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Environmental DNA and its role in identifying yeast biodiversity in mangrove ecosystem: a literature review

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Abstract. Yeast biodiversity in mangrove ecosystems is crucial for their health and ecological functions. However, traditional methods often fail to detect yeast species that are difficult to culture or slow growing, leaving a significant portion of this biodiversity undetected. This study explores the use of environmental DNA (eDNA) as an alternative method for identifying yeast species in mangrove ecosystems, addressing data gaps left by conventional methods. Data is collected from various relevant literature sources, including scientific journals, books, and research reports. The literature review reveals that eDNA analysis can improve conservation management by providing robust biodiversity assessments. Future research should focus on understanding eDNA persistence, ecological implications, and improving bioinformatics for better data interpretation. In-depth long-term studies are recommended to study the temporal and spatial dynamics of yeast communities in mangrove ecosystems. Further validation of the eDNA method in various environmental conditions is needed to ensure reliability. Research on yeast interactions with other ecosystem components and the impact of human activities like pollution and habitat change is also important.

1 Introduction

Mangrove ecosystems are incredibly diverse and productive habitats that thrive in the intertidal zones of tropical and subtropical coastlines [1]. These distinctive ecosystems are vital for sustaining diverse flora and fauna, promoting coastal protection, carbon sequestration, and sustaining local livelihoods [2]. One of the key challenges in understanding and conserving mangrove biodiversity is identifying the numerous species that inhabit these ecosystems, including yeast diversity [3]. Traditional biodiversity monitoring methods often fail to capture the full extent of microbial diversity in mangroves. However, environmental DNA (eDNA) has emerged as a powerful tool for surveying microbial communities, offering a non-invasive and comprehensive approach to characterizing biodiversity [4].

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This study investigates the capacity of eDNA to determine the variety of yeast species present in mangrove environments. The objective is to use eDNA analysis to reveal the diversity of species and geographic in these crucial and poorly researched environments. This study enhances our comprehension of microbial diversity in mangroves and provides insights into the ecological functions of yeasts in these intricate ecosystems.

1.1 Importance of yeast diversity in mangroves

Mangrove ecosystems utilize yeasts for nutrient cycling, plant interactions, and organic matter decomposition, with various yeast species producing enzymes and bioactive compounds for biotechnology [5-6]. *Candida*-genus mangrove yeasts widely distribute and decompose pollutants including phenol and toluene, which is essential for bioremediation [7]. Understanding mangrove ecosystem ecology requires research yeast diversity [8, 6]. Marine yeasts fulfilled effectively in environmental and medicinal applications, finding yeast diversity crucial to ecological functions and industrial applications [9]. Yeast species could additionally indicate mangrove ecosystem health and threats [7]. Environmental DNA can identify yeast species and provide mangrove ecosystem yeast distribution, abundance, and interactions [10-11]. Mangrove yeasts also have bioactive compounds which might be utilized to produce antibacterial, antifungal, or anticancer medicines [12]. Environmental DNA metabarcoding could enhance our understanding of yeast diversity in mangroves and provide quick, complete biodiversity evaluations for conservation [13].

1.2 Environmental DNA (eDNA): an overview

Environmental DNA (eDNA) is the genetic material shed by organisms into their environment, such as water or soil. This genetic information provides valuable insights into the diversity and abundance of species, offering a non-invasive way to monitor biodiversity [14]. The principles of eDNA technology are rooted in organisms leaving traces of their genetic material in the environment through sloughed skin cells, hair, feces, or urine [15]. Environmental DNA has been a valuable tool for studying biodiversity, from identifying elusive species to understanding the impacts of invasive species on native ecosystems [16]. In the context of mangrove ecosystems, eDNA analysis can provide crucial information about the presence and distribution of yeast species [13]. Sequencing, bioinformatics, and sample processing have improved eDNA technology, allowing more accurate species identification in varied environmental matrices [14]. Advances in eDNA technology may help explain yeast diversity in mangrove ecosystems and their ecological roles and interactions [17]. Environmental DNA technology combined with ecological research helps understand microbial interactions [18 -19].

1.3 Environmental DNA (eDNA) technology

Environmental DNA (eDNA) technology has revolutionized biodiversity monitoring by offering a non-invasive and high-throughput approach to studying microbial communities [10, 14, 19]. The process involves extracting and analyzing genetic material shed by organisms into the environment, providing a comprehensive snapshot of the species in a given ecosystem [13, 20].

1.3.1 Sample collection

To study yeast diversity, samples were collected from across the mangrove ecosystem to include multiple microenvironments and environmental circumstances [9]. The empirical data from diverse sample locations show large species abundance changes, which may be impacted by ecological and environmental variables, confounding species dispersion evaluation [21].

1.3.2 Environmental DNA extraction and sequencing

After sample collection, improved methods retrieved eDNA from soil and water samples to capture genetic diversity. Using high-throughput sequencing, yeast species in mangrove habitats were identified from extracted eDNA [13, 22].

1.3.3 Data analysis

Environmental DNA analysis is used to identify species, assess biodiversity, and monitoring environmental shifts, ahead of established approaches in efficiency and cost [23]. Metabarcoding, a non-invasive approach for eDNA data processing, analyzes environmental DNA sequences to rapidly estimate biodiversity. This method allows for evaluating ecosystem functions and highlights by identifying species composition and community structure [13]. Biological and abiotic variables such particle size, environment, and DNA physical state influence eDNA transportation and degradation, which could affect detection and analysis. All methods of sampling embrace uncertainties like false negatives. Hence modeling assists in predicting species occurrence in eDNA data analysis. These models consist of ecological variables and sample volume to enhance detection probability [24]. Genomic binning and metagenomic sequencing may improve eDNA analysis resolution, revealing distinct gene sets and functional profiles in microbial communities. Comparing taxonomic and functional profiles across samples and situations requires standardization of data, such as using QIIME2 [12]. Advanced sequencing and data modeling procedures in eDNA analysis expose ecosystem dynamics and species interactions, which makes it a vital tool for environmental monitoring and biodiversity assessment [13, 23, 24].

1.4 Advantages of eDNA technology

Environmental DNA technology offers advantages over traditional methods for ecological monitoring and conservation, including the ability to identify rare species and whole communities in aquatic settings [21]. eDNA can also identify invasive and endangered species, aiding conservation and management [14]. Some legal issues embrace eDNA technologies because they are dependable and fulfill scientific needs [24]. eDNA's sensitivity, specificity, and holistic view of biodiversity make it an essential tool for modern ecological research and management, despite potential DNA degradation and standardized protocols [20-21].

1.5 Microbial diversity and role of yeast in mangrove ecosystem

In addition to their rich plant and animal diversity, mangrove ecosystems harbor a wealth of microbial life, including yeasts [25]. Understanding microbial diversity, including yeast communities, is essential for comprehensively assessing mangrove ecosystems' health and ecological dynamics [26]. Identifying and characterizing yeast species through DNA analysis provides valuable insights into these microorganisms' ecological functions and contributions to the mangrove ecosystem [13]. As indicators of environmental health, yeast communities can provide valuable insights into the overall resilience of mangrove ecosystems in the face of environmental stressors, climate change, and human disturbances [27]. The complex interactions between yeasts, plants, and other microorganisms in mangroves contribute to the resilience of these ecosystems by supporting nutrient cycling, organic matter decomposition, and the maintenance of soil structure [28-29].

In the future, researchers should focus on investigating the temporal and spatial dynamics of yeast communities in mangrove ecosystems. Studying how yeast populations change over time and across different locations can offer insights into the resilience and adaptability of these ecosystems to environmental stresses [5, 30]. Integrating multi-omics approaches, such as metagenomics and metabolomics, with eDNA technology can offer a more comprehensive understanding of the functional roles of yeasts and their interactions with other microorganisms in mangroves [19]. By combining these molecular techniques, researchers can decipher the metabolic pathways, ecological functions, and adaptive strategies yeast communities employ in response to environmental stimuli [31]. Moreover, collaborative efforts between researchers, conservation practitioners, and local communities are imperative for the sustainable management of mangrove ecosystems. Engaging stakeholders in participatory monitoring and conservation initiatives can facilitate knowledge exchange, promote community stewardship, and enhance the overall effectiveness of conservation efforts aimed at safeguarding yeast diversity and the ecological integrity of mangroves [32].

The ecological implications of yeast diversity in mangroves extend beyond microbial interactions to encompass broader environmental processes and ecosystem functioning [33]. The intricate relationships between yeast communities and the surrounding environment significantly affect mangrove ecosystems' resilience, stability, and biodiversity [34]. Yeast plays a crucial part in the decomposition of organic matter and the recycling of essential nutrients, contributing to the overall productivity and nutrient dynamics of mangrove ecosystems. Understanding yeast diversity and functional attributes can provide valuable insights into the efficiency of nutrient-cycling processes and the maintenance of ecosystem productivity [5, 35]. Another ecological implication pertains to yeasts' potential role in mitigating environmental stressors and enhancing the adaptive capacity of mangrove ecosystems [28]. Certain yeast species have been found to possess mechanisms for tolerance to environmental stress, including salinity, pollutants, and other anthropogenic impacts [36].

1.6 Findings yeast diversity in mangrove ecosystems

Due to its various ecological functions and biotechnology potential, mangrove habitats attract attention to the yeast diversity. In Fujian, Guangdong, and Hainan Provinces in China, 269 yeast strains from mangrove plants and sediments comprising 22 genera and 45 species were isolated. The predominant strains were *Candida spp*. (44.6%), followed by *Kluyveromyces*, *Pichia*, and others, with some strains belonging to undescribed species, presenting a rich and unexplored diversity [7]. A comprehensive examination in China's intertidal zones identified 286 yeast species from 4436 strains, presenting astounding diversity across regions and ecological conditions. The research observed that mean annual temperature, salinity, and pH affect yeast community structures, with *Candida parapsilosis* and *Candida tropicalis* being the most frequently isolated species [9]. Biogeochemical cycles rely on the mangrove microbiome, particularly yeasts, which increases production and resilience. Vegetation types and human activities contribute to the microbiome's functional and taxonomic diversity [12]. Environmental DNA metabarcoding could fast and non-invasively analyze species composition and ecosystem health in mangrove habitats. This method may identify yeast variety and ecological activities in complicated ecosystems [13]. Yeast diversity in mangrove ecosystems is impacted by environmental and human factors, with significant implications for ecosystem functioning and biotechnology.

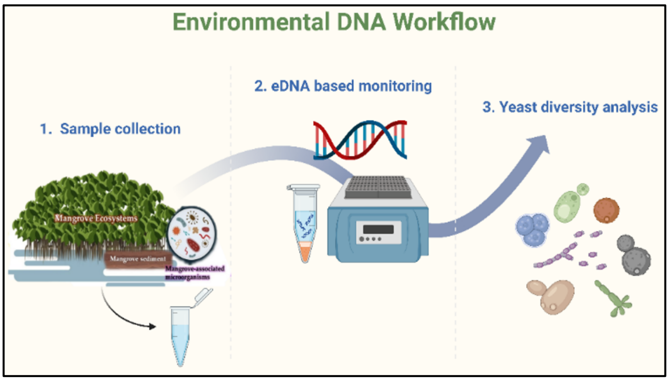

Fig. 1. The Environmental DNA workflow.

2 Methods

This research used a traditional literature review methodology to investigate the function of environmental DNA (eDNA) in identifying yeast biodiversity within mangrove habitats. The study will use secondary sources, such as peer-reviewed journal articles, books, and reputable studies, to consolidate current information. Primary data will provide empirical findings, while secondary data will include information on the methods used in eDNA research, the diversity of yeast species present in mangrove habitats, and their ecological roles. The secondary data will serve as the foundation for the literature review, including crucial context and background information.

The data analysis will use a qualitative method, using thematic analysis to discern reoccurring themes, patterns, and insights from the literature studied. The data analysis process will encompass: (1) identifying and selecting pertinent studies via systematic search methodologies in scientific databases, (2) categorizing the gathered data into thematic classifications, (3) strictly comparing and analyzing findings across various studies, and (4) synthesizing the information to elucidate key insights and deficiencies in the existing comprehension of eDNA's function in identifying yeast biodiversity within mangrove ecosystems.

3 Result and discussion

3.1 Technical and methodological challenges in eDNA analysis

Although eDNA technology has transformed the study of microbial diversity in environments like mangroves, it has technical and methodological hurdles. Extracting high-quality eDNA from complicated environmental materials like mangrove sediments and water is difficult [14]. The presence of PCR inhibitors, humic substances, and other contaminants in these samples can affect the efficacy of eDNA extraction and subsequent analysis [37]. Another significant challenge in eDNA analysis is the accurate amplification and sequencing of target DNA regions, mainly when dealing with diverse microbial communities. The design of primers and PCR conditions must be carefully optimized to ensure the specific amplification of target sequences while minimizing bias and artifacts in the eDNA data [21].

In addition, standardization of eDNA protocols and methodologies across different research groups is crucial for the comparability and reproducibility of results [38]. Harmonizing sampling techniques, DNA extraction methods, and bioinformatic pipelines can facilitate data integration and meta-analyses, ultimately advancing our understanding of yeast diversity and its ecological roles in mangroves [39].

3.2 Limitations in current eDNA databases and reference materials

eDNA technology has revolutionized mangrove microbial diversity research, yet it has technical and methodological challenges. Mangrove sediments and water are challenging to extract high-quality eDNA. These limitations make yeast community identification and characterization in mangrove ecosystem samples complicated [4,13]. The lack of comprehensive reference sequences for diverse yeast species hinders the accurate taxonomic assignment of eDNA sequences obtained from environmental samples [38]. Moreover, the availability of high-quality reference materials for validating and benchmarking eDNA-based analyses is crucial for ensuring the reliability and accuracy of microbial diversity assessments [40]. The need for more authenticated reference materials for diverse yeast taxa poses a significant limitation in validating the taxonomic assignments and species identification derived from eDNA data [41].

3.3 Environmental and temporal variability in eDNA sampling

Temporal variability, including seasonal fluctuations and long-term changes in environmental conditions, can also influence the composition and activity of yeast communities [42]. Longitudinal studies that span multiple seasons and years are necessary to capture the full spectrum of temporal variability and understand the resilience of yeast populations to environmental changes over time [36]. Incorporating robust sampling strategies considering environmental and temporal variability will be crucial for obtaining comprehensive insights into the dynamic nature of yeast communities in mangroves and their responses to ecological perturbations [43].

3.4 Interpretational challenges in eDNA data

Interpretation of DNA data presents significant challenges, especially when attempting to differentiate true microbial diversity from potential contamination or artifacts introduced during sample collection, processing, or sequencing [44]. The complexity of mangrove ecosystems and their various microbial populations makes this difficulty much greater. These problems need rigorous quality control and bioinformatic analyses to assure the credibility of eDNA-based microbial diversity estimations in mangrove ecosystems [13].

Interpreting eDNA data also becomes complex when considering the dynamic nature of yeast communities and their responses to environmental perturbations [42]. To accurately measure mangrove ecosystem microbial diversity and dynamics, sampling must account for environmental and temporal variability. Robust sampling procedures that account for these differences are essential for understanding mangrove yeast populations' dynamic character [45]. Furthermore, the accurate taxonomic assignment of eDNA sequences derived from complex environmental samples such as mangrove sediments and water remains a significant interpretational challenge [46].

3.5 Advancements in DNA sequencing technologies

Recent advancements in DNA sequencing technologies have provided unprecedented opportunities to enhance our understanding of yeast diversity in mangrove ecosystems [19]. High-throughput sequencing technology and bioinformatic techniques have transformed environmental microbiology, allowing researchers to study microbial populations more deeply [47]. New-generation sequencing platforms, such as Illumina and Nanopore, offer higher throughput, increased read lengths, and improved accuracy, allowing for the comprehensive profiling of yeast diversity in complex environmental samples [34]. These technological advancements facilitate the detection of rare and low-abundance yeast taxa, thereby capturing a more complete picture of microbial communities within mangrove ecosystems [48]. In addition to sequencing platform advancements, metagenomic and meta transcriptomic techniques in eDNA analysis reveal mangrove yeast community function and metabolic activities [49]. Furthermore, developing eDNA-specific bioinformatic pipelines and analytical tools has improved taxonomic assignment, species identification, and functional annotation accuracy and efficiency [10]. Researchers can overcome the interpretational problems of complicated eDNA datasets using bioinformatics, improving mangrove ecosystem microbial diversity estimations [13]. As we implement these new tools and methodologies, we must continue to address eDNA database constraints, environmental sample variances, and interpretation issues [23]. A multidisciplinary and integrative approach may help us use eDNA technology to investigate yeast community dynamics in mangrove ecosystems and their ecological value [20].

3.6 Integrating eDNA with other biological and ecological data

As we look to advance our understanding of yeast diversity in mangrove ecosystems, it is imperative to integrate eDNA data with other biological and ecological information [35]. This integration will provide a more holistic view of the interactions between yeast communities and their environment, offering valuable insights into these microorganisms' ecological roles and functions in mangroves [10]. Using eDNA analysis with field data and environmental data, researchers may better understand yeast distribution, abundance, and diversity in mangrove ecosystems in connection to environmental conditions and ecological trends [50]. Integrating eDNA with other biological and ecological data sources can enrich our understanding of yeast diversity and environmental functions, fostering a more comprehensive and nuanced perspective of microbial communities in mangrove ecosystems [12, 13]. This integrative approach will also support the development of effective conservation and management strategies grounded in a thorough understanding of the complex dynamics and contributions of yeast communities to the overall ecological integrity of mangroves [3].

3.7 Addressing bioinformatics and data analysis challenges

As the field of eDNA sequencing technologies continues to advance, it is essential to address the bioinformatics and data analysis challenges accompanying the generation of large and complex datasets [4]. One of the primary challenges lies in developing robust bioinformatic pipelines that can effectively handle the vast amount of sequencing data while maintaining high levels of accuracy and reliability in taxonomic assignment and functional annotation [51]. Furthermore, standardizing bioinformatic analyses for eDNA data is crucial for ensuring comparability across studies and reproducibility of results. This involves establishing best practices for data processing, quality control, statistical analyses, and implementing reference sequences for taxonomic classification [52]. Developing integrated bioinformatic workflows that can effectively combine and analyze diverse data types is essential for understanding microbial diversity, functional attributes, and ecological interactions in mangrove ecosystems [53].

Moreover, as the volume of eDNA data grows, addressing issues related to data storage, management, and accessibility is paramount [17]. Establishing infrastructure and repositories for the storage and sharing of eDNA datasets, along with the development of user-friendly data visualization and exploration tools, will facilitate collaboration and knowledge exchange within the scientific community [21].

By prioritizing the resolution of bioinformatics and data analysis challenges, researchers can ensure the robustness and reliability of eDNA-based studies, ultimately enhancing our understanding of yeast diversity and ecological functions in mangrove ecosystems [6]. This concerted effort will lay the foundation for comprehensive and rigorous investigations essential for informing conservation and management strategies aimed at preserving the integrity of these critical coastal habitats [9].

4 Conclusion

Environmental DNA research can improve our understanding of microbial communities in mangrove ecosystems by integrating eDNA analysis with traditional methods. This will provide a deeper understanding of yeast communities' ecological roles and resilience to environmental and human impacts. Technological advancements will make eDNA sequencing and analysis more accessible, allowing for more extensive investigations of yeast biodiversity across diverse mangrove regions. This research can guide conservation and management strategies, ensuring the ecological integrity and biodiversity of mangrove habitats globally. Integrating diverse perspectives with eDNA methods is crucial for sustainable and informed preservation strategies.

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