it could help raise awareness of these outbreaks [12]. Real-time genomics in infectious disease surveillance includes:

1) Rapid pathogen identification:

While traditional diagnostic approaches can take weeks or even months, genomic sequencing can provide a definite diagnosis of infections in a matter of hours or days. The development of genetic technology has led to a rise in the sophistication of infectious disease surveillance, providing new opportunities for tracking antibiotic resistance, quickly identifying pathogens, and investigating outbreaks..

The speed and precision of pathogen identification have been greatly increased by advances in genomic technologies. More accurate and expedient genomic approaches are supplementing, if not completely replacing, traditional methods that rely on biochemical assays and culture.

Pathogen identification in the context of food safety has been transformed by next-generation sequencing (NGS) technology. NGS enables risk assessment, functional prediction, and whole-genome construction for foodborne pathogens. When compared to conventional culture-based methods, this approach greatly shortens the time needed for pathogen detection [13]. The application of NGS in food safety shows off its capacity for quick and precise pathogen identification, enhancing the effectiveness and safety of diagnostic procedures.

Nanopore sequencing has proven to be successful in real-time wastewater surveillance, according to recent studies. High-precision identification of viral variations is made possible by nanopore sequencing, especially with the enhanced R10.4.1 version. For example, its use in tracking the prevalence of variants in SARS-CoV-2 has demonstrated its capacity to identify and monitor variants in real-time, even in the fragmented viral genomes that are typical of wastewater samples [14]. Rapid pathogen detection in environmental samples is improved by this method, which also detects novel mutations and issues early warning signals. This method improves the speed at which pathogens may be quickly identified in environmental samples by detecting new mutations and early warning signals.

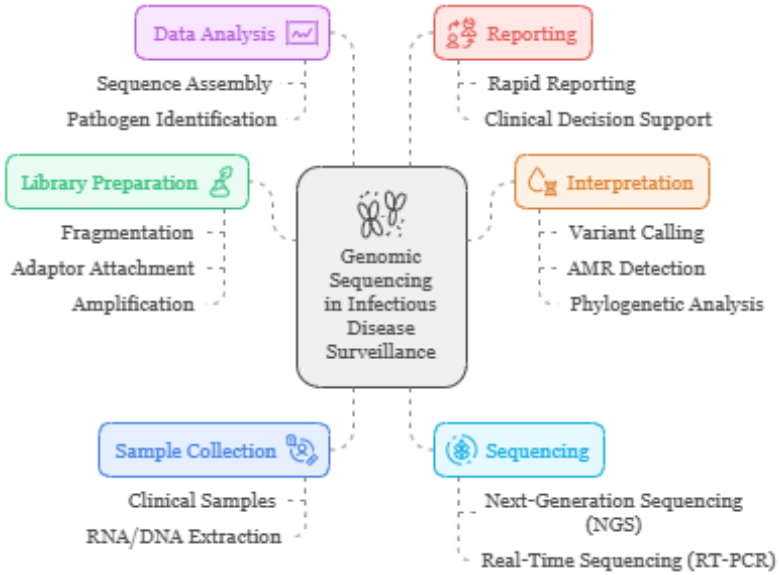

Fig2. Depicts how genomic data aids in tracking and investigating the spread of infectious diseases, linking cases to determine outbreaks and transmission pathways.

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2) Outbreak investigation:

Genomic technologies are vital in examining and comprehending the progression of infectious disease outbreaks by analyzing pathogens' genomes from various cases to pinpoint the outbreak's origin and monitor its transmission. By providing detailed genetic information, these tools help in tracking the spread and source of outbreaks, improving the efficacy of response measures.

DNA barcoding and metagenomic sequencing are two methods that metagenomics uses to quickly and accurately identify species in marine habitats. A large variety of marine creatures, including some that are difficult to identify using conventional approaches, can be identified using these methods, which also provide improved taxonomic precision [13]. Researchers can evaluate ecosystem health and biodiversity more accurately by incorporating these genetic techniques into marine monitoring programs.

When examining complicated outbreaks, like the multispecies plasmid-associated epidemic of NDM-5-producing Enterobacterales, whole-genome sequencing (WGS) has proven essential. The complicated nature of the outbreak was revealed by real-time WGS, which made it possible to identify plasmid transfer events and the dynamics of bacterial transmission throughout several hospital units [17]. Targeted intervention efforts are supported by the integration of genetic data with conventional infection control techniques, which improves our understanding of epidemic processes.

Cross-domain genomic data is important; a scoping review on the application of genomic epidemiology to zoonotic illnesses emphasizes this. Through the integration of genetic data from environmental, animal, and human sources, scientists are able to trace the spread of pathogens across many interfaces and pinpoint the main origins of infection [17]. This multi-domain method contributes to our understanding of how zoonotic illnesses propagate and guides the development of successful therapies.

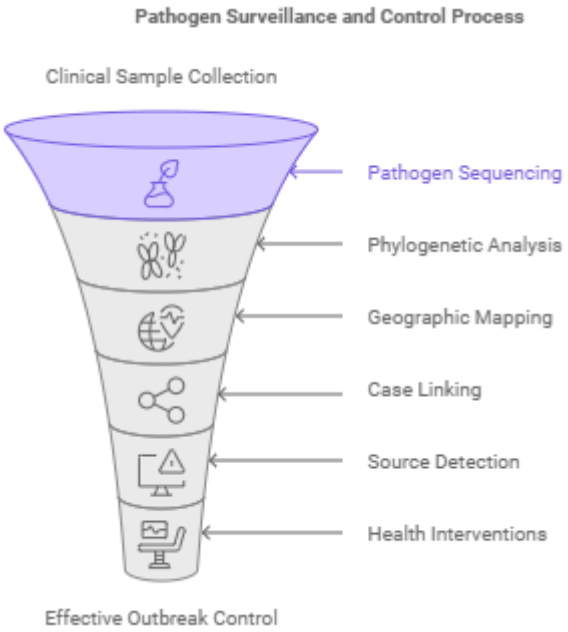

Fig3. A flowchart of the steps and processes involved in how genomic data aids in tracking and investigating the spread of infectious diseases

3) Antimicrobial resistance surveillance

Genomic sequencing can help track the rise and dissemination of antibiotic-resistant bacteria, allowing for the creation of specific measures to address this increasing health risk.

Surveillance of antimicrobial resistance (AMR) is critical for effective infection control and patient management. The integration of genomic technologies into AMR surveillance offers significant potential for real-time insights into resistance patterns and mechanisms.

The integration of genomic technologies into AMR surveillance in healthcare settings provides rapid and actionable information. This approach allows for near real-time monitoring of resistance patterns and informs infection prevention and control measures [18]. However, challenges such as cost, bioinformatics training, and the need for viable use cases must be addressed.

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Recommendations include defining cost-effective applications of genomic AMR surveillance and building capacity through regional hub-and-spoke models.

Table 1. A comparative table highlighting the advantages of WGS/NGS over traditional methods in various applications of outbreak investigation.

Application	Traditional Methods	WGS/NGS Advantage	Impact on Outbreak Investigation
Pathogen Identification	PCR, Culture methods	Complete genomic profile	Rapid and accurate strain identification
Mutation Detection	Target-specific PCR	Genome-wide mutation scanning	Early detection of emerging variants
Transmission Tracking	Epidemiological surveys	High-resolution genomic fingerprinting	Precise transmission chain mapping
Drug Resistance	Phenotypic testing	Genetic resistance marker detection	Rapid resistance profiling
Viral Evolution	Limited gene sequencing	Complete evolutionary analysis	Better prediction of outbreak patterns

The application of genomic technologies in infectious disease surveillance has transformed rapid pathogen identification, outbreak investigation, and antimicrobial resistance surveillance. By leveraging these advanced tools, researchers and healthcare professionals can achieve more accurate, timely, and actionable insights, ultimately enhancing public health responses and safety. Addressing associated challenges will be crucial for maximizing the benefits of these technologies in combating infectious diseases.

III. METAGENOMICS

Metagenomics is revolutionizing the field of ecosystem monitoring by providing powerful tools for species identification, population genetics, habitat connectivity, and conservation planning. By leveraging advances in genomic technologies, researchers can gain deeper insights into ecosystem dynamics and improve conservation strategies. Here's how metagenomics is applied across these critical areas.

A. *Metagenomics for Ecosystem Monitoring*

1) Species identification:

By examining environmental DNA (eDNA) that has been obtained from a variety of substrates, including soil, water, and sediments, metagenomics helps with species identification. Species that are uncommon or challenging to sample using conventional techniques can be found and identified with this method.

Non-invasive genetic approaches have been used in recent research to monitor severely endangered species such as Strigophus habroptilus, or kākāpō. Metagenomics is an efficient tool for identifying species distribution without direct observation, as demonstrated by the successful identification of individual kākāpō from soil samples by researchers utilizing environmental presence/absence analyses to more intricate evaluations of genetic diversity and fitness. This approach has the potential to expand the uses of eDNA. DNA metabarcoding and nanopore sequencing [19] from straightforward species

DNA barcoding and metagenomic sequencing are two methods that metagenomics uses to quickly and accurately identify species in marine habitats. A large variety of marine creatures, including some that are difficult to identify using conventional approaches, can be identified using these methods, which also provide improved taxonomic precision [20]. Researchers can evaluate ecosystem

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health and biodiversity more accurately by incorporating these genetic techniques into marine monitoring programs.Population Genetics.

The genetic diversity and population structure of organisms within an environment can be understood through the study of metagenomics. To comprehend population dynamics, genetic health, and the effects of environmental changes, one must have access to this information.

There have been suggestions for using genomic applications to improve our knowledge of population genetics in different species. We get knowledge on population structure and resilience through the examination of genetic relatedness, adaptive variants, and coevolutionary processes among microbes and hosts. [21]. Assessing genetic diversity and locating putative adaptation responses to environmental stresses are made easier with the aid of these genomic techniques.

Microbial diversity and functional potential in different habitats can be evaluated using metagenomic techniques, such as high-throughput sequencing. The genetic composition of microbial communities, including those engaged in crucial ecological processes like pollution degradation and nutrient cycling, can be better understood with the use of this technique [22]. The genetic foundations of ecological interactions and community dynamics can be better understood by researchers by analyzing microbial populations and their functional genes.

2) Habitat Connectivity:

Maintaining biological processes and species movement requires habitat connection. Understanding the distribution of genetic diversity throughout interconnected habitats and the potential effects of connectivity disruptions on ecosystem health is possible through the study of metagenomics.

The study of gene flow and habitat connectivity involves the application of genomic tools. Researchers can evaluate how topographical characteristics and human activity affect genetic exchange and population structure by examining genomic variation among various groups [21]. Having this knowledge is essential for creating conservation plans that preserve or improve habitat connectivity.

Metagenomic techniques are useful for tracking the genetic diversity and connectivity of marine populations in marine ecosystems. The spatial distribution of genetic diversity and connection patterns in marine environments can be understood through the use of techniques like metagenomic sequencing and SNP-based approaches [20]. This data supports the management of marine protected areas and the development of strategies to enhance habitat connectivity.

3) Conservation Planning:

Effective conservation planning requires a comprehensive understanding of species diversity, genetic health, and ecological interactions. Metagenomics offers valuable tools for informing conservation strategies and decision-making.

Metagenomics can guide conservation planning by providing detailed genetic information on species and ecosystems. For example, genomics can inform the selection of conservation areas, population supplementation, and restoration efforts based on genetic diversity and adaptive potential [21]. This approach helps in prioritizing conservation actions and optimizing resource allocation.

The use of real-time genomic techniques, such as nanopore sequencing, enhances conservation efforts by providing up-to-date information on species distribution and genetic health. This dynamic monitoring allows for timely interventions and adaptive management strategies to address emerging threats [19].

IV. OMICS

A. *Omics Technologies in Infectious Disease Diagnosis*

1) Multi-Omics Integration:

Advancements in metabolomic, transcriptomic, genomic, and proteomic technologies now allow for comprehensive analysis of molecular changes in the host response with clinical samples. The merging of multiple omic datasets enables researchers to utilize systems biology methods, discover new disease pathophysiology, create innovative diagnostic and predictive models, and gain a more thorough understanding of disease mechanisms.[23]

2) Host Response Analysis:

Discover new disease pathophysiology, create innovative diagnostic and predictive models, and gain a more thorough understanding of disease mechanisms[24].

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B. *Application of Omics in Specific Infectious Diseases*

1) Sepsis:

For the diagnosis and treatment of sepsis, early etiological diagnosis and the description of the host's reaction to infection are essential. The development of commercially available quick diagnostic tools, improved bedside diagnosis of immunological dysfunction, identification of patient "signatures" associated with various clinical outcomes, and the possibility of customized medicines have all resulted from novel microbiological techniques and omics analysis [25].

2) Lyme Disease:

In Lyme disease, inflammation related to innate and acquired immunity is crucial for both defending the host and determining disease severity. Omics technologies have shown potential for developing disease biomarkers for early, disseminated, and post-treatment stages, improving early detection and diagnosis, elucidating underlying molecular pathways, and identifying molecular targets for therapy [26].

V. NANOPORE SEQUENCING

Compared to conventional sequencing techniques, nanopore sequencing technology offers significant advantages, making it a potent tool for microbial genomics. Long reads, which are produced by nanopore sequencing as opposed to short-read sequencing technologies, are very helpful for de novo assembly of complicated genomes, finding structural variations, and analyzing repetitive sections. Furthermore, nanopore sequencing is suitable for real-time disease identification and surveillance because it is highly portable and useful in field situations.

Nanopore sequencing has been extensively used in many microbiological domains recently, including aetagenomics, surveillance of antibiotic resistance [27], and pathogen identification. With the use of this technology, public health interventions might be informed, and our understanding of microbial diversity and function could be completely transformed.

By sensing the breakdown of their internal ionic current, nanopores are tiny, purposefully modified protein pores that allow nucleotide sequencing. These holes allow strands of DNA and RNA to pass through as "squiggle" signals. This squiggle signal can be quickly incorporated into genomic data using specialized algorithms, such as effective neural networks, because certain nucleotide pairs produce recognizable pauses of the ionic current. [28]. Because of this, the squiggle signal model is free and can contain any atomic-level chemical characteristics of DNA and RNA strands, including epigenomic alterations. With powerful, parallelizable processors like graphics processing units (GPUs), this basecalling can happen fast, at the speed of sequencing itself. As a result, genetic information can be produced and evaluated right at the. DNA and RNA strands flow through these pores as "squiggle" signals. Because specific nucleotide pairings result in recognisable pauses of the ionic current, this squiggle signal can be rapidly base-called into genomic data using specialized algorithms such as efficient neural networks. [28]. This makes the squiggle signal model-free and able to incorporate any chemical features of DNA and RNA strands down to the atomic level, such as epigenomic modifications.. This basecalling can occur quickly, at the pace of sequencing itself, when combined with strong, parallelizable computers like graphics processing units (GPUs). Because of this, genetic data can be generated and assessed immediately at the point of care, for example, in a clinical or research setting [29] [30]. Its capacity to produce lengthy, uninterrupted reads has important ramifications for the preservation of biodiversity.

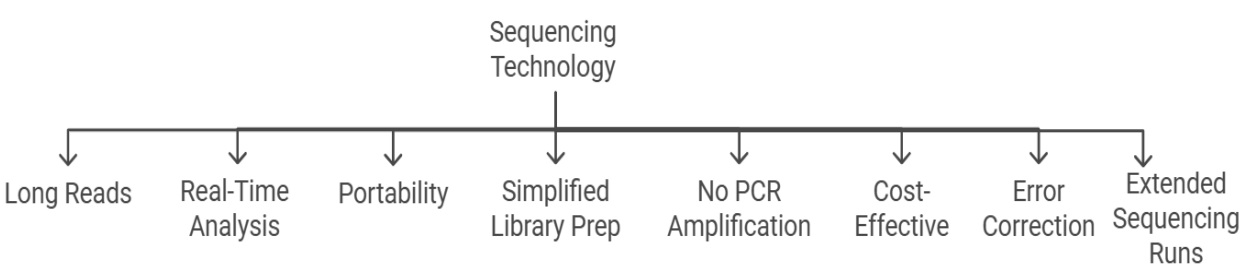

Fig4. A flowchart highlighting the key features and advantages of nanopore sequencing technology

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A. *Nanopore Sequencing in Biodiversity Conservation*

1) Species Identification and Taxonomy:

Examining novel disease development mechanisms and the regulation of gene expression by epigenetic changes to genomic material is an intriguing subject [31] [32]. For instance, the well-studied mechanism of transcriptional silence by methylation of DNA has historically made sequencing methylated areas difficult due to the temporary the type of methylation and the highly methylated areas' low sequence complexity [33]. Nanopore equipment has been effective in conducting methylation investigations. Davenport et al. used standardized nanopore sequencing kits with the older R9.5 chemistry to find probable tumor suppressor genes that may be epigenetically silenced in hepatocellular carcinomas in order to uncover the hypermethylation of cytosines [34]. In good concordance with conventional bisulfite conversion, nanopore detection of genome-wide 5meC identified 482 methylated genes that short-read sequencing platforms had overlooked. By merging hierarchical Dirichlet processes with hidden Markov models, further techniques have been devised to enhance the identification of methylated residues from the ionic current signal data of ONT nanopore sequencers. [35] [27]. Portable nanopore sequencers enable species identification in the field, facilitating real-time biodiversity surveys and monitoring.

2) Population Genetics and Phylogeography:

a) *Genetic Diversity*

Since several loci contribute to genetic diversity, the majority of traits in humans, crops, and livestock are polygenic. The phenotype as a whole is influenced by a continuum of effects at these loci, from frequent low-effect variants to uncommon high-effect variants. It is possible to forecast phenotypes in novel individuals by using statistical techniques that have been developed to compute the impact of these loci. These techniques, known as polygenic risk scores, are used to quantify an individual's disease risk quantitatively in humans. In agriculture, they are used to choose superior individuals based on genomic breeding values. SNP array genotypes are commonly used in both domains for analysis.

b) *Phylogeography*

By analyzing genetic variation across geographic regions, nanopore sequencing can help reconstruct the evolutionary history of species and identify important refugia.

B. *Nanopores to Create a Real-Time Traceability and Monitoring System*

The short-read sequencing method used by the present foodborne pathogen detection network has drawbacks when it comes to real-time analysis.[36] . Nanopore real-time sequencing can enable quick identification of pollution sources and transmission routes. In surveillance and traceability systems, metagenomics is a crucial tool that offers fresh insights into foodborne microbial outbreaks, source attribution, and risk assessment. It can swiftly detect new or emerging microbes in the food supply chain and track genes linked to antibiotic resistance in foods with intricate genomic backgrounds. [37] Nonetheless, abiotic genetic material in high quantities within food can tamper with sequencing data. By locating SNPs and SVs, nanopore sequencing-based WGS can enhance metagenomics analysis[38]. For source attribution and phylogenetic analysis, real-time sequencing data can be employed.

An RNA transcript can be obtained by nanopore sequencing. When it comes to read length, managing complex microbiome and non-bacterial transcriptome backgrounds, and other relevant aspects, nanopore transcriptome sequencing offers benefits over traditional methods. One of the most potent benefits of nanopore sequencing technology is its direct RNA detection capability [39]. RNA must currently be reverse transcribed to cDNA during the library preparation phase of both first- and second-generation sequencing.

1) Portable nanopore sequencers enable species identification in the field, facilitating real-time biodiversity surveys and monitoring:

Nanopore sequencing yields sequencing data in hours, as Emily Rames and Joanne Macdonald
[40] showed. This technology can analyze enterovirus genes from clinical and environmental sources. The application of nanopore sequencing technology holds potential to improve the thorough investigation of various biological pathways and clarify the complexities associated with mRNA processing and modification in a variety of illnesses[41]. Sanger sequencing has drawbacks; it cannot analyze polluted or mixed DNA samples containing two or more donors, and it is limited to offering one read for each amplified PCR product (amplicon).
[42] This constraint may be addressed by newly developed HTS technologies like ONT's MinION, which provide economical

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data for forensic applications on a reasonable platform.[43] Because nanopore sequencing can be readily applied to sequence libraries made by PCR amplification of popular forensic DNA markers, it shows good sensitivity to the quantity and quality of input DNA, even at low input DNA concentrations. Although nanopore sequencing can produce very long-read sequences (up to 106 bases per read), it is helpful for short amplicon sequencing down to roughly 200 bases (the lowest read length required by the ONT platforms)[44]. Provided that the technological obstacles of sequence quality and data processing are surmountable, nanopore sequencing appears to have many potential applications in non-human forensic science. The most direct avenue for species identification in animal DNA forensics is by nanopore sequencing. The utilization of different gene sections [45] [46] and methods for performing sequence similarity searches [47] in conjunction with DNA sequencing for species identification has already been validated. Using the sequencing process and data gathering tools to produce Sanger sequence data (sample chromatograms) is comparable to going through several phases of analysis. Validation studies of these particular steps are not necessary, even though these steps must function properly to produce the result data. Moreover, the manufacturer's instructions are typically followed exactly, and in the rare cases when a user does interfere, it won't change the DNA sequences that were taken [43]. Researchers can concurrently find nucleotide sequences and related epigenetic modifications through the use of nanopore sequencing. Vasiljevic et al. [48] conducted the initial confirmation of the non-human forensic species identification using molecular genetic evidence from MinION sequencing. They examined the NGSpeciesID [49] software's newest version, which includes all necessary steps for generating reliable consensus sequences. Using nanopore data from six species, the study evaluated the effect of sequence data variance on the accuracy of species identification. When combined with the NGSpeciesID approach, the validation findings amply illustrated the reliability of nanopore data for species identification in forensic genetics. Results of validation amply supported the application of NGSpeciesID in forensic genetics by demonstrating how to employ the method in conjunction with nanopore data for reliable species identification.

In order to identify cryptic species quickly, accurately, and in a variety of ways, nanopore sequencing has become a very useful technique. Conservation efforts can be aided by nanopore sequencing, which can reveal hidden biodiversity by studying genetic differences between individuals. The availability of reference databases, computing resources, and ethical considerations are only a few of the issues that must be resolved for nanopore sequencing to be successfully applied in the identification of cryptic species. To fully utilize nanopore sequencing in this field, technological and data analysis tool developments must continue. Nanopore sequencing offers a promising new direction in our knowledge of and preservation of Earth's biodiversity. This technology can help save the natural heritage of our world by helping to discover cryptic species and developing conservation strategies.

VI. CONCLUSION

Real-time genomics is developing at a rapid pace, and this is becoming a key factor in managing infectious diseases and conserving biodiversity. We can improve our ability to diagnose and treat infections in real time by utilizing cutting-edge methods like nanopore sequencing and complete omics approaches. A greater understanding of pathogen transmission patterns and resistance mechanisms is made possible by the integration of genetic data into public health frameworks. This integration also makes it possible to apply targeted interventions that can slow the spread of infectious illnesses.

Furthermore, the use of genomic technology in environmental monitoring offers important new perspectives on how biodiversity is affected by habitat loss and climate change. Through the process of explaining genetic degeneration in threatened species, these techniques enable conservationists to come up with more practical plans for protecting ecosystems that are coming under more and more pressure from human activities. The relevance of genomics as a crucial instrument in preserving ecological integrity is further highlighted by the capacity to track invasive species and evaluate hybridization occurrences in real time.

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Table 2. Outlining the potential challenges and future directions in the integration of real-time genomics, metagenomics, and omics technologies for comprehensive One Health solutions

Integration Challenges and Future Directions in One Health Genomics

Category	Current Challenges	Future Directions	Expected Impact
Technical Infrastructure	• Real-time data processing bottlenecks • Limited computational resources in field settings • Data storage and management constraints • Integration of multiple data types	• Edge computing implementation • Cloud-based analysis platforms • Scalable storage solutions • Standardized data integration pipelines	• Faster outbreak detection • Improved field capabilities • Better data accessibility • Enhanced analysis accuracy
Data Generation & Quality	• Sample quality variability • Standardization across laboratories • Field sampling limitations • Cost of sequencing technologies	• Automated quality control • Universal protocols • Portable sequencing devices • Cost-effective methods	• Higher data quality • Better reproducibility • Increased coverage • Wider adoption
Analysis & Integration	• Complex multi-omic data analysis • Limited reference databases • Bioinformatics expertise gaps • Real-time analysis constraints	• Machine learning algorithms • Expanded reference databases • Automated analysis pipelines • Real-time analysis tools	• Better pattern detection • Improved accuracy • Faster results • Enhanced insights
Surveillance & Monitoring	• Geographic coverage gaps • Delayed detection systems • Limited cross-sector coordination • Resource constraints	• Global surveillance networks • Early warning systems • Integrated platforms • Resource sharing initiatives	• Better coverage • Faster response • Improved coordination • Efficient resource use
Implementation & Training	• Limited expertise availability • Training resource gaps • Technology adoption barriers • Standardization issues	• Capacity building programs • Online training platforms • User-friendly tools • Standard operating procedures	• Wider adoption • Better expertise • Improved standardization • Enhanced capabilities

Long-read sequencing and portable genomic techniques have completely changed the realm of animal forensics by enabling us to track the provenance of wildlife products and stop illicit poaching. These methods not only support increased accountability and understanding of animal protection, but they also improve law enforcement activities. In an era where infectious diseases are a constant concern and the environment is changing quickly, the collaboration of genetic science and conventional ecological methods will be crucial. In addition to bolstering our public health responses, ongoing investment in and use of real-time genetic technologies will support the sustainability of our natural ecosystems. In the end, adopting these advances will empower us to make data-driven, well-informed decisions that promote biodiversity preservation and human health, guaranteeing a robust and sustainable future for future generations.

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