EJTAS
ISSN 2786-7447
EUROPEAN JOURNAL OF THEORETICAL AND APPLIED SCIENCES
OPEN ACCESS
PEER REVIEWED

Role of Microbial Communities in Compost and Plant Growth: Structure and Function

Atiqullah Sarwari
Department of Biology, Faculty of Education, Helmand University, Helmand, Afghanistan;
Department of Biology and Biotechnology, Al-Farabi Kazakh National University, Almaty,050038, Kazakhstan

G. Zh. Abdieva
Candidate of biological sciences, Kazakh National University named after al-Farabi University,
associate professor of biotechnology department, Almaty city. 050038, Kazakhstan

Mohammad Hassan Hassand
Department of Biology, Faculty of Education, Kandahar University, Kandahar, Afghanistan;
Department of Biology and Biotechnology, Al-Farabi Kazakh National University, Almaty,050038, Kazakhsta

Uzair Mohammad Kakar
Department of Chemistry, Faculty of Education, Logar University, Logar, Afghanistan;
Department of physical and chemical science, faculty of chemistry and chemical technology Almaty,050038 Kazakhstan

Parwiz Niazi
Department of Biology, Faculty of Education, Kandahar University, Kandahar, Afghanistan

Suggested Citation
Sarwari, A., Abdieva, G.Zh., Hassand, M.H., Mohammad, K.U. & Niazi, P. (2024). Role of Microbial Communities in Compost and Plant Growth: Structure and Function. *European Journal of Theoretical and Applied Sciences, 2*(2), 23-37.
DOI: 10.59324/ejtas.2024.2(2).03

Abstract:

The review explores the microbial communities within composite composts, focusing on their role in decomposition and nutrient cycling, using advanced molecular techniques and traditional microbiological assays, the researchers examine the diverse bacteria, fungi, and archaea in compost matrices, they highlight the richness and complexity of these ecosystems, their adaptability to various environmental conditions, and their substrate compositions. Certain important groups of microorganisms are essential for breaking down organic material, releasing nutrients, and creating humic substances that are vital for soil health and plant development. The research also shows how the makeup of the microbial community and the conditions of composting work together, which has a big impact on how well the compost matures and how good the final product is.

Keywords: *Microbial communities, Plant Growth, Soil fertility, Environmental factors, Techniques, Management.*

Introduction

Composting, which is a sustainable waste management practice at its root, is based on the elaborate maintenance of the involvement of microbial communities in the organic matter transformation into a high-nutrient humus. Recognizing not only the structural and functional properties but also the relationship between these biodiversity microbial consortia within composite composts can be considered the main priority for the optimization of composting methods and the application of soil enrichment and agricultural productivity (Younis, A., et al., 2022). The microorganisms, which comprise bacteria until archaea, are the ones responsible for the compost feedstock degradation of complex organic compounds; thus, they are able to release essential nutrients along with promoting the formation of stable organic matter. Microbial communities structure predominantly through substrate composition, moisture, and temperature, which dictate the rate and efficiency by which organic materials break down. What is more, functional features of microbial communities, including enzymatic activities and metabolic pathways, control key processes in which cellulose and lignin turn into simpler organic compounds or nitrogen, which are fixed in the soil through complex processes called humification (Sánchez, Ó. J., et al., 2017). Elucidating the complex web of microbial interaction and functional redundancy among these microbial communities through which composting is optimized, characterizing the byproducts of the process, and isolating compost-adapted microbes is crucial for maximizing efficiency, minimizing impacts on the environment, and promoting the long-term sustainability of organic waste management. Therefore, this introductory fact will build on a foundation that will later provide knowledge about the structures and functions of microbial processes as they play a role in nutrient circulation, soil health, and ecosystem structural stability Wei, H., et al., 2018).

Microbial Diversity in Composite Composts

Factors Influencing Microbial Diversity in Composts

Through interactions of processes such as competition, predation, and mutualism, the composition of microorganisms, their internal functioning, and their external characteristics will be overseen by different factors that shape the structure and function of these microbial communities within compost matrixes. Feedstock composition has a deep impact due to the fact that it determines which type of organic materials will be used for the production of energy substrates that support only particular species of microorganisms. Temperature is of paramount importance, with thermophilic temperatures supporting the multiplication of heat-tolerant microorganisms that make it possible for rapid organic matter degradation to take place (Niazi, P., et al., 2023). The latter, however, are microbial communities that are mesophilic and psychrophilic. Microbial activity and community composition in these terrestrial ecosystems are very much dependent on the content of moisture, which enhances the working of enzymes and nutrient metabolism when optimum moisture is provided. The availability of oxygen, pH, and C/N ratios, among others, closely correlate with microbial diversity and metabolism pathways, thus playing an intricate role in the environmental conditions of composting processes. Knowing the complex relationships between these factors and the way they influence composting efficiency and quality for farmland and environmental needs is key to controlling microbial populations and ensuring they have a good quantity and quality (Li, L., et al., 2018, Luepke KH, et al., 2017).

Methods for Assessing Microbial Diversity in Composts

There are different strategies employed to diagnose microbial diversity in composts, which explore the overall structure and function of the microbial ecosystems within composite compost matrices. With PCR and related molecular techniques like gene amplification (for example, 16S rRNA for bacteria, ITS for fungi, and the archaeal genes), specific genetic markers can be precisely identified, and therefore an absolute measurement of microbial taxa populations in compost samples is now possible. Relying only on traditional isolations does not allow you to know the overall population and capabilities of the microorganisms involved; therefore, metagenomic analysis provides the opportunity to directly sequence the DNA from environmental samples, aiming for a more comprehensive approach. The sequencing and analysis of metatranscriptomics provide more clarified pathways for the metabolic activities of the microbial populations involved and illuminate the functional network behind the composting process. The application of these molecular techniques together with traditional microbiological tests and chemical analyses leads to an understanding of microbial composition and activity, which in turn helps in the development of schemes aimed at the effective compost age of waste (Chandna, P., et al., 2013, Agrawal, P. K., et al., 2015).

Structural Characteristics of Microbial Communities

The taxonomic diversity and spatial organization of microbial communities within composite compost receiving different shreddings are crucial features of composite compost. Such microbial communities have a noticeable spatial pattern, and some elements of this pattern could occur when they clump around biodegradable materials and form biofilms on compost surfaces. Such a collaboration allows for the achievement of the appropriate complexity and balance between resident community microorganisms. Also, microbial communities show stratification both horizontally and vertically in different regions of the compost piles, as the populations that lie on the floors of the pile have entirely different oxygen requirements, i.e., moisture content and nutrient gradients, as compared to the surface populations that thrive in the primary stage of composting. Recognizing these structural differences would be essential for the construction of compost compounds' microbial network, nutrient cycling scheme, and decomposition route, therefore laying the foundations for the development of strategies for efficiency enhancement and obtaining uncompromised quality of the product (Singh, P., et al., 2022; Aguilar-Paredes, A., et al., 2023).

Spatial Distribution of Microbial Populations within Compost Matrices

The spatial pattern of microbial populations within the microscale compost structure is key to deciphering the features of composite composts. Microorganisms in composts show complex patterns that are affected by lessening temperature, diminished moisture, and the facilitation of nutrients. These interconnected communities exploit a diverse range of niches available within the compost matrix, so the compositional makeup of these networks differs. The results of the structural analysis show that among the various taxonomic groups of microorganisms, bacteria, fungi, and archaea, each of the latter has its own unique role in the degradation of organics. Functional characterization exhibits the microbial synergetic communications among microbial agglomerations, whereby some local processes take place, such as organic destruction, nutrient cycling, and disease suppression (Kuang, J., et al., 2016).

Successional Changes in Microbial Community Structure During Composting

Microbial community structures Variations during composting are reflected in the community dynamics during the decomposition process, which reveal shifts in microbial composition and activity. First, the composition of the microbe species starts with a higher concentration of mesophilic microorganisms (like Actinobacteria and thermo-uridized fungi). However, as the composting process goes on, the microbe species undergo a succession, and the population of thermophilic bacteria increases eventually. Along the compost aging cycle and with the microbial community undergoing additional changes, the mesophilic and thermophilic bacteria gradually give way to more cellulolytic and ligninolytic fungi. These important fungi are waiting to break down recalcitrant organic compounds. These recolonization patterns are followed by some diversification processes that occur at two different physiological levels, i.e., decomposition of organic matter, nutrient cycling, and suppression of pathogens. The aerobic and anaerobic successions of microbes and the behavior of composite composts point out the role of microorganisms in the cycling of nutrients and waste degradation (Ding, J., et al., 2020).

Influence of Environmental Factors on the Structure of Microbial Communities

The structure of microbial communities throughout the composite compost is greatly influenced by the parameters of environmental factors, which contribute to the microbes being shaped and function throughout the entire composting process. A few interrelated factors that include environmental variables, such as temperature, water activity, pH, oxygen, and nutrients, are actual determinants of microbial communities. - Extreme heat swings cause changes in the composition of the microbial populations as more thermophilic bacteria are active while there is a reduced activity of the mesophilic ones, and the moisture level determines the level of microbial activity and the ease of access to the substrates by the microbes. pH effects the metabolic activities of microbial communities, thus aiding or depriving them access to some nutrients and making the decomposition process go on in a slow or quick manner (Niazi, P., et al., 2023). Moreover, the oxygen content drives the entry of aerobic and anaerobic microbial taxa, which then shape the community. The complex network of environmental factors like aeration, moisture, temperature, pH value, and substrate comprise the dynamic composition and functionality of microbial communities inside the composting system, ultimately determining how rapidly organic matter degrades, what nutrients are cycled, and the overall quality of the compost product (Hou, D., et al., 2017, Meng, Q., et al., 2019).

Functional Characteristics of Microbial Communities

The diversity and complexity of functional microbiota in composts are astounding, and their applications extend well beyond mere organic matter decomposition and nutrient recycling but also involve vital processes that establish an ecological balance. The metabolic pathways of bacterial communities are facilitated by the enzymatic functions that help in the degradation of complex organic molecules like cellulose, lignin, and proteins into simple breakdown products that can be utilized for microbial growth (Azizi, A., et al., 2023). Beyond that, some common groups of microbes are engaged in nutrient transport, which produces essential nutrients such as nitrogen, phosphorus, and potassium available for the plants to absorb. On the same note, the inhabitants of the microbial world stand in line for disease prevention through competitive interactions and the biosynthesis of antibomicrobial compounds, developing a stable and healthy compost ecosystem. More emphatically, the microbial functions in composite composts clearly illustrate how these communities play the most critical enzymatic role in the chemical reactions that account for soil fertility, plant growth, and ecosystem stability (Aguilar-Paredes, A., et al., 2023).

Role of Microbial Communities in Organic Matter Degradation

The microbial races are those that form the basis of the biological decomposition of the organic waste in composite composts by a network of enzymatic activities and metabolic processes in a complex manner. Such locales assemble a microbial assemblage with a wide spectrum of taxa containing enzymes that can perform many jobs related to organic compound degradation, such as breaking down cellulose, hemicellulose, lignin, proteins, or lipids. It is an array of silver-hue collections of bacteria, fungi, and actinomycetes, each of which has a unique enzymatic capability for a different substrate that is involved in the decomposition process. Even some bacteria are notable for their ability to split complicated polymers into small molecules, whereas a few species of fungi are marvelous at lignin metabolites, and actinomycetes are an important contributor to the breakdown of tough substances. The interplay of microbial communities in such a way facilitates the fabulous efficiency in the degradation of organic matter and triggers the availability and release of necessary nutrients and energy that sustain the growth of the microorganisms and the composting processes. Compost formula and bioprocesses are tightly interconnected, as the composition and functions of microbial residents in compost's microscopic environment create the tempo and level of organic matter decomposition, and thus the quality and nutrient content in the end-product of compost (Condron, L., et al., 2010).

Microbial Nutrient Cycling in Composting Processes

Here is a key factor in composting: it is the result of microbial communities having multiple species with different structures and functions that are involved in nutrient cycling in the compost. Microorganisms, which play a key role, would be involved and assist in the transformation and recycling process of the nutrients carbon, nitrogen, phosphorus, and sulfur available in that organic matter. The composting practice, in reality, causes less production of methane compared to the breakdown of those organic matters through the processes in which the microorganisms work to produce carbon dioxide. A nitrate and ammonium form is also created in the process, which would be available to plants to utilize. Taking the plus, the biological nitrogen fixation process by microorganisms is responsible for not just the process of nitrogen-fixing; it also endows atmospheric nitrogen compounds with nitrogen by converting ammonia into nitrogen. Microbial microorganisms convert phosphorus by containing phosphate in organic compounds that plants can assimilate. Nevertheless, ethylene-cycling microbes are the facilitators that carry out specific functions and enable the microbes to interact with biomass elements; in turn, the plants grow. Involvement of microorganisms with and without metals is an important factor for nitrogen and phosphorus cycling processes to be actively engaged in composting operations, leading to the upgrading of nutrient content in compost and thus helping in plant growth and soil fertility after its application (Liu, X., et al., 2023).

Contribution of Microbial Communities to Compost Stability and Maturity

The microbial community is responsible for quite a number of changes and developments that are needed for the complete degradation of waste materials and their conversion into a stable and nutrient-rich end product. During composting, the microorganisms mix their populations to convert the complex organic matter into components that are not easily utilized by the mold or microbes and produce soils that are stable and have great water-holding capacity. During this process, humic substances, a source of compost stability and a repository of carbon dioxide, are generated through the process of humification. Furthermore, microbial activities create heat during composting, which at the existent temperature can collaborate to kill weeds, pathogens, and phytotoxic compounds. Through succession, the microbial communities in compost undergo a shift, with populations found among microbes reacting to the degradation of hard-to-break compounds, i.e., recalcitrant compounds, gaining greater dominance. These microbial-driven processes in general contribute to the maintenance of compost stability and maturity, which are definitely characterized by reduced phytotoxicity, increased nutrient content, and enhanced soil conditioning properties, while concluding that the microbial communities play a seemingly outweighing role in composting (Aguilar-Paredes, A., et al., 2023 , Palaniveloo, K., et al., 2020).

Key Microbial Players in Composting

The array of key microbes that participate in composting are from these different taxa and perform different roles in organic matter breakdown and the nutrient cycle (Niazi, P., et al., 2023). A family of bacteria, which can be broadly categorized as *Bacillus, Pseudomonas*, and *Thermus genus*, is vital during the composting process. They can break down different organic substrates through metabolism and thrive in diverse conditions. Besides bacteria, fungi, in particular *Aspergillus*, *Penicillium*, and *Trichoderma*, are understood to play major roles in cellulosic fiber degradation, tearing complex polymers such as cellulose and lignin. *Actinomycetes*, including *Streptomyces* and *Actinomyces*, participate in the decomposition of resistant organic matter related to composting and produce the cells of extra ethylases involved in composting directly. These microorganisms, as well as archaea and protozoa, cooperate within complex microbial consortia that efficiently degrade organic matter and utilize the nutrients for a good-quality compost with appropriate stability and maturity.

This microscopic structure and its function contribute to the development of beneficial microbial communities in composite composts. It's this collective behavior of microbes that determines the quality and nutritional value of the finished compost products (Zhao, Y., et al., 2022).

Identification and Characterization of Key Microbial Taxa Involved in Composting

The isolation and characterization of microbial taxa from an aerated composting system manifests a diverse microbial community with multiple intricate functions in organic matter degradation and nutrient cycling. Bacteria constitute the prominent microbial community in composts, and this instigates the genera *Pseudomonas, Bacillus*, and *Thermus*, which prevail in these environments owing to their metabolic versatility and ability to thrive in different environmental conditions (Nadeem, H., et al., 2021). Different types of fungi, for instance, *Aspergillus, Penicillium*, and *Trichoderma* kinds, perform an important role in breaking down lignocellulose materials, converting complex polymers such as cellulose and lignin into their soluble form. The *actinomycetes,* which are represented by the Streptomyces species, constitute the group responsible for the decomposition of recalcitrant organic matter and excrete a wide variety of enzymes important to composting. Microbes such as bacteria, archaea, and protozoa are present and help the composting process, though they play a lesser role. These key bacterial taxa contribute to composting not only through efficient organic degradation and releasing nutrients into the soil but also through improvements in compost stability and uniformity. They highlight the importance of microbial recycling and soil health management through composting. (Wang, Y., et al., 2020, Yang, Z., et al., 2021).

Functional Roles of Dominant Microbial Species/Groups in Compost Ecosystems

The root microorganisms that prevail in the compost ecosystem as the predominant species have well-differentiated structural and functional characteristics, which they collectively act on to accelerate the decomposition rate of organic matter and cycle the nutrients. Bacteria known for their unicellular structure have a great capability of degradation, which defines their function of decomposing complex organic molecules such as cellulose and lignin while also taking charge of pH regulation across their metabolic activities. Fungi, with their multi-cell structure and filamentous hyphae, have evolved to be among the best in the world at breaking lignin, which is the most recalcitrant part of plant, humus, and mycorrhizal association formation, which increases nutrient uptake and plant growth. The heterokonts, which have the properties of bacteria as well as fungi, play an important role in cellulose and lignin decomposition, produce antibiotics that will prevent microbial assault, and modify the soil's atom structure. Due to their highly diverse structure, protozoa (eukaryotic, one-celled organisms) feed on microbial populations by consuming and regulating nitrogen mineralization, providing the lowest level of microbial community hierarchical structure. Depending on dominant microorganisms living in compost ecosystems, communication between them enables the repurposing of organic matter, thus nourishing nutritive soils and providing the basis for responsible agriculture (Matheri, F., et al., 2023).

Interactions Among Microbial Populations and Their Impact on Composting Dynamics

The resident bacteria colony dynamics of the compost soil microenvironment are complicated and ever-transforming, and they facilitate composting activity greatly. In wastewater, bacteria, fungi, actinomycetes, and protozoa come together in complex communities that interrelate, consuming organic matter, and form the base of the food chain, which is made of bacteria and algae (Monib, A. W., et al., 2024). Being the fastest and most flexible organisms, bacteria are the first stage of biodegradation and fracture the initial big organic compounds into more simple forms. Fungus, especially the organism with lignin degradation and hyphal networks, along with bacteria, are other co-operators that boost the degradation process and formation of humus from the complex substances. *Actinomycetes,* together with cellulose and lignin decomposition, also play a role in antibiotics that can shape the community structure through inherent processes. Cyanobacteria, being secondary producers, are carbon fixers that fulfill multiple functions in the ecosystem; hence, they are termed ecosystem engineers. Through direct interactions, microbes are the conductors that ensure efficient transformation of organic materials, which are broken down into rich nutrient compost, thus underscoring the essential role of microbial communities in composting processes (Wang, P., et al., 2023).

Influence of Feedstock Composition on Microbial Communities

The microbial communities in compost sites are heavily influenced by the composition of the feedstock and, both structurally and functionally, by the composite of compost strengths. The decomposition rate of an organic material in the compost system will be affected by the feedstock nutrient concentration levels, carbon to nitrogen ratio, moisture content, and organic matter complexity, which will in turn illustrate the relevant niches and the metabolic activities of the microbes that inhabit the compost environment. Straw or wood chips, which contain a couple of high-carbon materials, are very good soil amendments, and they can be digested by soil microorganisms to release carbon, while the main nitrogen source, like manure, can increase the growth of nitrogen-utilizing microbes (Monib, A. W., et al., 2023). The kind and structure of available nutrients and substrates in the feedstocks directly affect the population, abundance, and community composition of microorganisms. For the practical dimension, there are specific actions taken by microbial communities, i.e., they utilize the metabolic processes to expedite bio-degradation, ultimately altering the compost maturity, nutrient cycling efficiency, and the quality of the compost. Consequently, the communion of microbial systems with feedstock composition has great significance for compost transformation processes and for producing high-grade compost (Blasco, Let al., 2022).

Effects of Different Feedstock Materials on Microbial Community Composition and Function

Microbial communities of compost mixes under different feedstock materials are complex due to the diversity of metabolic capabilities and specific ecological preferences of the microbes involved in the process. Fodder materials having varying carbon-to-nitrogen ratios, like green waste, animal manures, or agricultural residues, are responsible for a variety of selective pressures on microbial commute, so that due to diverse community composition and traits, community functions get varied. An example is the case where the presence of carbohydrate-rich materials such as straw or sawdust increases the numbers of cellulolytic bacteria and lignin-degrading fungi. As a result, the decomposition rate of organic matter is increased, and humus formation is enhanced. Manure is full of nitrogen, which boosts the soil with nitrogen-fixing bacteria or fungi to speed up soil enrichment and boost the compost with bioavailable nitrogen salts. Dried-up community competitiveness, influenced by the alternations of microbial community structure, spills over to functional diversity and causes the variation of decomposition kinetics, nutrient transformation pathways, and fertilization effects—the key factors determining the characteristics of the compost product. In this respect, feedstock materials are of utmost importance as they form the basis for microbial communities' composition and diversity in composite composts, thereby having an impact on the composting effectiveness and the final production's suitability for any agricultural or gardening purposes (Lv, Z., Chen, et al., 2019).

Strategies for Optimizing Composting Processes Based on Feedstock Characteristics

The role of various substrates in reshaping the structure and function of complex microbial communities is diverse, as organisms possess specific metabolic strategies and environmental preferences. For instance, feedstock raw materials with varying C:N ratios, like green waste, animal manure, or agriculture residues, are responsible for differential regulation of the microbial communities under which the microorganisms of different gene compositions and functional properties prevail. For example, the biodegradation of lignocellulosic biomasses that are rich in carbon, like straws or sawdust, stimulates the development of cellulolytic microorganisms and lignin-dehydrogenizing fungi, whose roles are to increase the formation of humus. On the other hand, manure is regarded as a nitrogen-loading type that causes the development of nitrogen-eating bacteria (bacteria or fungi), and through their existence, the process of N-cycling is accelerated and the compost is enriched with bioavailable N-compounds. These changes in microbial community structure result in expanding functional diversity, and therefore, not only the speed of decomposition but also the ways of nutrient cycling and the general quality and stability of the resulting compost are affected. This enables the tailoring of microbial communities in composite composts through the choice of feedstock material quantity as well as quality, and this in turn has a bearing on the ultimate composting performance and thereby determines the suitability of the end compost for agriculture as well as horticultural uses (Reyes-Torres, M., et al., 2018).

Environmental Factors Shaping Microbial Communities

Composite composts, with their strong microbial populations, put the role of environmental factors at the forefront of their making because of their beneficial effects on the elements and interactions for biophysical properties known as structure and function. The complex relationship among abiotic elements, including temperature, moisture, pH, oxygen, and nutrient content, markedly affects the types, numbers, and activity of microbes outside of the composting habitat. Between every couple of phases, we will be able to tell the temperature fluctuations by studying the metabolic rate of microorganisms. The faster high-temperature organisms are dominant during the thermophilic phase; these break down complex organic matter. Moisture level variations affect microbe activity as well as the accessibility of substrates, whereas pH level regulation ensures the type of microbe communities and enzymatic processes. Moreover, oxygen availability samples determine whether it is oxidation or fermentation, the evidence of which pathway occurs, and the nature of the products. The variety and abundance of nutrient sources such as carbon, nitrogen, and phosphorus determine the microbial growth rate, community structure, and microbial efficiency of organic matter degradation and nutrient transformations during composting. Environmental factors also play a collective role in building up the compositional structures of microbial communities in compost composts, which ultimately affects the composting process and the finished product quality (Wu, Z., et al., 2018).

Impact of Temperature, Moisture, pH, and Aeration on Microbial Community Dynamics

The microbial community dynamics in composite composts react to environmental factors, such as temperature, moisture, pH, and aeration, on a structural and functional level. Temperature regimes result in limited microbial metabolisms, with thermophilic bacteria being at their growth peak during the hot-temperature state, thereby precipitating the degradation of organic matter and the spread of heat-resisting microorganisms (Monib, A. W., et al., 2023). The portion of moisture content is highly crucial for microbial activity as well as the availability of fillers for enzymatic reactions and uptake of nutrients, while the exorbitant amount of moisture leads to an anaerobic condition and hence reduces the aerobic decomposition processes. Microbial community interactions and enzymatic function depend on pH levels, which are typically slightly alkaline for microbial activity to oxidize most organic matter (Niazi, P., et al., 2023). Proper aeration guarantees access to oxygen. The process of aerobic decomposition occurs, and aerobic microbial development is encouraged, whereas in cases of poor aeration, anaerobic conditions are created. Anaerobic conditions lead to changes in microbial dynamics, with compost maturation and biomass decomposition processes delayed. In regards to composite composts, these environmental factors collectively act dynamically to form the compositional, biomass, and hormesis of microbially associated communities, which finally decide the speeds and directions of organic matter disintegration and of nutrient cycle operations (Ge, M., et al., 2022,: Ma, T., et al., 2022).

Strategies for Controlling Environmental Parameters to Promote Desired Microbial Activities in Composting

Controlling microbes through the use of appropriate strategies for environmental management will create ideal conditions for desirable activities of microbes during composting and increase the structural and functional features of microbial populations in composted manure. The heat management practice is geared towards recording and maintaining temperatures favorable enough for the growth of thermophilic microbinz throughout the two phases, with the thermophilic phase being focused, therefore enhancing the degradation of complex organic matter. Managing the preferred moisture level is very important and successful only when microbial activity and substrate accessibility are ensured. This can be done through monitoring the moisture level periodically and either when the necessary addition of moisture or drainage is performed. The acid-base (PH) adjustment does allow for creating a specific microbial-friendly environment, and certain additives like lime and sulfur can be used to make compost pH more suitable. In cases of inadequate aeration, aerobic decomposition would be impeded by anaerobic conditions, which are unfavorable for microorganisms. The best way to achieve this is by turning the compost regularly or through mechanical aeration, which enhances the process of oxygen diffusion in the composting mass. These measures can be used to control environmental factors in such a way that they facilitate the occurrence of the desired microbial activity as well as its efficiency during the composting process, which then leads to the production of a high-quality compost (Andraskar, J., et al., 2021).

Application of Molecular Techniques in Studying Microbial Communities

The application of molecular approaches in the characterization of the microbiota of compost materials through the use of sodocompost technology and its molecular techniques generates unique data that gives a picture of the structure and function of these microbes within such materials. For example, next-generation sequencing (NGS) helps in doing a high-resolution analysis of the microbial diversity in the compost, which enables the identification and quantification of different microbial taxa present in certain mixtures. Metagenomic and metatranscriptomic procedures give us an understanding of the functions of microbial society and its parts, revealing the contribution of these microbial communities to organic matter degradation, nutrient cycling, and fermentation processes. Moreover, polymerase chain reaction (PCR) allows for the detection of individual groups of microorganisms or functional genes of interest that are involved in crucial degradation steps and the follow-up of microbial group dynamics in response to environmental changes. These molecular methods allow researchers to unveil the complex interactions that exist between the microorganisms involved, the environmental conditions, and the popularity of compost production, paving the way for improved strategies for the production of soil-improving composts (Heisey S, et al., 2022).

Advantages and Limitations of Molecular Techniques in Compost Microbiome Research

The molecular techniques exhibit several aspects of preference in microbiome studies of compost, including sensitivity and a special ability to detect and count scant microbial taxa or functional genes that are crucial for the composting process. In addition, the said techniques are considered independent of culture, allowing for the identification of microbial communities that do not necessarily require labor-intensive isolation and cultivation methods. The use of molecular tools allows scientists to show intricate microbial interactions and biochemical pathways happening inside the microbial community, which become better understood structurally and functionally. On the other hand, one has to take into consideration the accuracy and applicability of the results that are affected during DNA extraction, amplification, and sequencing processes, which may later serve as a basis for subsequent findings and interpretations. Additionally, molecular tools may necessitate the use of complex instrumentation, competent manpower, and adequate bioinformatic facilities, which is and remains a great problem for the researchers that have no access. Even though the described limitations characterize the molecular approaches of microbial community studies and the optimization of composting procedures, molecular approaches remain important and trustworthy tools for the study and advancement of microbial communities in compost and for proper control of the composting process (Bhatia, A., et al., 2015).

Implications for Compost Management and Utilization

The ability to identify the molecular and mechanical variables of microbial communities within multi-component composts is crucial to the regulation and usage of such compost practices. By shedding light on the principal microorganisms and the metabolic ways involved in organic matter disintegration for the utilization of nutrient processes, this knowledge thus increases the utilization of targeted interventions for optimizing composting efficiency and the resultant high-quality composts. The techniques for regulating environmental processes, including temperature, moisture, pH, and air provision, can be individually modified based on the development of microbial communities and, therefore, increase the rate of composting. For example, information on the composition and function of microbial communities allows designers to select the right composting additives or inoculants to stimulate faster digestion of organic matter or to make up for any deficiencies in nutrients. Eventually, the comprehension of the microbiomes from compost helps to have sustainable waste management, efficient nutrient recycling, and the production of different types of compost with wide applications in agriculture, horticulture, and finally, the conservation and protection of resources in the environment (Ayilara, M. S., et al., 2020).

Utilization of Microbial Community Data for Optimizing Composting Processes

The utilization of microorganism community data in the management of composting processes requires extracting knowledge from the microorganism community's structural and functional features within compost products to produce composting efficiency and quality as the outcome. Through the examination of microbial diversity, abundance, and activity characteristics, as well as the expression of functional genes, the compost managers can be able to pick essential microbial taxa and metabolic pathways that determine organic matter degradation and nutrient cycling. This data facilitates us to take hold of the turning levers of environmental elements, such as temperature, moisture, pH, and aeration, whereupon we might be able to derive the appropriate milieu for the desirable microbial activity and thereby shorten the composting period. Also, data from microbial communities can support the choice of composting amendments or adding microbial cells that are beneficial in increasing the activity of preferable pathways or can be used to treat imbalanced nutrients, ending up with an improvement in compost quality and nutrition (Ozturk, H., et al., 2023). Through the incorporation of microbial communities into the composting management system, stakeholders will achieve a holistic, sustainable approach to waste management, minimize the impact on the environment, and produce compost with a variety of agricultural as well as horticultural applications (Senadheera, U. E., et al., 2023).

Strategies for Enhancing Compost Quality and Efficacy Based on Microbial Insights

The implementation of strategies of compost quality switching and improving through the utilization of microbial features and the understanding of microbial communities within composite composts focused on the structural, ecological, and metabolic traits of these communities is the basis of these strategies. Compost managers can achieve this by understanding how the main microbial taxa and metabolic pathways are driving organic matter decomposition and nutrient cycling. With this information, compost managers can determine what approaches can enhance the performance of their composting activities. These entail quietly adjusting environmental parameters such as temperature, moisture, pH, and aeration to create beneficial conditions for the fast-growing microbes in order to quicken the composting rate and promote the production of immaculate compost (Monib, A. W., et al., 2023). Similarly, biological insights can be used to narrow composting conditions for the use of suitable composting additives, or microbial inoculants that help to advance certain composting pathways and resolve nutrient deficiencies to obtain a high-quality compost that is efficient in different organic farming and gardening processes. Participating in microbiology in composting process control means the implementation of more effective steps aimed at waste revalorization, lowering negative impacts on the environment and fertile soil, as well as earth health and soil fertility management (Ayilara, M. S., et al., 2020).

Potential Applications of Compost Microbial Communities in Biotechnological and Agricultural Settings

Microbial communities in compost chemical entities have great potential for application in biotechnology and agriculture; their fields are varied and meaningful. Biotechnology engages microbial communities as a source of unique enzymes and elements, such as bioactive compounds, that are used in industries for environmental purification, biofuel production, and pharmaceuticals. The microbial populations involved in compost are rich in biofertilizers and biostimulants that can be used advantageously in agriculture to improve soil fertility, promote plant development, and enable stress tolerance. The knowledge of the microbial composition and their interactions in compost through structural and functional characteristics can be precisely applied to optimize them in biotechnology and agriculture by selecting specialized microbial consortia and engineering microbial strains for superior performance in the respective fields. The compost microbial communities have the potential to influence positive practices in the bioproduction and agriculture industries to a maximum. They will then contribute to the power of environmentally friendly matters to a significant extent (Jurado, M., et al., 2014, Yu, Z., Tang, J., et al., 2018).

Conclusion

The types of microorganisms living in the compost and their characteristics play a big role in how well the composting process works and what the final compost will be like. Knowing about the structure of microorganisms' communities, diversity, mass, and metabolic activities will help in the use of compost to its fullness, close nutrient loops, and make the compost higher quality. By using advanced techniques and understanding how microorganisms work, compost managers can adjust their methods to create the best conditions for the microbes they want to thrive. This helps speed up the breakdown of materials and make better compost, another big use of the microbial activity of compost is in biotechnological facilities as well as in agriculture, where the microorganisms are used to produce novel bioproducts, biofertilizers, and biostimulants, contributing to sustainable waste management and ecological farming, the review involving the structural and functional characterization of native microorganisms in compost microbial communities is the basis for the design of more efficient and eco-friendly technologies to process waste and manage soil fertility.

Funding

This research received no external funding.

References

Agrawal, P. K., Agrawal, S., & Shrivastava, R. (2015). Modern molecular approaches for analyzing microbial diversity from mushroom compost ecosystem. 3 *Biotech, 5*(6), 853-866. https://doi.org/10.1007%2Fs13205-015-0289-2

Aguilar-Paredes, A., Valdés, G., Araneda, N., Valdebenito, E., Hansen, F., & Nuti, M. (2023). Microbial Community in the Composting Process and Its Positive Impact on the Soil Biota in Sustainable Agriculture. *Agronomy, 13*(2), 542. https://doi.org/10.3390/agronomy13020542

Andraskar, J., Yadav, S., & Kapley, A. (2021). Challenges and control strategies of odor emission from composting operation. *Applied Biochemistry and Biotechnology, 193,* 2331-2356. https://doi.org/10.1007/s12010-021-03490-3

Ayilara, M. S., Olanrewaju, O. S., Babalola, O. O., & Odeyemi, O. (2020). Waste management through composting: Challenges and potentials. *Sustainability, 12*(11), 4456. http://dx.doi.org/10.3390/su12114456

Azizi, A., Mahboob, M., Monib, A. W., Hassand, M. H., Sediqi, S., & Niazi, P. (2023). The Role of Plants in Human Health. *British Journal of Biology Studies, 3(1), 08-12.* http://dx.doi.org/10.32996/bjbs.2023.3.1.2

Bhatia, A., Rajpal, A., Madan, S., & Kazmi, A. A. (2015). Techniques to analyze microbial diversity during composting—A mini review.

Blasco, L., Kahala, M., Ervasti, S., & Tampio, E. (2022). Dynamics of microbial community in response to co-feedstock composition in anaerobic digestion. *Bioresource Technology, 364,* 128039. https://doi.org/10.1016/j.biortech.2022.128039

Chandna, P., Nain, L., Singh, S., & Kuhad, R. C. (2013). Assessment of bacterial diversity during composting of agricultural byproducts. *BMC microbiology, 13*(1), 1-14. https://doi.org/10.1186/1471-2180-13-99

Condron, L., Stark, C., O'Callaghan, M., Clinton, P., & Huang, Z. (2010). The role of microbial communities in the formation and decomposition of soil organic matter. *Soil microbiology and sustainable crop production,* 81-118. http://dx.doi.org/10.1007/978-90-481-9479-7_4

Ding, J., Wei, D., An, Z., Zhang, C., Jin, L., Wang, L., & Li, Q. (2020). Succession of the bacterial community structure and functional prediction in two composting systems viewed through metatranscriptomics. *Bioresource Technology, 313,* 123688. https://doi.org/10.1016/j.biortech.2020.123688

Ge, M., Shen, Y., Ding, J., Meng, H., Zhou, H., Zhou, J., & Liu, J. (2022). New insight into the impact of moisture content and pH on dissolved organic matter and microbial dynamics during cattle manure composting. *Bioresource Technology, 344,* 126236. https://doi.org/10.1016/j.biortech.2021.126236

He, Y., Xie, K., Xu, P., Huang, X., Gu, W., Zhang, F., & Tang, S. (2013). Evolution of microbial community diversity and enzymatic activity during composting. *Research in microbiology, 164*(2), 189-198. https://doi.org/10.1016/j.resmic.2012.11.001

Heisey, S., Ryals, R.A., Maaz, T.M., & Nguyen, N.H. (2022). A Single Application of Compost Can Leave Lasting Impacts on Soil Microbial Community Structure and Alter Cross-Domain Interaction Networks. *Frontiers in Soil Science*, 2, 749212. https://doi.org/10.3389/fsoil.2022.749212

Hou, D., Huang, Z., Zeng, S., Liu, J., Wei, D., Deng, X., & He, J. (2017). Environmental factors shape water microbial community structure and function in shrimp cultural enclosure ecosystems. *Frontiers in microbiology, 8,* 2359. https://doi.org/10.3389%2Ffmicb.2017.02359

Jurado, M., López, M. J., Suárez-Estrella, F., Vargas-García, M. C., López-González, J. A., & Moreno, J. (2014). Exploiting composting biodiversity: study of the persistent and biotechnologically relevant microorganisms from lignocellulose-based composting.

Bioresource technology, 162, 283-293. https://doi.org/10.1016/j.biortech.2014.03.145

Kuang, J., Huang, L., He, Z., Chen, L., Hua, Z., Jia, P., & Shu, W. (2016). Predicting taxonomic and functional structure of microbial communities in acid mine drainage. *The ISME journal, 10*(6), 1527-1539. https://doi.org/10.1038/ismej.2015.201

Li, L., Xu, M., Eyakub Ali, M., Zhang, W., Duan, Y., & Li, D. (2018). Factors affecting soil microbial biomass and functional diversity with the application of organic amendments in three contrasting cropland soils during a field experiment. *PLoS One, 13*(9), e0203812. https://doi.org/10.1371%2Fjournal.pone.0203812

Liu, X., Rong, X., Yang, J., Li, H., Hu, W., Yang, Y., & Zhang, J. (2023). Community succession of microbial populations related to CNPS biological transformations regulates product maturity during cow-manure-driven composting. *Bioresource Technology, 369*, 128493. https://doi.org/10.1016/j.biortech.2022.128493

Luepke, K. H., & Mohr, J. F., 3rd (2017). The antibiotic pipeline: reviving research and development and speeding drugs to market. *Expert review of anti-infective therapy*, *15*(5), 425–433. https://doi.org/10.1080/14787210.2017.1308251

Lv, Z., Chen, Z., Chen, X., Liang, J., Jiang, J., & Loake, G. J. (2019). Effects of various feedstocks on isotope fractionation of biogas and microbial community structure during anaerobic digestion. *Waste Management, 84,* 211-219. https://doi.org/10.1016/j.wasman.2018.11.043

Ma, T., Zhan, Y., Chen, W., Xu, S., Wang, Z., Tao, Y., & Wei, Y. (2022). Impact of aeration rate on phosphorus conversion and bacterial community dynamics in phosphorus-enriched composting. *Bioresource Technology, 364,* 128016. https://doi.org/10.1016/j.biortech.2022.128016

Matheri, F., Kambura, A. K., Mwangi, M., Ongeso, N., Karanja, E., Adamtey, N., & Runo, S. (2023). Composition, structure, and functional shifts of prokaryotic communities in response to co-composting of various nitrogenous green feedstocks. *BMC microbiology, 23*(1), 50. http://dx.doi.org/10.1186/s12866-023-02798-w

Meng, Q., Yang, W., Men, M., Bello, A., Xu, X., Xu, B., & Zhu, H. (2019). Microbial community succession and response to environmental variables during cow manure and corn straw composting. *Frontiers in microbiology, 10,* 529. https://doi.org/10.3389/fmicb.2019.00529

Monib, A. W., Niazi, P., & Sediqi, S. (2023). Investigating Approaches for Optimizing Agricultural Yield: A Comprehensive Review of the Crucial Role of Micronutrients in Enhancing Plant Growth and Maximizing Production. *Journal for Research in Applied Sciences and Biotechnology*, *2*(5), 168-180. https://doi.org/10.55544/jrasb.2.5.26

Monib, A. W., Alimyar, O., Mohammad, M. U., Akhundzada, M. S., & Niazi, P. (2023). Macronutrients for Plants Growth and Humans Health. *Journal for Research in Applied Sciences and Biotechnology*, *2*(2), 268-279. https://doi.org/10.55544/jrasb.2.2.38

Monib, A. W., Niazi, P., Barai, S. M., Sawicka, B., Baseer, A. Q., Nikpay, A., ... & Thea, B. (2024). Nitrogen Cycling Dynamics: Investigating Volatilization and its Interplay with N2 Fixation. *Journal for Research in Applied Sciences and Biotechnology*, *3*(1), 17-31. http://dx.doi.org/10.55544/jrasb.3.1.4

Monib, A. W., Niazi, P., Azizi, A., Sediqi, S., & Baseer, A. Q. (2024). Heavy Metal Contamination in Urban Soils: Health Impacts on Humans and Plants: A Review. *European Journal of Theoretical and Applied Sciences*, *2*(1), 546-565. http://doi.org/10.59324/ejtas.2024.2(1).48

Niazi, P., Hekmatullah, Z., Mohammad, M. U., Monib, A. W., Hassand, M. H., Ozturk, H., ... & Alimyar, O. (2023). Biochar as a Fertilizer Replacement for Sustainable Agriculture. *Journal for Research in Applied Sciences and Biotechnology*, *2*(4), 8-18. https://doi.org/10.55544/jrasb.2.4.2

Niazi, P., Monib, A. W., Ozturk, H., Mansoor, M., Azizi, A., & Hassand, M. H. (2023). Review on Surface Elements and Bacterial Biofilms in Plant-Bacterial Associations. *Journal for Research in Applied Sciences and Biotechnology*, *2*(1), 204-214. http://dx.doi.org/10.55544/jrasb.2.1.30

Niazi, P., Alimyar, O., Azizi, A., Monib, A. W., & Ozturk, H. (2023). People-plant Interaction: Plant Impact on Humans and Environment. *Journal of Environmental and Agricultural Studies*, *4*(2), 01-07. http://dx.doi.org/10.32996/jeas.2023.4.2.1

Niazi, P., Monib, A. W., & Azizi, A. (2023). A Review on Plants and Plant/Microbial Systems in Reducing Exposure. *Journal for Research in Applied Sciences and Biotechnology*, *2*(2), 1-7. http://dx.doi.org/10.55544/jrasb.2.2.1

Nadeem, H., Niazi, P., Asif, M., Kaskavalci, G., & Ahmad, F. (2021). Bacterial strains integrated with surfactin molecules of Bacillus subtilis MTCC441 enrich nematocidal activity against Meloidogyne incognita. *Plant Biology*, *23*(6), 1027-1036. https://doi.org/10.1111/plb.13301

Ozturk, H., Niazi, P., Mansoor, M., Monib, A. W., Alikhail, M., & Azizi, A. (2023). The Function of Zinc in Animal, Plant, and Human Nutrition. *Journal for Research in Applied Sciences and Biotechnology*, *2*(2), 35-43. https://doi.org/10.55544/jrasb.2.2.6

Palaniveloo, K., Amran, M. A., Norhashim, N. A., Mohamad-Fauzi, N., Peng-Hui, F., Hui-Wen, L., & Razak, S. A. (2020). Food waste composting and microbial community structure profiling. *Processes, 8*(6), 723. https://doi.org/10.3390/pr8060723

Reyes-Torres, M., Oviedo-Ocaña, E. R., Dominguez, I., Komilis, D., & Sánchez, A. (2018). A systematic review on the composting of green waste: Feedstock quality and optimization strategies. *Waste management, 77,* 486-499. https://doi.org/10.1016/j.wasman.2018.04.037

Sánchez, Ó. J., Ospina, D. A., & Montoya, S. (2017). Compost supplementation with nutrients and microorganisms in composting process. *Waste management, 69,* 136-153. https://doi.org/10.1016/j.wasman.2017.08.012

Senadheera, U. E., Jayasanka, J., Udayanga, D., & Hewawasam, C. (2023). Natural and designer cellulosomes: A potential tool for enhancing microbial additive-mediated lignocellulosic agricultural waste composting. B*ioresource Technology Reports, 25,* 101695. https://doi.org/10.1016/j.biteb.2023.101695

Singh, P., Jain, K. R., Lakhmapurkar, J., Gavali, D., Desai, C., & Madamwar, D. (2022). Microbial community structure and functions during chronosequence-based phytoremediation programme of Lignite tailing soil. *Environmental Technology & Innovation, 27,* 102447. https://doi.org/10.1016/j.eti.2022.102447

Wang, P., Han, S., & Lin, Y. (2023). Role of microbes and microbial dynamics during composting. In *Current Developments in Biotechnology and Bioengineering* (pp. 169-220). Elsevier.

Wang, Y., Liu, L., Yang, J., Duan, Y., Luo, Y., Taherzadeh, M. J., & Zhao, Z. (2020). The diversity of microbial community and function varied in response to different agricultural residues composting. *Science of the Total Environment, 715,* 136983. https://doi.org/10.1016/j.scitotenv.2020.136983

Wei, H., Wang, L., Hassan, M., & Xie, B. (2018). Succession of the functional microbial communities and the metabolic functions in maize straw composting process. *Bioresource technology, 256,* 333-341. http://dx.doi.org/10.1016/j.biortech.2018.02.050

Wu, Z., Liu, Q., Li, Z., Cheng, W., Sun, J., Guo, Z., & Yin, H. (2018). Environmental factors shaping the diversity of bacterial communities that promote rice production. *BMC microbiology, 18*(1), 1-11. https://doi.org/10.1186/s12866-018-1174-z

Yang, Z., Chen, Z., Lee, K., Owens, E., Boufadel, M. C., An, C., & Taylor, E. (2021). Decision support tools for oil spill response (OSR-DSTs): Approaches, challenges, and future research perspectives. *Marine Pollution Bulletin, 167,* 112313.

http://dx.doi.org/10.1016/j.marpolbul.2021.112313

Younis, A., Ahsan, M., Akram, A., Lim, K. B., Zulfiqar, F., & Tariq, U. (2022). 9 Use of Organic Substrates in Sustainable Horticulture. Biostimulants for crop production and sustainable agriculture/Mirza Hasanuzzaman, 122.

Yu, Z., Tang, J., Liao, H., Liu, X., Zhou, P., Chen, Z., & Zhou, S. (2018). The distinctive microbial community improves composting efficiency in a full-scale hyperthermophilic composting plant. *Bioresource technology, 265,* 146-154. https://doi.org/10.1016/j.biortech.2018.06.011

Zhao, Y., Zhuge, C., Weng, Q., & Hu, B. (2022). Additional strains acting as key microbes promoted composting process. *Chemosphere*, *287*(3), 132304. https://doi.org/10.1016/j.chemosphere.2021.132304