Original Review Article

Journal of Biological Research

& Biotechnology

Bio-Research Vol. 22 No.1; pp. 2223-2233 (2024). ISSN (print):1596-7409; eISSN (online):2705-3822

The role of ecogenomics in environmental and forensic discoveries

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Abstract

Ecogenomics is the application of genetic information and environmental science to understand the genetic diversity and functional potential of microbial communities in various environments. It involves the analysis of DNA and RNA sequences to gain insights into the structure, function, and dynamics of ecosystems. In the context of the environment, ecogenomics plays a crucial role in understanding the impact of human activities on natural ecosystems. By studying the genetic composition of microbial communities, researchers can assess the health and resilience of ecosystems, identify key species involved in nutrient cycling and energy flow, and monitor the effects of pollution and climate change. Ecogenomics also has significant applications in forensic research. By analyzing the microbial DNA present at crime scenes, forensic scientists can gain valuable information about the individuals involved. Microbes are ubiquitous and can be transferred from person to person, leaving behind a unique microbial signature that can be used for identification purposes. This approach, known as microbial forensics, can complement traditional forensic techniques and provide additional evidence in criminal investigations. By harnessing the power of genomics, researchers can uncover hidden microbial diversity, track ecosystem changes, and provide valuable insights into criminal investigations.

Keywords: Crime, Ecosystem, Genomics, Microbiome, Sequencing

Received September 11, 2023; **Revised** February 04, 2024; **Accepted** February 10, 2024; **Published** March 03, 2024

https://dx.doi.org/10.4314/br.v22i1.1
Journal Homepage: http://www.bioresearch.com.ng.
Publisher: *Faculty of Biological Sciences, University of Nigeria, Nsukka, Nigeria.*

INTRODUCTION

Ecogenomics is a field of study that combines ecology and genomics to understand the genetic diversity and functional potential of microbial communities in various ecosystems. It involves the analysis of the genomes of multiple organisms within a community to gain insights into their interactions, roles, and contributions to ecosystem processes (Roy *et al*., 2011). The scope of ecogenomics is broad and encompasses the study of microbial communities in diverse environments such as soil, water, air, and the human body. It aims to uncover the genetic and functional diversity of these communities, as well as the factors that shape their composition and dynamics (Maphosa *et al*., 2012). Ecogenomics utilizes high-throughput sequencing technologies and bioinformatics tools to analyze the genetic material (DNA or RNA) extracted from environmental samples (Kumar *et al*., 2022). By sequencing and comparing the genomes of different organisms within a community, researchers can identify and characterize the genes and metabolic pathways that are important for ecosystem functioning.

The applications of ecogenomics are wide-ranging. It can be used to study the impact of environmental changes on microbial communities, such as climate change or pollution. It can also help in the discovery of novel genes and enzymes with potential applications in biotechnology, agriculture, and medicine. Additionally, ecogenomics can provide insights into the role of microbial communities in nutrient cycling, carbon sequestration, and other ecosystem processes (Zaya and Ashley, 2012).). The interdisciplinary nature of ecogenomics allows researchers to integrate knowledge and techniques from molecular biology, ecology, bioinformatics, and statistics to gain a comprehensive understanding of the genetic diversity, ecological roles, and functional potential of microbial communities in different ecosystems. This interdisciplinary approach is crucial for addressing complex ecological questions and advancing our understanding of the interactions between organisms and their environment.

Molecular biology techniques such as DNA sequencing, polymerase chain reaction (PCR), and gene expression analysis are used to study the genetic diversity, gene expression patterns, and functional potential of microbial communities in different ecosystems (Creer *et al*., 2016). Ecogenomics incorporates ecological principles to understand the distribution, abundance, and dynamics of microbial communities in various ecosystems (Haro-Moreno *et al*., 2020). By studying the genetic makeup of these communities, ecogenomics helps in understanding their ecological roles, such as nutrient cycling, energy flow, and symbiotic relationships.

Bioinformatics plays a crucial role in ecogenomics by providing computational tools and methods to analyze large-scale genomic data (Orton *et al*., 2016). It involves the development and application of algorithms, databases, and statistical models to process, analyze, and interpret genomic information. Bioinformatics tools are used in ecogenomics to analyze DNA sequences, identify genes, predict functional annotations, and compare microbial communities across different environments.

Statistics is essential in ecogenomics to analyze and interpret the large and complex datasets generated from genomic studies. Statistical methods are used to identify patterns, correlations, and associations within the data, as well as to infer ecological and evolutionary processes. Statistical techniques such as multivariate analysis, regression analysis, and hypothesis testing are employed to understand the relationships between environmental factors and microbial community composition or function (Yinglin and Jun, 2017).

Ecogenomics has the potential to revolutionize our understanding of the environment and forensic research. By harnessing the power of genomics, researchers can uncover hidden microbial diversity, track ecosystem changes, and provide valuable insights into criminal investigations. This interdisciplinary field holds great promise for addressing environmental challenges and advancing forensic science.

Applications of Ecogenomics in Environmental Research

Ecogenomics has several applications in environmental research. These applications are as follows;

Monitoring Environmental Changes

Ecogenomics allows for the monitoring of environmental changes and their impacts on biodiversity and ecosystem health. By repeatedly sampling and analyzing genetic material from the same ecosystem over time, researchers can detect changes in microbial communities and functional genes. This helps in understanding the effects of factors such as climate change, pollution, or land-use changes on ecosystem health and biodiversity. For example, ecogenomics can be used to study the impact of climate change on coral reefs. By analyzing the genomic data of coral species, researchers can identify genes that are associated with thermal tolerance and resilience to rising ocean temperatures (Elder *et al*., 2022). This information can help in predicting which coral species are more likely to survive and adapt to future climate change scenarios (Wang *et al*., 2021; Fenglei *et al*., 2023). Ecogenomics can be used to study the impact of habitat degradation on fish and bird populations. By analyzing the genomic data of different fish species, researchers can identify genetic variations that are associated with their ability to adapt to degraded habitats, such as polluted waters or reduced food availability (Cermakova *et al*., 2023; Hamilton *et al*., 2016; Wu *et al*., 2021; Hohenlohe *et al*., 2021). This information can help in understanding which fish populations are more resilient to habitat degradation and can guide conservation efforts to restore and protect their habitats.

Microbial Diversity Assessment

Ecogenomics allows researchers to identify and characterize the microbial diversity present in an ecosystem. By analyzing the DNA or RNA extracted from environmental samples, scientists can determine the types and abundance of microorganisms, including bacteria, archaea, fungi, and viruses (Roux *et al*., 2021). This information helps in understanding the overall biodiversity of the ecosystem.

Functional Gene Analysis

Ecogenomics enables the study of functional genes present in microbial communities. Functional genes are responsible for various ecological processes, such as nutrient cycling, degradation of pollutants, and production of bioactive compounds. By analyzing the genetic material, researchers can identify the functional genes and assess their abundance and diversity. This provides insights into the ecosystem's capacity to perform essential functions and maintain its health (Orton *et al*., 2016)

Indicator Species Identification

Ecogenomics can help identify indicator species that are sensitive to environmental changes or disturbances. By comparing the microbial communities in different ecosystems or over time, researchers can identify specific microbial taxa or functional genes that are associated with healthy or degraded ecosystems (Felipe *et al*., 2018). These indicator species can serve as early warning signs of ecosystem health decline and guide conservation efforts. Ecogenomics can be used to study the impact of invasive species on native ecosystems. By comparing the genomic data of invasive species with that of native species, researchers can identify genetic differences that may contribute to the invasiveness of the species (Matheson and McGaughran, 2022; Turner *et al*., 2021; Neinavaie *et al*., 2021). This information can help in understanding the mechanisms behind their success and guide management strategies to control their spread and minimize their impact on native biodiversity.

Assessment of Ecosystem Services

Ecogenomics can provide information on the potential ecosystem services provided by microbial communities. For example, by analyzing the genes involved in nitrogen fixation or carbon sequestration, researchers can estimate the ecosystem's capacity to provide these services (Yanbin *et al*., 2022). This information is crucial for understanding the overall health and functioning of ecosystems and their contributions to human well-being.

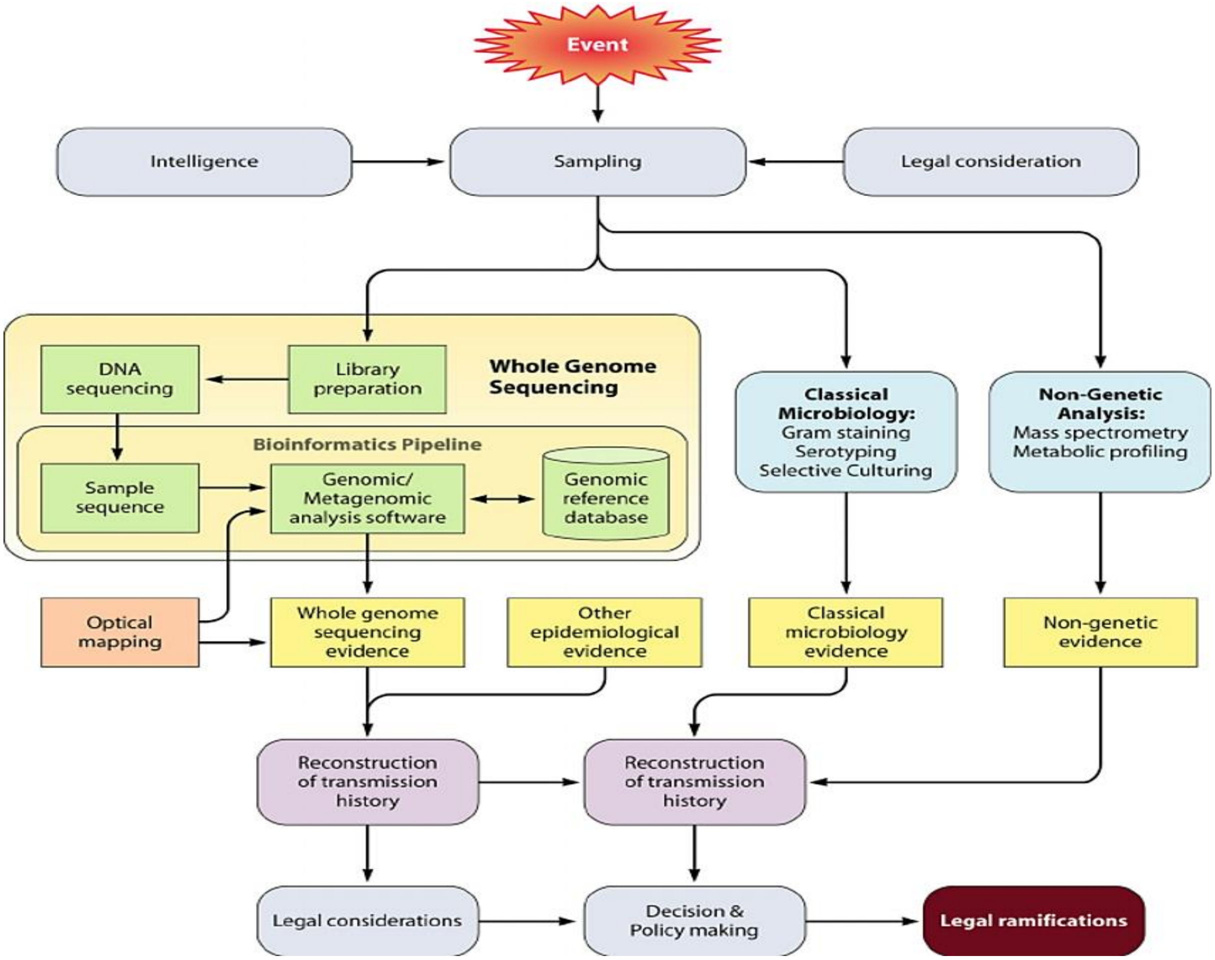
Overall, ecogenomics provides a powerful tool for assessing biodiversity and ecosystem health by analyzing the genetic material present in environmental samples. It allows researchers to understand the composition, diversity, and functioning of microbial communities, identify indicator species, assess ecosystem services, and monitor environmental changes. This knowledge is crucial for effective conservation and management of ecosystems.

Applications of Ecogenomics in Forensic Research

Ecogenomics has several applications in forensic research. While traditionally applied to environmental studies, ecogenomics has gained attention in forensic science, particularly in trace evidence analysis. Forensic trace evidence analysis aims to identify and compare various types of microscopic evidence found at crime scenes or on individuals. This includes things like hair, fibers, soil, pollen, and other small particles that can provide crucial information in criminal investigations (UFH, 2022). Incorporating ecogenomics into this process can enhance the precision and depth of analysis. This can provide information about the geographic origin of the evidence, the presence of specific organisms or contaminants, and the movements of suspects or victims. This information is crucial for understanding the patterns of illegal trade, identifying hotspots of poaching or logging, and targeting conservation efforts effectively. The workflow of forensic DNA analysis using ecogenomics techniques is shown in **Figure 1.**

Forensic Microbiome Analysis

Ecogenomics can be used to analyze the microbial communities present at crime scenes or on evidence. This can provide valuable information about the environment and the individuals involved in a crime. For example, the analysis of microbial DNA on a weapon or clothing can help identify the geographic origin of the suspect or provide information about their lifestyle (Santiago-Rodriguez *et al*., 2016; Schmedes *et al*., 2016)



Source (Gilchrist *et al*., 2015)

Figure 1: workflow of forensic DNA analysis using ecogenomics techniques.

Forensic Entomology

Forensic entomology is the use of insect evidence to assist in legal investigations, often involving the estimation of the time of death (postmortem interval) and the location of death (crime scene analysis). The integration of ecogenomics into forensic entomology has led to several valuable advancements: Ecogenomics can be used to study the DNA of insects found at crime scenes, such as flies or beetles. By analyzing the insect's DNA, researchers can determine the time of death, the location of the crime, and even the presence of drugs or toxins in the victim's body (Durdle, 2020; Sharma *et al*., 2015).

Forensic Botany

Ecogenomics can be used to analyze plant DNA found at crime scenes or on evidence. This can help identify the type of plant, its geographic origin, and its role in the crime. For example, the analysis of pollen grains can provide information about the location and time of a crime, as well as the movements of suspects or victims (Sawyer, 2020). By analyzing the genetic markers of plants, researchers can trace the origin of plant material found at a crime scene (Robertson *et al*., 2022; Zaya and Ashley, 2012). This can be particularly useful in cases involving illegal trade of endangered plant species, environmental crimes, or cases where the geographical origin of the plant is relevant. Ecogenomic techniques can help establish a timeline of events by examining the succession of plant species in a particular area. This can be useful in cases involving missing persons or bodies that have been exposed to the elements for an extended period.

3.4. Forensic Wildlife Analysis

Ecogenomics can be used to study the DNA of wildlife species found at crime scenes, such as hairs, feathers, or droppings. This can help identify the species involved in a crime, track the movements of suspects or victims, and provide evidence for illegal wildlife trade or poaching (Cindy, 2023). By analyzing genetic data from different crime scenes, ecogenomics can link different illegal activities to the same individuals or groups. This can help investigators build stronger cases against wildlife criminals who may be involved in multiple incidents. Ecogenomics can establish a genetic database of individuals or populations, which can be used to trace the origin of seized wildlife products back to specific populations (Sahajpal *et al*., 2021). This traceability helps investigators understand the routes of illegal trade and target key areas for enforcement. DNA analysis allows scientists to accurately identify the species of a confiscated sample, even if it is in a fragmented or degraded state. This is particularly useful in cases where smugglers attempt to disguise or mislabel the wildlife products they are trafficking. By comparing the DNA sequence of the sample to a reference database, scientists can determine the species involved, helping authorities to enforce regulations and protect endangered species. DNA analysis can also identify individual animals within a species. This is crucial in cases where poachers or traffickers claim that the confiscated wildlife products are from legal sources or captive-bred animals. By comparing the DNA profiles of the confiscated samples to a database of known individuals, scientists can determine if the animals were illegally obtained from the wild or bred in captivity.

Determination of Cause of Death

Ecogenomics plays a vital role in determining the cause of death in wildlife. By analyzing the DNA of deceased animals, scientists can identify pathogens, toxins, or other genetic markers associated with specific diseases or causes of death (Li *et al*., 2020). This information helps in understanding the factors contributing to mortality events, such as disease outbreaks or environmental contaminants. It also aids in wildlife management and conservation efforts by identifying potential threats to populations and implementing appropriate measures to mitigate them.

Successful Forensic Cases where Ecogenomics Played a Crucial Role in Solving Crimes or Providing Evidence.

The "Golden State Killer" Case: In 2018, ecogenomics played a pivotal role in identifying and capturing Joseph James DeAngelo, also known as the Golden State Killer. Investigators used DNA samples collected from crime scenes in the 1970s and 1980s to create a genetic profile. This profile was then compared to publicly available genetic data on genealogy websites, leading them to distant relatives of the suspect (*Los Angeles Times*, 2020). By building a family tree and narrowing down potential suspects, investigators were able to collect discarded DNA from DeAngelo, confirming his identity and linking him to multiple crimes.

The "Grim Sleeper" Case: Lonnie David Franklin Jr., known as the Grim Sleeper, was a serial killer who operated in Los Angeles from the 1980s to 2002 (Harmon, 2020). In 2010, investigators used ecogenomics to identify and apprehend him. DNA samples collected from crime scenes were analyzed, and a partial match was found in the California DNA database. To confirm the match, investigators used familial DNA searching, which led them to Franklin's son. By collecting a discarded DNA sample from Franklin, they were able to conclusively link him to the crimes.

The "Boston Strangler" Case: In 2013, ecogenomics helped solve a decades-old mystery surrounding the identity of the Boston Strangler (Mcphee, 2013). Albert DeSalvo was widely believed to be the Boston Strangler, responsible for a series of murders in the 1960s. However, his guilt was never proven. In 2013, investigators exhumed DeSalvo's body and used ecogenomics to compare his DNA with DNA evidence from the crime scenes. The results showed a match, providing strong evidence that DeSalvo was indeed the Boston Strangler.

The "Buckskin Girl" Case: In 1981, an unidentified female body was found in Ohio, and she became known as the "Buckskin Girl" due to the distinctive clothing she was wearing. Despite extensive efforts, her identity remained unknown for over three decades. In 2018, ecogenomics played a crucial role in solving the case. DNA extracted from the victim's remains was analyzed, and a genetic profile was created. This profile was then compared to public genealogy databases, leading investigators to a potential family connection. Through further investigation and DNA testing of relatives, the victim was identified as Marcia King, providing closure to her family and enabling progress in the investigation (*CBS News*, 2018).

These cases highlight how ecogenomics, combined with traditional forensic techniques, has been instrumental in solving crimes, identifying perpetrators, and providing closure to victims' families.

Table 1: Summary of Some Recent Discoveries in Environmental and Forensic Research

Environmental discoveries	Reference (s)
CRISPR-based Environmental DNA (eDNA) Analysis	(Li *et al*., 2023)
Microplastic Pollution Monitoring in Water Bodies	(Kallenbach *et al*., 2022)
Remote Sensing for Environmental Monitoring	(Rumiano *et al*., 2020)
Predictive Ecology- Integration of genomic data with ecological models.	(Campbell *et al*., 2023)
Niche Differentiation for Specific Environmental Tolerance using Groundwater Phages.	(Kothari *et al*., 2021)
Next Generation Sequencing (NGS)-Based Approaches for Discovery of New Circular DNA Single-Stranded Viral Species.	(Enrique *et al*., 2024)
Multi-environment ecogenomics analysis of diverse bacterial phylum.	(Mujakić *et al*., 2023)
Forensic Discoveries	
Stable Isotope Analysis for Forensic Geolocation.	(Arai *et al.,* 2023), (Putman & Bowen, 2019)
DNA Phenotyping in Forensic Investigations.	(Zaguia *et al*., 2022)
Forensic Entomology and Decomposition Studies.	(Bambaradeniya, 2023)
Post-Mortem Interval and Microbiome Analysis.	(Tozzo *et al*., 2022)
Massively Parallel Sequencing (MPS) of Damaged samples.	(Carratto *et al*., 2022)
Single Cell Genomics Applications in Forensic Science.	(Huffman and Ballantyne, 2023)
Microbiome Technology in Forensic Analysis.	(Zhang *et al*., 2023)

Challenges and Future Directions of Ecogenomics in Environmental and Forensic Research

Ecogenomics has emerged as a powerful tool in environmental and forensic research. It allows researchers to understand the diversity, function, and interactions of organisms in their natural habitats, as well as to identify and track organisms in forensic investigations. However, there are several challenges and future directions that need to be addressed to fully harness the potential of ecogenomics in these fields.

Challenges

One of the primary challenges of ecogenomics is the high cost of sequencing technologies. The process of sequencing the genomes of multiple organisms within an ecosystem can be expensive, especially when dealing with complex and diverse ecosystems (Helmy *et al*., 2016). The cost of sequencing has decreased significantly over the years, but it remains a barrier for many researchers and limits the scale and scope of ecogenomic studies. Also, there are vast amount of data generated by high-throughput sequencing technologies. The analysis and interpretation of this data require advanced computational and bioinformatics tools. Developing efficient algorithms and software for data analysis, as well as improving data storage and management systems, are crucial for the advancement of ecogenomics.

Another challenge is the lack of reference genomes for many organisms in environmental and forensic samples. Reference genomes are essential for accurate taxonomic and functional assignment of sequences (Almeida *et al*., 2021). Efforts should be made to expand the existing reference databases and to develop methods for de novo assembly of genomes from metagenomic data. While DNA analysis is a powerful tool, it does have some limitations. Obtaining high-quality DNA samples from confiscated wildlife products can be challenging, especially if the samples are degraded or mixed with other materials. The lack of comprehensive reference databases for all species and regions can limit the accuracy of geographic origin determination. To effectively use DNA analysis in wildlife crime investigations, it is essential to establish comprehensive DNA databases. These databases should include reference samples from known individuals, captive populations, and wild populations across different regions. By continuously expanding and updating these databases, scientists can improve the accuracy and reliability of DNA analysis in identifying species, individuals, and their geographic origins.

Ethical considerations also play a crucial role in ecogenomics. The collection and analysis of genomic data from organisms in their natural habitats raise concerns about privacy, consent, and potential harm to the ecosystem (Arshad *et al*., 2021). Researchers must ensure that proper consent is obtained from individuals or communities involved in the study, and that the data is used responsibly and by ethical guidelines. Additionally, there is a need for transparency and open communication with the public to address concerns and build trust.

Furthermore, ecogenomics faces limitations in terms of sample collection and representation. It is often challenging to obtain representative samples from diverse ecosystems, especially those that are remote or inaccessible. Bias in sample collection can lead to incomplete or skewed understanding of the ecosystem's genomic composition. Additionally, the reliance on DNA-based approaches may overlook important functional aspects of ecosystems, such as epigenetic modifications or interactions between organisms.

Future direction

There are several ongoing research efforts aimed at improving sequencing technologies, developing standardized protocols, and enhancing data analysis methods. Some of these efforts include:

Improving sequencing technologies: Development of new sequencing platforms: Researchers are working on developing new sequencing platforms that can provide faster, more accurate, and cost-effective sequencing. Examples include nanopore sequencing, single-molecule real-time (SMRT) sequencing, and synthetic long-read sequencing (Ram *et al*., 2019).

Developing scalable and efficient data storage solutions: As the volume of sequencing data continues to grow, researchers are working on developing scalable and efficient data storage solutions. This includes the use of cloud computing, distributed file systems, and compression algorithms to handle large-scale genomic data.

Improving data sharing and collaboration platforms: Efforts are being made to develop platforms and databases that facilitate data sharing, collaboration, and reproducibility in genomics research. This includes initiatives like the Global Alliance for Genomics and Health (GA4GH) and the European Genome-phenome Archive (EGA) (Freeberg *et al*., 2021).

Enhancing read length and accuracy: Efforts are being made to improve the read length and accuracy of sequencing technologies. This includes developing new chemistries, improving base-calling algorithms, and reducing sequencing errors. Researchers are continuously developing new bioinformatics tools and algorithms to analyze sequencing data (Pereira *et al*., 2020). This includes tools for read alignment, variant calling, de novo assembly, and functional annotation. Efforts are also being made to improve the accuracy and efficiency of these tools. With the advancement of multi-omics technologies, efforts are being made to develop methods for integrating and analyzing data from different omics layers, such as genomics, transcriptomics, proteomics, and metabolomics. This integration can provide a more comprehensive understanding of biological systems

Standardizing protocols: Researchers are working on developing standardized protocols for library preparation, which is a crucial step in sequencing (Hess *et al*., 2020). Standardization helps ensure reproducibility and comparability of sequencing data across different laboratories and platforms. Also, efforts are being made to develop reference materials and quality control standards that can be used to assess the performance of sequencing technologies and protocols. This helps in benchmarking and improving the accuracy and reliability of sequencing data.

These ongoing research efforts aim to overcome the current limitations of sequencing technologies, standardize protocols, and enhance data analysis methods, ultimately advancing our understanding of genomics and its applications in various fields such as medicine, agriculture, and environmental sciences.

In environmental research, one of the future directions of ecogenomics is to understand the functional potential of microbial communities in different ecosystems. This can be achieved by integrating metagenomic data with other omics data, such as metatranscriptomics and metaproteomics, to study gene expression and protein function in environmental samples. This will provide insights into the roles of different organisms in ecosystem processes and their responses to environmental changes.

In forensic research, ecogenomics has the potential to revolutionize the field of forensic identification and traceability. By analyzing the microbial communities associated with different environments, such as soil, water, or human skin, it is possible to link individuals or objects to specific locations or events. However, more research is needed to establish the reliability and robustness of microbial forensic techniques, as well as to develop standardized protocols and databases for forensic ecogenomics.

Generally, ecogenomics has the potential to provide valuable insights into the functioning of ecosystems and to improve forensic investigations. However, addressing the challenges and exploring the future directions outlined above will be crucial for the advancement and widespread application of ecogenomics in environmental and forensic research.

CONCLUSION

Ecogenomics has proven to be a valuable tool in both environmental and forensic research. It allows scientists to study the genetic diversity and interactions of organisms in their natural environments, providing insights into ecosystem functioning and biodiversity conservation. In environmental research, ecogenomics has been used to identify and monitor species, assess the impact of environmental disturbances, and develop strategies for ecosystem restoration and management. In forensic research, ecogenomics has been used to identify and trace the source of biological materials, such as in wildlife crime investigations or the analysis of microbial communities in crime scenes. Generally, ecogenomics has revolutionized the way we study and understand the environment and has the potential to contribute significantly to both scientific knowledge and practical applications in the future. While ecogenomics holds great promise for advancing our understanding of ecosystems, it faces challenges and limitations. The high cost of sequencing technologies, data analysis complexities, ethical considerations, and limitations in sample collection and representation all need to be addressed to fully harness the potential of ecogenomics. Overcoming these challenges will require interdisciplinary collaborations, technological advancements, and ethical frameworks to ensure responsible and impactful research.

Conflict of Interest

The authors declare no actual or potential conflict of interest.

Acknowledgements

We profoundly grateful to the ethics and publication committee of Alex Ekwueme Federal University Ndufu Alike, Ebonyi State for the review of this work. This article received no funding.

Authors Contributions

NKE, IAG and UCD were involved in the conception and design of the work and in drafting the manuscript. AP and ENE were involved in writing and editing the work.

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