MALAYSIAN JOURNAL OF SCIENCE
MJS
ISSN 1394-3065

Regular Issue

Malaysian Journal of Science 44 (2): 86-103 (June 2025)
https://mjs.um.edu.my

Exploring Fertilizer-Microbiome Interactions Through Next-Generation Sequencing (NGS): Insights for Sustainable Agriculture

Mohd Khairil Radzali[1a], Amalia Mohd Hashim[2ab], Miratul Hada Mohd Ali[3a], Wan Zuhainis Saad[4a]*, Zakiah Anis Nawawi[5a]

Abstract: With the global demand for food production escalating, concerns about the long-term sustainability and environmental impact of traditional farming practices, particularly the application of chemical fertilizers, have gained prominence. Recognizing the importance of addressing these issues, this review explores the evolving dynamic between fertilizers and microbial communities, emphasizing the need for a more profound understanding of these interactions. The transformative impact of next-generation sequencing (NGS) technologies in unraveling microbial intricacies within agricultural ecosystems is highlighted as a crucial tool for advancing this understanding. Investigation extends to discerning the nuanced effects of both chemical and non-chemical fertilizers on soil microbiomes, considering variations in soil type and crop specificity. Linking these findings to the Sustainable Development Goals (SDGs), the review highlights the critical connection between fertilizer use, microbial diversity, and the achievement of sustainability objectives. Despite the potential of NGS, the review acknowledges current limitations, sparking discussions on potential technological advancements and methodological improvements. Emphasizing the necessity for interdisciplinary collaboration, it advocates for comprehensive insights that bridge gaps between microbiology, agriculture, and sustainability. In conclusion, the article synthesizes historical perspectives, cutting-edge technologies, and sustainable development objectives to provide a holistic understanding of the intricate interplay between fertilizers, microbial diversity, and the imperative path toward a more sustainable agricultural future.

Keywords: *Fertilizers, microbial diversity, sustainable agricultural practices, next-generation sequencing (NGS) technologies, sustainable development goals (SDGs)*

1. Introduction

Background

Agriculture is the backbone of human civilization, providing sustenance, economic stability, and a foundation for societal development. Its global significance is indisputable, as it not only supports the basic human need for food but also fuels economies (Shen et al., 2023), shapes landscapes (Martello et al., 2023), and influences cultural identities (Zheng et al., 2023). The unprecedented growth of the world's population and the escalating demand for food resources have intensified the pressure on agricultural systems, necessitating innovative approaches to ensure sustainable food production.

At the core of modern agricultural practices lies the pivotal role of fertilizers. Fertilizers have become vital tools for farmers seeking to enhance crop yields and meet the escalating demands of a growing population (Mustafa et al., 2023). These chemical and non-chemical formulations offer valuable nutrients to plants, augmenting soil fertility and addressing nutrient deficiencies. While fertilizers have played a critical role in boosting agricultural productivity, their widespread use has raised concerns about environmental impact, including soil acidification, greenhouse gas emissions, depletion of the ozone layer, and loss of biodiversity (Bai et al., 2020; Mustafa et al., 2023). As we delve into the intricate relationship among fertilizers and microbial communities, it becomes apparent that a nuanced understanding of these dynamics is essential for sustainably shaping the future of agriculture. This review investigates the transformative potential of Next Generation Sequencing (NGS) in unraveling the complex interplay between fertilizers and microorganisms, offering insights that can pave the way for achieving Sustainable Development Goals (SDGs) in agriculture.

Rationale for the Review

The escalating global demand for food production drives the imperative to reassess and optimize agricultural practices. With the world's population steadily climbing, the need for increased food yields places unprecedented pressure on the agricultural sector. This heightened demand necessitates a critical evaluation of existing farming methods to ensure both quantity and the quality and sustainability of our food supply. Simultaneously, the reliance on conventional fertilizers has sparked environmental and sustainability challenges that cannot be ignored. Runoff from these chemical inputs contributes to water pollution, adversely

Authors information:
[a]Department of Microbiology, Faculty of Biotechnology and Biomolecular Sciences, Universiti Putra Malaysia, 43400, Serdang, Selangor, MALAYSIA. E-mail: gs50774@student.upm.edu.my[1]; amalia@upm.edu.my[2]; miratulali@gmail.com[3]; mohdtermizi@upm.edu.my[4]; zuhainis@upm.edu.my[5]; zakiahanisnawawi@gmail.com[6]
[b]Halal Produt Research Institute, Universiti Putra Malaysia, 43400, Serdang, Selangor, MALAYSIA. E-mail: amalia@upm.edu.my[2]
*Corresponding Author: zuhainis@upm.edu.my

Received: January, 2024
Accepted: July, 2024
Published: June, 2025

DOI: https://doi.org/10.22452/mjs.vol44no2.9

impacting aquatic ecosystems, while the accumulation of excess nutrients in the soil can lead to degradation and long-term loss of fertility (AbdelRahman et al., 2022; Li et al., 2022a). Addressing these challenges requires a major shift towards more environmentally conscious and sustainable agricultural practices.

Amidst these challenges, the introduction of NGS emerges as a transformative tool to deepen our understanding of microbial dynamics in agriculture. NGS technologies, including both shotgun and amplicon sequencing, enable researchers to investigate the genetic landscapes of microbial communities, offering unparalleled insights into their composition, diversity, and functional potential (Liu et al., 2021a; de Vries et al., 2023; Maretto et al., 2023; Tang et al., 2023). It holds the promise of unraveling the complex relationships between fertilizers and microorganisms and guiding the development of sustainable agricultural practices for the future (Chouhan et al., 2023). This review aims to investigate the synergy between fertilizer use, microbial dynamics, and NGS technologies, highlighting on the path toward achieving Sustainable Development Goals in agriculture.

2. Fertilizers and Microbial Diversity: a Historical Perspective

Historically, the relationship between fertilizers and microorganisms has been focused primarily on nutrient provision to plants. Traditional agricultural practices often treated soil as a mere substrate for plant growth (Thompson, 1992; Lafaille, 2017), with little consideration for the intricate web of microbial life beneath the surface. While effective in boosting crop yields, this limited perspective failed to account for the broader ecological consequences of altering microbial ecosystems. It aimed to replenish essential nutrients without heavily understanding the dynamic interplay between these chemical inputs and the diverse microbial communities inhabiting the soil and plant root systems (Russel & Williams, 1977; Inubushi & Acquaye, 2004). However, the traditional mindset that viewed soil merely as a medium for plant growth is gradually transforming into a holistic approach that considers the soil as a living ecosystem (Ponge, 2015).

As agriculture evolved and intensified, the limitations of these traditional views became increasingly apparent that the indiscriminate use of chemical fertilizers led to soil degradation, negative impacts on microbial biodiversity, and environmental pollution (Feng et al., 2022; Mukhles et al., 2022; Wang et al., 2022; Nguyen et al., 2023). The emergence of these challenges underscored the need for a deeper understanding of the intricate relationships between fertilizers and microorganisms. The dynamic nature of microbial communities, their symbiotic relationships with plants, and their roles in nutrient cycling and soil health became focal points for researchers seeking sustainable agricultural solutions (Abid et al., 2021; Iqbal et al., 2023; Wei et al., 2023a; Zhang et al., 2023a). Acknowledging the complexity of these interactions is vital for mitigating the unintended consequences of fertilization and steering agricultural practices toward greater ecological resilience.

The historical shift towards environmentally-friendly agricultural practices, as highlighted in the Sustainable Development Goals (SDGs) and underscored by scholars like Dubey et al. (2021) and Shahmohamadloo et al. (2021), reflects a growing awareness of the complex interplay between human activities and the environment. This departure from historical practices, often focused solely on maximizing yields with little regard for long-term ecological consequences, is now characterized by a commitment to biodiversity conservation, climate resilience, and reducing ecological footprint. Aligning agricultural strategies with sustainable development objectives underscores a historical trajectory towards a more responsible and conscientious approach, recognizing the importance of integrating sustainable practices to ensure the long-term well-being of ecosystems and harmony between food production and ecological health preservation.

3. Next Generation Sequencing: Revolutionizing Agricultural Microbiology

The aim of sustainable agriculture relies on microbial diversity. These microscopic organisms, including bacteria, fungi, and archaea, contribute to soil fertility, nutrient cycling, and plant health (May et al., 2023; Xiang et al., 2023). A rich and diverse microbial community can enhance plant tolerance to soil salinity (Feng et al., 2023; Wang et al., 2023), suppress pathogenic organisms (Ehau-Taumaunu & Hockett, 2023; Yang et al., 2023a), and improve nutrient availability for plants (Arunrat et al., 2023; Li et al., 2023a). As the agricultural community recognizes the multifaceted benefits of microbial diversity, there is a growing shift towards holistic and regenerative practices that aim to maximize crop yields and foster long-term soil health.

NGS technologies have emerged as powerful tools, propelling agricultural microbiology into a new era of precision and depth. Two primary methodologies, shotgun and amplicon sequencing, form the cornerstone of NGS applications in studying microbial communities. Shotgun Sequencing involves the random sequencing of DNA fragments, providing a comprehensive snapshot of the entire genetic content present in a sample (Doni et al., 2023). Amplicon sequencing, on the other hand, targets specific gene regions such as 16S ribosomal RNA (16S) and Internal Transcribed Spacer (ITS), allowing for a more focused analysis of microbial diversity (Liu et al., 2021a). These approaches help researchers to investigate the genetic complexities of microbial communities with unprecedented resolution, shedding light on the composition, functional potential, and dynamics of these microscopic ecosystems (Liu et al., 2021a; de Vries et al., 2023; Maretto et al., 2023; Tang et al., 2023).

By unlocking the genetic codes of diverse microorganisms through NGS technologies, researchers can elucidate their roles in nutrient cycling, plant-microbe interactions, and overall soil health (Windisch et al., 2021; Kim et al., 2022; Xiang et al., 2023). NGS aids in the identification and quantification of microbial species, offering insights into their functional capabilities and interactions. By exploring the microbial ecosystems, NGS enables

DOI: https//doi.org/10.22452/mjs.vol44no2.9

the comprehensive analysis of microbial diversity at a scale and precision unattainable by traditional methods such as PCR-Denaturing Gradient Gel Electrophoresis (PCR-DGGE), Terminal Restriction Fragment Length Polymorphism (T-RFLP), and Fluorescent in Situ Hybridization (FISH) (Wolsing & Priemé, 2004; Caracciolo et al., 2005; Wenhui et al., 2007; Bokulich & Mills, 2012). This transformative capability extends beyond taxonomy, allowing a deeper understanding of the functional attributes governing microbial contributions to agricultural ecosystems.

The application of NGS in agricultural microbiology goes beyond mere taxonomic identification and explores the functional dynamics of microbial communities. Metagenomics, a primary application of NGS, enables the direct study of genomic material extracted from environmental samples, providing valuable insights into the functional potential of microbial communities (Tas et al., 2021). Metatranscriptomics further extends this capability by analyzing the actively expressed genes, allowing researchers to analyze real-time functional activities within microbial ecosystems (Mukherjee & Reddy, 2020). This understanding of genetic composition and functional activities empowers scientists to identify microbial contributions to nutrient cycling, disease suppression, and plant resilience (Chuckran et al., 2021; Mendes et al., 2023; Pande et al., 2023). The integration of metagenomic and metatranscriptomic data opens avenues for targeted interventions, allowing for the development of precision agricultural practices that leverage the specific functions of microbial communities to improve crop health and yield.

The shift from traditional to NGS-based approaches represents a paradigmatic leap in our capacity to assess microbial diversity. NGS offers several advantages over outdated conventional methods, including higher throughput, reduced cost per base pair, and the ability to detect rare and novel microbial taxa (Zhao et al., 2020; Adhikari et al., 2021; Greay et al., 2021). The technology's capacity to provide quantitative data on microbial abundances, community structures, and functional potentials in a single experiment is unparalleled (Hiiesalu et al., 2012; Azarbad et al., 2022). NGS minimizes biases inherent in cultivation-dependent methods, allowing for the identification of previously unculturable microorganisms (Chaudhary et al., 2019; Qaisrani et al., 2019; Sessou et al., 2023; Deinert et al., 2023). It is a transformative tool that broadens our understanding of microbial ecosystems and guides the development of targeted strategies for enhancing agricultural productivity and resilience toward sustainable practices.

4. Fertilizer Impact on Microbial Communities: Insights from NGS Studies

Chemical Fertilizers and Their Effects on Microbiomes

The widespread application of chemical fertilizers in modern agriculture has significantly changed the dynamics of soil microbial communities, prompting a closer examination of their impacts through the NGS. Chemical fertilizers, rich in nitrogen (N), phosphorus (P), and potassium (K), are known to influence soil pH, nutrient availability, and overall soil structure (Li et al., 2020a; Liu et al., 2020). However, the consequences of these alterations on microbial diversity and function have become increasingly apparent with the application of NGS technologies.

Apart from demonstrating an increase in the abundance of the denitrification-related gene nirK (Carrascosa et al., 2023), chemical fertilization exhibited an increased abundance of genes associated with methane oxidation, soil nitrogen degradation, nitrification, and anammox, emphasizing a distinct influence on nutrient cycling as shown by the 16S amplicon studies (Hu et al., 2022a). The NPK fertilization also positively influenced acidophilic groups, such as nitrifiers and denitrifiers, based on 16S and ITS amplicon sequencing, and concurrently increased the alpha diversity of arbuscular mycorrhizal (AM) fungi in the root endosphere (Semenov et al., 2020; Ma et al., 2021). According to Hu et al. (2022b), nitrogen (N) fertilization induced the saprotroph fungal functional group, which may suggest its potential role in decomposing and absorbing organic matter from dead or decaying organisms using the ITS sequencing approach.

Recent studies using shotgun metagenomic sequencing are further discussed and have revealed novel insights into how the taxonomic makeup of soil microorganisms changes when exposed to chemical fertilizers. High inorganic nitrogen fertilizer led to higher relative abundance in Bacillaceae and Carnobacteriaceae families, while certain bacterial families like Pseudonocardiaceae, Clostridiaceae, Cytophagaceae, Micromonosporaceae, and others were relatively less abundant (Enebe & Babalola, 2021). Apart from increasing soil nutrient availability, excessive K2SO4 application in tobacco-planting soil increased copiotrophic groups such as Burkholderiaceae and Rhodospirillaceae families, as well as Ellin6067 genus, while negatively impacting oligotrophic taxa (Lu et al., 2022). Li et al. (2020b) found that applying NPK fertilizer reduced Proteobacteria and Bradyrhizobium at the genus level and increased Acidobacteria at the phylum level. In a separate study, Li et al. (2022b) reported that NPK fertilizer resulted in decreased Proteobacteria abundance, increased Actinobacteria abundance, the lowest Acidobacteria abundance, and the highest Chloroflexi abundance. Fadiji et al. (2020) found that using inorganic fertilizer (NK) led to the dominance of Dothideomycetes at the class level and endophytic Leptosphaeria at the genus level. Leptosphaeria sp. has been reported to promote plant growth by increasing root volume and plant tolerance to salinity and drought (Poveda, 2022; Zhao et al., 2024). These findings highlight the impact of nutrient changes on microorganisms, influencing specific groups that, in turn, can promote plant growth, emphasizing the potential for targeted approaches to enhance overall plant health and productivity.

These studies uncover previously overlooked microorganisms, revealing details of nutrient cycling, organic matter decomposition, and plant-microbe interactions. By integrating data from diverse ecosystems and crops, these investigations offer a complete understanding of the intricate connections between chemical fertilizers and microbial communities. This awareness aids in refining fertilizer applications, lessening environmental impact, and fostering robust and productive farming practices. The research also takes economic factors into

DOI: https://doi.org/10.22452/mjs.vol44no2.9

account, directing efforts toward cost-effective and sustainable approaches. Moreover, it addresses social considerations by advocating for microbiome-conscious agriculture, contributing to a more promising future.

Non-Chemical Fertilizers and Their Influence on Microbial Diversity

In contrast to chemical fertilizers, non-chemical alternatives, such as organic or bio-based fertilizers, have gained prominence in agricultural systems aiming for sustainability and reduced environmental impact. The impact of these non-chemical fertilizers on microbial diversity has become a focal point of the investigation, leveraging the capabilities of NGS to delve into the subtleties of microbial responses.

NGS studies have facilitated a signified comparative analysis of the impacts of non-chemical and chemical fertilizers on microbial diversity. By adopting a comparative approach, researchers have unraveled the intricate interactions between diverse fertilizer types and the soil microbiome, with multiple studies highlighting the beneficial effects of both organic matter and fertilizers on agriculture. Zhu et al. (2023a) found that composting enhances microbial diversity, promoting the activity of beneficial genera like Corynebacterium and Lactobacillus, while influencing nutrient cycling and emissions. Composting also showcases Marinimicrobium and Thermobifida's crucial roles in ammonia assimilation, highlighting the diverse microbial contributions (Zhu et al., 2023b). Moreover, bark compost boosts beneficial fungi, including Penicillium and Inocybe, with potential benefits for nutrient uptake and plant health (Malewski et al., 2023) whereas the combination of compost and citrus rootstocks significantly influences rhizobiome bacterial abundance and diversity, correlating with essential nutrient concentrations for plant health and productivity (Castellano-Hinojosa et al., 2023). Sophora alopecuroides L., or Kudouzi in China, traditionally used for medicinal purposes, is also employed as an organic fertilizer, enhancing sugar content and promoting beneficial microorganisms, as indicated by Hua et al. (2023).

Manure serves as an alternative to compost for organic fertilizer. Khatri et al. (2023) claim that green manure applications lead to higher microbial abundance, reduced disease development, and increased abundance of beneficial phyla, thereby contributing to sustainable agriculture. Erythrobacter sp. YH-07-inoculated organic manure enhances microbial diversity, suppresses Fusarium wilt, and alters community composition. This demonstrates its potential for disease control, as Tang et al. (2023) highlighted. Another finding reveals that Hanwoo manure positively impacts soil organic matter, crude ash, and phosphorus, providing a valuable alternative to chemical fertilizers (Lee et al., 2023). Lastly, implementing reduced tillage with green manure for a decade enhances soil organic carbon and total nitrogen, maintaining almond yields and promoting sustainability, albeit with changes in the bacterial community structure (Özbolat et al., 2023). These findings showcase their significant potential in fostering sustainable agriculture, enhancing soil health, and mitigating disease risks, emphasizing a promising shift towards eco-friendly farming practices.

One notable trend from the comparative studies is the potential for non-chemical fertilizers to foster greater microbial diversity than their chemical counterparts. Organic amendments, for instance, introduce a spectrum of organic matter that serves as a substrate for a diverse array of microorganisms (Saunders et al., 2012; Verma et al., 2020). This diversity, in turn, contributes to enhanced nutrient cycling, disease suppression, and overall soil health as discussed previously. The comparative insights gained from NGS studies not only inform on the immediate impacts of fertilizer choices but also provide a foundation for developing strategies that optimize microbial diversity in ways that align with sustainable development goals in agriculture (Meuniern & Bayır, 2021; Ashraf et al., 2022).

The Role of Soil Type and Crop Specificity in Shaping Microbial Communities

The relationships between fertilizers and microbial communities are not only influenced by the type of fertilizer. However, they are equally shaped by the unique characteristics of soil types and the specific crops being cultivated. NGS studies have been instrumental in elucidating the complex interplay between soil types, crop specificity, and the dynamic microbial ecosystems they harbor.

Understanding the impact of soil type on microbial communities is crucial, as various soils possess distinct physical and chemical properties that influence microbial life. NGS technologies have unveiled how microbial compositions respond differently to fertilizers in clayey, loamy, and sandy soils. High clay content in the soil offered enhanced physicochemical protection for microbial biomass pools and mitigated water stress, impacting the efficacy of N fertilization on soil microbial communities (Kallenbach & Grandy, 2011; Fierer et al., 2012; Yu et al., 2019). The 16S rRNA sequencing results indicated shifts in bacterial composition post-fertilization, which led to a decrease in the relative abundance of Chloroflexi, Acidobacteria, and Nitrospirae at the phylum level while increasing Proteobacteria and Actinobacteria (Liu et al., 2021b). The relative abundance of Gemmatimonadota and Firmicutes significantly increased with NPK treatments, accompanied by a decrease in Bacteroidetes (Chen et al., 2023).

On the contrary, sandy loam soils demonstrate a well-rounded capacity for water retention, stable structure formation, adequate aeration, and maintenance of a moderate soil temperature (Lakesh et al., 2022). Fertilizer applications resulted in a major shift in microbial composition, with a lower relative abundance of Bacteroidetes and elevated levels of Proteobacteria and Verrucomicrobia compared to the control (Zhang et al., 2022a). Meanwhile, fertilized sandy loam soils exhibit significant increases in Ambispora, Funneliformis, and Glomus, accompanied by a marked decline in Paraglomus at the genus level of the arbuscular mycorrhizal fungal community (Liu et al., 2022). These findings collectively highlight the multifaceted impact of fertilization on microbial attributes, influencing bacterial and fungal communities in different soil types.

In addition, the crop specificity of microbial communities adds another layer of complexity to the fertilization equation in the NGS studies. A study by Zhang et al. (2023b) reveals that rotating rice and oilseed rape crops significantly enhances soil microbes, particularly those associated with nitrogen, phosphorus, and overall soil quality. A similar study on crop rotation of peppers and eggplants created helpful microbes that protected bananas from diseases, aiding in sustainable banana farming (Hong et al., 2023). Compared to annually rotated crops, corn and soybean crops influenced bacterial communities differently, with grass cover crops having minimal impact, emphasizing the greater role of soil pH and organic matter for bacteria (Chamberlain et al., 2020).

Biochar had different effects on wheat and mash bean soils, increasing specific genes in both, with wheat showing an additional gene increase; the crop type played a major role in how biochar and fertilizer influenced microbes in mash bean soils (Azeem et al., 2020). A study by Woo et al. (2022) found that pea farming clearly reduced microbe diversity compared to wheat, pea-wheat rotations, and fallow fields, impacting diverse fungi, and influencing nitrogen, water, as well as both beneficial and harmful fungi in the Canadian prairies. Consequently, the choice of fertilizer can exert variable effects on microbial communities based on the specific crop it is intended for (Dincă et al., 2022; Gupta et al., 2022; Williams et al., 2023). Integrating crop-specific insights from NGS studies into fertilizer management can enhance nutrient uptake, disease resistance, and overall crop performance. These studies offer a roadmap for customizing agricultural practices based on the intricate relationships among fertilizers, soil types, and crop specificity. This holistic approach acknowledges unique microbial dynamics in diverse agroecosystems, which are crucial for creating sustainable and resilient agricultural systems in the face of global challenges.

5. Sustainable Development Goals (SDGS) and Agricultural Microbial Diversity

Linking Fertilizer Use, Microbial Diversity, and SDGs

The intersection of fertilizer use, microbial diversity, and the ambitious targets set by the SDGs forms a critical nexus in pursuing a more sustainable and equitable global agriculture (Figure 1). Fertilizers, both chemical and non-chemical, play a pivotal role in meeting the SDG mandate to eradicate hunger (SDG 2) by bolstering crop yields (Heidkamp et al., 2021; Saqib et al., 2020; Ishfaq et al., 2023). However, the implications of fertilizer use extend beyond mere productivity, resonating with several other SDGs that collectively underscore the need for holistic and environmentally responsible agricultural practices (United Nations, 2023).

Microbial diversity emerges as a linchpin in achieving these broader sustainability goals. NGS studies have illuminated the intricate relationships between fertilizers and microbial communities, revealing their profound impact on soil health, nutrient cycling, and ecosystem resilience (Ma et al., 2023; May et al., 2023; Xiang et al., 2023). Recognizing the symbiotic alliances between plants and microorganisms facilitated by appropriate fertilization (Li et al., 2023b) aligns with SDG 15 (Life on Land), promoting the conservation, restoration, and sustainable use of terrestrial ecosystems (Kumawat et al., 2023). Moreover, fostering microbial diversity through judicious fertilizer management contributes to SDG 13 (Climate Action) by enhancing soil carbon sequestration and mitigating greenhouse gas emissions (Jiang et al., 2021; Zhou et al., 2022). The potential to reduce agriculture's environmental footprint while simultaneously increasing its productivity positions microbial-conscious fertilization as a key player in the global effort to combat climate change.

Furthermore, the relationship between fertilizer use, microbial diversity, and the SDGs extends into water resource management, aligning with SDG 6 (Clean Water and Sanitation). Proper fertilization practices that promote microbial diversity contribute to enhanced water retention in soils (Wang et al., 2021; Xu et al., 2023a), reducing the risk of nutrient runoff and contamination of water bodies (Menzies Pluer et al., 2020). By mitigating water pollution and ensuring sustainable water use in agriculture, this integrated approach addresses a critical aspect of the SDGs related to clean and accessible water. Implementing microbial-conscious fertilization supports agricultural productivity and safeguards vital water resources, marking a significant stride towards achieving the broader agenda of sustainable development.

Linking fertilizer application, microbial diversity, and SDGs demonstrates the need for an integrative approach to agricultural practices. Harnessing the insights gleaned from NGS studies, this linkage provides a pathway for sustainable intensification, ensuring that the gains in crop production are harmonized with environmental conservation, social equity, and the overarching objectives of the Sustainable Development Agenda.

DOI: https//doi.org/10.22452/mjs.vol44no2.9

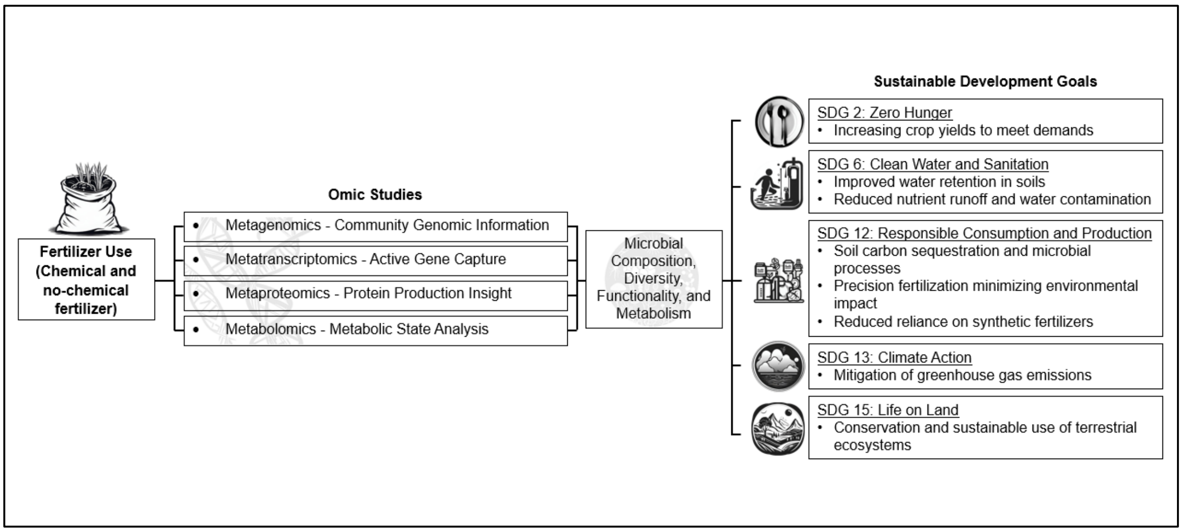

Figure 1. An illustration showing how fertilizer applications and multi-omics studies contribute to the achievement of Sustainable Development Goals

NGS as a Tool for Aligning Agricultural Practices with Sustainability Goals

NGS is a transformative tool that dissects the complex relationships between fertilizers, microbial diversity, and agricultural ecosystems and aligns agricultural practices with the broader canvas of sustainability goals. In the context of the SDGs, NGS acts as a linchpin by providing a comprehensive understanding of microbial communities' responses to different fertilizers and their implications for sustainable agriculture.

NGS offers a holistic view of the soil microbiome, enabling researchers and practitioners to identify microbial signatures associated with sustainable practices. By delineating the impacts of various fertilizers on microbial diversity, NGS facilitates the development of precision fertilization strategies that optimize crop yields efficiently while minimizing environmental harm (Kurzemann et al., 2020; Iqbal et al., 2022; Wyszkowska et al., 2022). This aligns with SDG 12 (Responsible Consumption and Production) by reducing the need for excessive resource consumption, minimizing environmental degradation, and supporting the goal of ensuring sustainable consumption and production patterns for a healthier planet.

Furthermore, NGS-driven insights contribute to achieving SDG 2 (Zero Hunger) by fostering resilient agricultural systems. Better understanding the microbial dynamics in response to fertilizers enables the design of strategies that enhance nutrient availability, improve soil health, and, consequently, increase food security (Kurzemann et al., 2020; Nwachukwu & Babalola, 2022; Arunrat et al., 2023). NGS's capacity to uncover microbial contributions to carbon sequestration (Zhou et al., 2022) aligns with SDG 13 (Climate Action), offering methods to reduce climate change through sustainable agriculture.

Moreover, NGS contributes significantly to the pursuit of SDG 15 (Life on Land) by shedding light on the impact of fertilizers on microbial diversity and its cascading effects on terrestrial ecosystems. The ability of NGS to uncover the intricate relationships between microbial communities and the surrounding environment enables a nuanced understanding of the role of these microorganisms in promoting biodiversity and ecosystem resilience (Wang & Xiong, 2022; Meng et al., 2023; Xu et al., 2023b). This aligns with the broader objective of conserving land ecosystems, restoration, and sustainable use (Küfeoğlu, 2022). Through soil analysis, NGS helps farmers boost agricultural productivity and support ecosystem health. Integrating NGS data into land management strategies preserves biodiversity, prevents soil degradation, and promotes species coexistence. NGS is a powerful tool aligning agriculture with sustainability goals by understanding fertilizer-microbe interactions, enabling precision agriculture for enhanced productivity, environmental protection, and fulfillment of SDGs.

Addressing Global Challenges Through a Microbial Perspective

Embracing a microbial perspective in agriculture is pivotal for addressing the multifaceted global challenges outlined in the SDGs. Using NGS to explore soil microorganisms presents an unprecedented opportunity to address global challenges by gaining insights into their effects on soil health and ecosystem resilience. Agriculture gains a tool for fostering sustainable practices that simultaneously enhance productivity and mitigate environmental impact from the lens of microbial diversity. The microbial perspective contributes directly to SDG 15 (Life on Land) by emphasizing terrestrial ecosystems' conservation and sustainable use (Kumawat et al., 2023; Li et al., 2023b). Besides that, climate change-induced abiotic stresses exacerbate agricultural challenges, particularly when compounded by chemical fertilizer application, which degrades soil health (Wijitkosum, 2018; Azahari & Sukarman, 2023). Nonetheless, leveraging beneficial microorganisms presents a sustainable solution, aligning with SDG 15 by fostering soil resilience and enhancing plant stress tolerance, thus promoting sustainable agricultural practices in the face of climate change.

Understanding and optimizing microbial communities through precision fertilization strategies aligns with SDG 12 (Responsible Consumption and Production), optimizing the application of fertilizers to enhance plant growth while minimizing environmental impact. Precision fertilization leverages microbial processes, such as nitrogen fixation, to make nutrients available to plants, thereby reducing the reliance on synthetic fertilizers (Shi et al., 2021; Lin et al., 2021). This aligns with responsible consumption and production, lowering the environmental footprint of chemical input production and use.

Moreover, a microbial perspective offers innovative solutions to combat climate change (SDG 13). Microorganisms contribute to combating climate change by enhancing soil fertility and structure through the breakdown of organic matter and storing carbon in the soil as a natural sink (Kozjek et al., 2023). Additionally, certain microbes, such as methanotrophic bacteria, play a crucial role in converting methane, a potent greenhouse gas, into less harmful byproducts, aiding in the reduction of overall greenhouse gas emissions (He et al., 2023). The understanding and harnessing microbial processes offer innovative solutions for managing greenhouse gas dynamics, contributing to global efforts to mitigate climate change (Hussain et al., 2022). Harnessing NGS technologies to decipher the microbial contributions to climate mitigation provides a pathway for agriculture to address global climate challenges proactively. By acknowledging the central role of microorganisms in the intricate balance of agroecosystems, the global community can forge a path toward achieving the broader aspirations of the Sustainable Development Agenda.

6. Challenges and Future Directions

Current Limitations in NGS-Based Studies

While NGS has revolutionized our understanding of microbial dynamics in response to fertilizers, several challenges persist in NGS-based studies. One notable limitation is the sheer volume and complexity of generated data (Larson et al., 2023). The extensive datasets produced by NGS technologies present storage, processing, and analysis challenges, demanding sophisticated computational infrastructure and expertise (Larson et al., 2023). This computational bottleneck poses challenges for researchers, particularly those with limited access to high-performance computing resources.

Additionally, the inherent biases and errors introduced during the sequencing process can impact the accuracy and reliability of results. Amplification biases, sequencing errors, and variations in bioinformatics pipelines may contribute to artifacts in the data, necessitating stringent quality control measures (Beckers et al., 2017; Notario et al., 2023). Addressing these technical challenges is vital to ensure the fidelity of NGS-generated information and to foster confidence in the conclusions drawn from such studies. The interpretability of NGS data remains a challenge. As our knowledge of microbial functions and interactions expands, so does the complexity of interpreting the functional implications of microbial diversity changes revealed by NGS (Toole et al., 2021). Integrating multi-omics data and advancing bioinformatics tools are essential for unraveling the functional significance of microbial shifts, thereby bridging the gap between taxonomic identification and ecological understanding.

In addition to technical challenges, issues related to standardization and comparability across studies pose hurdles in NGS-based agricultural microbiome research. The lack of standardized protocols for sample collection, DNA extraction, and data analysis can lead to variations in results, reducing the comparability of findings across other related studies (Serrano-Silva & Calderon-Ezquerro, 2018; Malczynski et al., 2021). Establishing a set of best practices and guidelines for NGS-based studies in agricultural microbiome research would enhance the consistency and reliability of results (Forry et al., 2023; Hiergeist et al., 2023). Collaborative efforts within the scientific community to develop and adopt standardized methodologies will build a more robust foundation for interpreting and synthesizing insights from diverse studies (Biswas et al., 2023). By addressing technical and standardization challenges, NGS can more effectively contribute to advancing our understanding of microbial responses to fertilizers and supporting the development of sustainable agricultural practices.

As NGS continues to be at the forefront of agricultural microbiome research, addressing these limitations will be pivotal for maximizing the technology's potential and ensuring that insights gained contribute meaningfully to developing sustainable agricultural practices. The ongoing refinement of methodologies, improvement in computational tools, and collaborative efforts across scientific disciplines will shape the future directions of NGS-based studies in unraveling the intricate relationships between fertilizers and microbial communities.

Potential Technological Advancements and Methodological Improvements

The future of NGS studies in agricultural microbiome research holds promise with anticipated technological advancements and methodological innovations. One area ripe for improvement is the enhancement of sequencing technologies themselves. Ongoing efforts to increase read lengths, reduce error rates, and elevate sequencing throughput will alleviate existing challenges in data generation (Callahan et al., 2021; Zhou et al., 2021), making NGS studies more accessible and cost-effective for a broader range of research endeavors. Long-read sequencing platforms like Oxford Nanopore and PacBio offer longer read lengths than traditional short-read platforms (Cook et al., 2024). Error correction tools such as Nanocorr and Canu help improve the accuracy of long-read data (Hu et al., 2020; Marić et al., 2024). For hybrid assembly pipelines, tools such as Unicycler and St. Petersburg Genome Assembler (SPAdes) combine long-read and short-read data for more accurate assemblies (Latorre-Pérez et al., 2020; Xu et al., 2022).

Moreover, the integration of multi-omics approaches is poised to refine our understanding of microbial responses to fertilizers. Coupling metagenomics with meta-transcriptomics, meta-proteomics, and metabolomics can provide a comprehensive view of microbial functions, shedding light on the dynamic interplay between microbial communities and their environment

(Yamazaki et al., 2021; Qiu et al., 2023; Yang et al., 2023b). Moreover, integrating metagenomic and metatranscriptomic analyses using NGS has allowed researchers to move beyond taxonomic identification and understand the functional consequences of chemical fertilizer applications at the molecular level. Metagenomic studies reveal the complete genetic makeup of microbial communities, exposing the genes and pathways involved in important ecological processes. In contrast, metatranscriptomics captures actively expressed genes, offering insights into the functional dynamics of microbial communities (Qian et al., 2020). These advanced analyses have revealed shifts in gene expression associated with nutrient uptake, stress response, and the synthesis of secondary metabolites (Chevrette et al., 2022; Law et al., 2022; Tartaglia et al., 2023). Identifying specific functional genes involved in these processes enhances our ability to predict and manage the ecological outcomes of chemical fertilizer use.

The integration between metagenomics and metabolomics also provides a comprehensive understanding of microbial functionality by revealing both the taxonomic composition of microbial communities and insights into the actual biochemical processes and metabolites. Zhao et al. (2023) demonstrates that long-term fertilization enhances soil quality by promoting the growth of beneficial bacteria and fungi and releasing essential compounds to support plant growth and maintain overall productivity. Additionally, Tian et al. (2023) found that mulching reduces NO3−-N content and influences specific genes (nxrA and nasA), accelerating microbial metabolism and stimulating the production of various metabolites linked to key biological processes. The P-fertilizer application resulted in a decrease in the diversity of bacterial and fungal genes in the soil. The fertilizer also affected the soil metabolite spectrum, notably influencing seven primary metabolic pathways related to amino acids, plant hormones, and secondary metabolites (Cheng et al., 2022). Integrating metagenomic and metabolomic approaches is crucial for developing sustainable fertilization strategies that optimize nutrient use, minimize environmental impact, and foster a resilient soil microbiome, translating microbial diversity data into actionable insights for sustainable agriculture.

Advancements in bioinformatics tools will play a pivotal role in overcoming current data analysis and interpretation limitations. Machine learning algorithms, for instance, have the potential to discern complex patterns within large and intricate datasets, facilitating more accurate taxonomic assignments and functional predictions (Lee et al., 2022; Zhang et al., 2022b; Cheng et al., 2023). Additionally, user-friendly pipelines that streamline data processing and enhance accessibility will democratize the use of NGS technologies, enabling researchers with diverse backgrounds to leverage these powerful tools.

As technology continues to evolve, the integration of advanced studies, like NGS commonly used in medicine, along with other emerging technologies such as high-resolution imaging and remote sensing (Wang et al., 2020; Zhang et al., 2020; Wei et al., 2023b), holds promise for gaining a more holistic understanding of agroecosystems. These multidisciplinary approaches will enable researchers to explore microbial dynamics at various scales, from the microscopic to the field-level, fostering a more nuanced comprehension of the intricate relationships between fertilizers, microbial communities, and sustainable agricultural practices.

The Importance of Interdisciplinary Collaboration for Comprehensive Insights

Addressing the complex challenges and unlocking the full potential of NGS in agricultural microbiome research requires a concerted effort in interdisciplinary collaboration (Chiusano, 2015). Integrating expertise from diverse fields such as microbiology, agronomy, bioinformatics, and data science is imperative for advancing our understanding of the relationships between fertilizers and microbial communities.

Microbial responses to fertilizers unfold within the broader context of agroecosystems, encompassing soil health, plant-microbe interactions, and environmental sustainability. An interdisciplinary approach ensures that researchers can navigate this complexity, drawing on various disciplines' insights to interpret NGS-generated data comprehensively. Microbiologists contribute their knowledge of microbial ecology, agronomists provide insights into crop-specific needs, and bioinformaticians bring essential tools for processing and analyzing large-scale genomic datasets.

Furthermore, collaboration between academia, industry, and policy-making entities is essential to bridge the gap between research findings and real-world applications (John et al., 2023). Industry professionals can offer practical insights into the scalability and feasibility of implementing NGS-informed strategies in diverse agricultural settings. Policymakers play a crucial role in translating research into actionable guidelines that promote sustainable and microbiome-conscious agricultural practices on a broader scale.

The challenges NGS studies face in agricultural microbiome research are multifaceted, and their resolution demands a collective effort. By fostering a culture of interdisciplinary collaboration, researchers can harness the strengths of different fields, enriching the depth and applicability of insights gained from NGS technologies. As we look to the future, synergy between diverse disciplines will be pivotal for overcoming challenges and realizing the full potential of NGS in shaping the sustainable future of agriculture.

4. Conclusion

In the journey through the nexus of fertilizers, microbial communities, and sustainable agriculture, this review has unveiled findings elucidated by NGS. NGS studies have provided unprecedented insights into the dynamic relationships between chemical and non-chemical fertilizers, soil types, crop specificity, and microbial diversity. Through comprehensive analyses, researchers have deciphered fertilizer applications' taxonomic and functional implications, offering a deeper understanding of agroecosystem dynamics. These insights underscore the pivotal role of microbial diversity in shaping resilient and sustainable

DOI: https//doi.org/10.22452/mjs.vol44no2.9

agricultural systems.

The potential impact of NGS on reshaping agricultural practices cannot be overstated. The depth and precision of information provided by NGS technologies empower farmers, researchers, and policymakers to make informed decisions that balance productivity with environmental and social considerations. NGS lays the foundation for a paradigm shift in agriculture from precision fertilization strategies tailored to specific soil types and crops to the development of microbiome-conscious agricultural policies. The technology's capacity to uncover microbial functions, predict ecosystem responses, and guide sustainable practices positions NGS as a transformative force with far-reaching implications for the future of global agriculture.

As we stand at the cusp of agricultural innovation, a resounding call to action echoes from the insights gained through NGS studies. It is incumbent upon the global community, including farmers, researchers, policymakers, and industry stakeholders, to embrace sustainable and microbiome-conscious agricultural practices. Leveraging the knowledge derived from NGS, we can design and implement strategies that enhance crop yields and prioritize soil health, biodiversity conservation, and climate resilience. This call to action implores us to bridge the gap between scientific knowledge and practical application, fostering a holistic approach that aligns with the principles of the SDGs. Through collaborative efforts, informed decision-making, and a commitment to stewardship of our agroecosystems, we could shape a productive but also sustainable, resilient, and harmonious agricultural future with the microbial world beneath our feet.

5. References

AbdelRahman, M. A., Metwaly, M. M., Afifi, A. A., D'Antonio, P., & Scopa, A. (2022). Assessment of soil fertility status under soil degradation rate using geomatics in West Nile Delta. *Land*, *11*(8), 1256. https://doi.org/10.3390/land11081256

Abid, M., Wu, J., Seyedsalehi, M., Hu, Y. Y., & Tian, G. (2021). Novel insights of impacts of solid content on high solid anaerobic digestion of cow manure: Kinetics and microbial community dynamics. *Bioresource Technology*, *333*, 125205. https://doi.org/10.1016/j.biortech.2021.125205

Adhikari, M., Kim, S. W., Kim, H. S., Kim, K. Y., Park, H. B., Kim, K. J., & Lee, Y. S. (2021). Bacterial Community and Diversity from the Watermelon Cultivated Soils through Next Generation Sequencing Approach. *The Plant Pathology Journal*, *37*(6), 521. https://doi.org/10.5423%2FPPJ.OA.07.2021.0106

Arunrat, N., Sereenonchai, S., Sansupa, C., Kongsurakan, P., & Hatano, R. (2023). Effect of Rice Straw and Stubble Burning on Soil Physicochemical Properties and Bacterial Communities in Central Thailand. *Biology*, *12*(4), 501. https://doi.org/10.3390/biology12040501

Ashraf, M. F., Hou, D., Hussain, Q., Imran, M., Pei, J., Ali, M., Shehzad, A., Anwar, M., Noman, A., Waseem, M., & Lin, X. (2022). Entailing the next-generation sequencing and metabolome for sustainable agriculture by improving plant tolerance. *International Journal of Molecular Sciences*, *23*(2), 651. https://doi.org/10.3390/ijms23020651

Azahari, D. H. (2023, September). Impact of chemical fertilizer on soil fertility of oil palm plantations in relation to productivity and environment. In *IOP Conference Series: Earth and Environmental Science* (Vol. 1243, No. 1, p. 012020). IOP Publishing. https://doi.org/10.1088/1755-1315/1243/1/012020

Azarbad, H., Tremblay, J., Bainard, L. D., & Yergeau, E. (2022). Relative and quantitative rhizosphere microbiome profiling results in distinct abundance patterns. *Frontiers in Microbiology*, *12*, 798023. https://doi.org/10.3389/fmicb.2021.798023

Azeem, M., Sun, D., Crowley, D., Hayat, R., Hussain, Q., Ali, A., Tahir, M. I., Jeyasundar, P. G. S. A., Rinklebe, J., & Zhang, Z. (2020). Crop types have stronger effects on soil microbial communities and functionalities than biochar or fertilizer during two cycles of legume-cereal rotations of dry land. *Science of The Total Environment,* *715*, 136958. https://doi.org/10.1016/j.scitotenv.2020.136958

Bai, Y. C., Chang, Y. Y., Hussain, M., Lu, B., Zhang, J. P., Song, X. B., Lei, X. S., & Pei, D. (2020). Soil chemical and microbiological properties are changed by long-term chemical fertilizers that limit ecosystem functioning. *Microorganisms*, *8*(5), 694. https://doi.org/10.3390/microorganisms8050694

Beckers, M., Mohorianu, I., Stocks, M., Applegate, C., Dalmay, T., & Moulton, V. (2017). Comprehensive processing of high-throughput small RNA sequencing data including quality checking, normalization, and differential expression analysis using the UEA sRNA Workbench. *RNA*, *23*(6), 823-835. https://doi.org/10.1261/rna.059360.116

Biswas, A., Kumari, A., Gaikwad, D. S., & Pandey, D. K. (2023). Revolutionizing Biological Science: The Synergy of Genomics in Health, Bioinformatics, Agriculture, and Artificial Intelligence. OMICS: *A Journal of Integrative Biology, 27*(12), 550-569. https://doi.org/10.1089/omi.2023.0197

Bokulich, N. A., & Mills, D. A. (2012). Next-generation approaches to the microbial ecology of food fermentations. *BMB Reports*, *45*(7), 377-389. http://dx.doi.org/10.5483/BMBRep.2012.45.7.148

Callahan, B. J., Grinevich, D., Thakur, S., Balamotis, M. A., & Yehezkel, T. B. (2021). Ultra-accurate microbial amplicon sequencing with synthetic long reads. *Microbiome*, *9*(1), 1-13. https://doi.org/10.1186/s40168-021-01072-3

DOI: https//doi.org/10.22452/mjs.vol44no2.9

Caracciolo, A. B., Grenni, P., Ciccoli, R., Di Landa, G., & Cremisini, C. (2005). Simazine biodegradation in soil: analysis of bacterial community structure by in situ hybridization. *Pest Management Science: formerly Pesticide Science, 61*(9), 863-869. https://doi.org/10.1002/ps.1096

Carrascosa, A., Pascual, J. A., López-García, Á., Romo-Vaquero, M., De Santiago, A., Ros, M., Petropoulos, S. A., & Alguacil, M. D. M. (2023). Effects of inorganic and compost tea fertilizers application on the taxonomic and functional microbial diversity of the purslane rhizosphere. *Frontiers in Plant Science, 14*, 1159823. https://doi.org/10.3389/fpls.2023.1159823

Castellano-Hinojosa, A., Albrecht, U., & Strauss, S. L. (2023). Interactions between rootstocks and compost influence the active rhizosphere bacterial communities in citrus. *Microbiome, 11*(1), 1-16. https://doi.org/10.1186/s40168-023-01524-y

Chamberlain, L. A., Bolton, M. L., Cox, M. S., Suen, G., Conley, S. P., & Ane, J. M. (2020). Crop rotation, but not cover crops, influenced soil bacterial community composition in a corn-soybean system in southern Wisconsin. *Applied Soil Ecology, 154*, 103603. https://doi.org/10.1016/j.apsoil.2020.103603

Chaudhary, D. K., Khulan, A., & Kim, J. (2019). Development of a novel cultivation technique for uncultured soil bacteria. *Scientific Reports*, *9*(1), 6666. https://doi.org/10.1038/s41598-019-43182-x

Chen, M., Zhang, S., Liu, L., & Ding, X. (2023). Influence of organic fertilization on clay mineral transformation and soil phosphorous retention: Evidence from an 8-year fertilization experiment. *Soil and Tillage Research*, *230*, 105702. https://doi.org/10.1016/j.still.2023.105702

Cheng, H., Yuan, M., Tang, L., Shen, Y., Yu, Q., & Li, S. (2022). Integrated microbiology and metabolomics analysis reveal responses of soil microorganisms and metabolic functions to phosphorus fertilizer on semiarid farm. *Science of the Total Environment, 817*, 152878. https://doi.org/10.1016/j.scitotenv.2021.152878

Cheng, Z., Zheng, Q., Shi, J., He, Y., Yang, X., Huang, X., Wu, L., & Xu, J. (2023). Metagenomic and machine learning-aided identification of biomarkers driving distinctive Cd accumulation features in the root-associated microbiome of two rice cultivars. *ISME Communications*, *3*(1), 14. https://doi.org/10.1038/s43705-023-00213-z

Chevrette, M. G., Thomas, C. S., Hurley, A., Rosario-Meléndez, N., Sankaran, K., Tu, Y., Hall, A., Magesh, S., & Handelsman, J. (2022). Microbiome composition modulates secondary metabolism in a multispecies bacterial community. *Proceedings of the National Academy of Sciences, 119*(42), e2212930119. https://doi.org/10.1073/pnas.2212930119

Chiusano, M. L. (2015). On the multifaceted aspects of bioinformatics in the next generation era: the run that must keep the quality. *Next Generation: Sequencing & Applications*, *2*, e106. http://dx.doi.org/10.4172/jngsa.1000e106

Chouhan, A., Kushwaha, E. M., & Mahalakshmi, P. (2023). 7 AGRICULTURE BIOINFORMATICS IN THE AGE OF NEXT-GENERATION SEQUENCING. *Applications of Environmental Biotechnology for Global Sustainability*, 51.

Chuckran, P. F., Fofanov, V., Hungate, B. A., Morrissey, E. M., Schwartz, E., Walkup, J., & Dijkstra, P. (2021). Rapid response of nitrogen cycling gene transcription to labile carbon amendments in a soil microbial community. *MSystems, 6*(3), e00161-21. https://doi.org/10.1128/msystems.00161-21

Cook, R., Brown, N., Rihtman, B., Michniewski, S., Redgwell, T., Clokie, M., Stekel, D. J., Chen, Y., Scanlan, D. J., Hobman, J. L., Nelson, A., Jones, M. A., Smith, D., & Millard, A. (2024). The long and short of it: benchmarking viromics using Illumina, Nanopore and PacBio sequencing technologies. *Microbial Genomics, 10*(2), 001198. https://doi.org/10.1099/mgen.0.001198

de Vries, J., Saleem, F., Li, E., Chan, A. W. Y., Naphtali, J., Naphtali, P., Paschos, A., & Schellhorn, H. E. (2023). Comparative Analysis of Metagenomic (Amplicon and Shotgun) DNA Sequencing to Characterize Microbial Communities in Household On-Site Wastewater Treatment Systems. *Water*, *15*(2), 271. https://doi.org/10.3390/w15020271

Deinert, L., Ikoyi, I., Egeter, B., Forrestal, P., & Schmalenberger, A. (2023). Short-Term Impact of Recycling-Derived Fertilizers on Their P Supply for Perennial Ryegrass (*Lolium perenne*). *Plants, 12*(15), 2762. https://doi.org/10.3390/plants12152762

Dincă, L. C., Grenni, P., Onet, C., & Onet, A. (2022). Fertilization and soil microbial community: a review. *Applied Sciences*, *12*(3), 1198. https://doi.org/10.3390/app12031198

Doni, L., Martinez-Urtaza, J., & Vezzulli, L. (2023). Searching pathogenic bacteria in the rare biosphere of the ocean. *Current Opinion in Biotechnology*, *80*, 102894. https://doi.org/10.1016/j.copbio.2023.102894

Dubey, P. K., Singh, A., Chaurasia, R., Pandey, K. K., Bundela, A. K., Dubey, R. K., & Abhilash, P. C. (2021). Planet friendly agriculture: Farming for people and the planet. *Current Research in Environmental Sustainability, 3*, 100041. https://doi.org/10.1016/j.crsust.2021.100041

Ehau-Taumaunu, H., & Hockett, K. L. (2023). Passaging phyllosphere microbial communities develop suppression towards bacterial speck disease in tomato. *Phytobiomes*

Journal, 7(2), 233-243. https://doi.org/10.1094/PBIOMES-05-22-0030-FI

Enebe, M. C., & Babalola, O. O. (2021). The influence of soil fertilization on the distribution and diversity of phosphorus cycling genes and microbes community of maize rhizosphere using shotgun metagenomics. *Genes, 12*(7), 1022. https://doi.org/10.3390/genes12071022

Fadiji, A. E., Ayangbenro, A. S., & Babalola, O. O. (2020). Organic farming enhances the diversity and community structure of endophytic archaea and fungi in maize plant: A shotgun approach. *Journal of Soil Science and Plant Nutrition, 20*, 2587-2599. https://doi.org/10.1007/s42729-020-00324-9

Feng, Q., Cao, S., Liao, S., Wassie, M., Sun, X., Chen, L., & Xie, Y. (2023). *Fusarium equiseti*-inoculation altered rhizosphere soil microbial community, potentially driving perennial ryegrass growth and salt tolerance. *Science of The Total Environment*, *871*, 162153. https://doi.org/10.1016/j.scitotenv.2023.162153

Feng, Y., Delgado-Baquerizo, M., Zhu, Y., Han, X., Han, X., Xin, X., Li, W., Guo, Z., Dang, T., Li, C., Zhu, B., Cai, Z., Li, D., & Zhang, J. (2022). Responses of soil bacterial diversity to fertilization are driven by local environmental context across China. *Engineering*, *12*, 164-170. https://doi.org/10.1016/j.eng.2021.09.012

Fierer, N., Lauber, C. L., Ramirez, K. S., Zaneveld, J., Bradford, M. A., & Knight, R. (2012). Comparative metagenomic, phylogenetic and physiological analyses of soil microbial communities across nitrogen gradients. *The ISME Journal*, *6*(5), 1007-1017. https://doi.org/10.1038/ismej.2011.159

Forry, S. P., Servetas, S. L., Kralj, J. G., Soh, K., Hadjithomas, M., Cano, R., Carlin, M., de Amorim, M. G., Auch, B., Bakker, M. G., Bartelli, T. F., Bustamante, J. P., Cassol, I., Chalita, M., Dias-Neto, E., Del Duca, A., Gohl, D. M., Kazantseva, J., Haruna, M. T., Menzel, P., Moda, B. S., Neuberger-Castillo, L., Nunes, D. N., Patel, I. R., Peralta, R. D., Saliou, A., Schwarzer, R., Sevilla, S., Takenaka, I. K. T. M., Wang, J. R., Knight, R., Gevers, D., & Jackson, S. A. (2023). Variability and Bias in Microbiome Metagenomic Sequencing: an Interlaboratory Study Comparing Experimental Protocols. *bioRxiv*, 2023-04. https://doi.org/10.1101/2023.04.28.538741

Greay, T. L., Evasco, K. L., Evans, M. L., Oskam, C. L., Magni, P. A., Ryan, U. M., & Irwin, P. J. (2021). Illuminating the bacterial microbiome of Australian ticks with 16S and Rickettsia-specific next-generation sequencing. *Current Research in Parasitology & Vector-Borne Diseases, 1,* 100037. https://doi.org/10.1016/j.crpvbd.2021.100037

Gupta, A., Singh, U. B., Sahu, P. K., Paul, S., Kumar, A., Malviya, D., Singh, S., Kuppusamy, P., Singh, P., Paul, D., Rai, J. P., Singh, H. V., Manna, M. C., Crusberg, T. C., Kumar, A., & Saxena, A. K. (2022). Linking soil microbial diversity to modern agriculture practices: A review. *International Journal of Environmental Research and Public Health*, *19*(5), 3141. https://doi.org/10.3390/ijerph19053141

He, Z., Shen, J., Zhu, Y., Feng, J., & Pan, X. (2023). Enhanced anaerobic oxidation of methane with the coexistence of iron oxides and sulfate fertilizer in paddy soil. *Chemosphere*, *329*, 138623. https://doi.org/10.1016/j.chemosphere.2023.138623

Heidkamp, R. A., Piwoz, E., Gillespie, S., Keats, E. C., D'Alimonte, M. R., Menon, P., Das, J. K., Flory, A., Clift, J. W., Ruel, M. T., Vosti, S., Akuoku, J. K., Bhutta, Z. A. (2021). Mobilising evidence, data, and resources to achieve global maternal and child undernutrition targets and the Sustainable Development Goals: an agenda for action. *The Lancet*, *397*(10282), 1400-1418. https://doi.org/10.1016/S0140-6736(21)00568-7

Hiergeist, A., Ruelle, J., Emler, S., & Gessner, A. (2023). Reliability of species detection in 16S microbiome analysis: Comparison of five widely used pipelines and recommendations for a more standardized approach. *PLoS One, 18*(2), e0280870. https://doi.org/10.1371/journal.pone.0280870

Hiiesalu, I., Öpik, M., Metsis, M., Lilje, L., Davison, J., Vasar, M., Moora, M., Zobel, M., Wilson, S. D., & Pärtel, M. (2012). Plant species richness belowground: higher richness and new patterns revealed by next-generation sequencing. *Molecular Ecology, 21*(8), 2004-2016. https://doi.org/10.1111/j.1365-294X.2011.05390.x

Hong, S., Yuan, X., Yang, J., Yang, Y., Jv, H., Li, R., Jia, Z., & Ruan, Y. (2023). Selection of rhizosphere communities of diverse rotation crops reveals unique core microbiome associated with reduced banana *Fusarium* wilt disease. *New Phytologist*, *5*(238), 2194-2209. https://doi.org/10.1111/nph.18816

Hu, X., Gu, H., Liu, J., Wei, D., Zhu, P., Zhou, B., Chen, X., Jin, J., Liu, X., & Wang, G. (2022a). Metagenomics reveals divergent functional profiles of soil carbon and nitrogen cycling under long-term addition of chemical and organic fertilizers in the black soil region. *Geoderma, 418*, 115846. https://doi.org/10.1016/j.geoderma.2022.115846

Hu, X., Gu, H., Liu, J., Zhou, B., Wei, D., Chen, X., & Wang, G. (2022b). High variation of fungal communities and associated potential plant pathogens induced by long-term addition of N fertilizers rather than P, K fertilizers: A case study in a Mollisol field. *Soil Ecology Letters,* *4*(4), 348-361. https://doi.org/10.1007/s42832-021-0120-4

Hu, Y., Fang, L., Nicholson, C., & Wang, K. (2020). Implications of error-prone long-read whole-genome shotgun sequencing on characterizing reference microbiomes. *IScience, 23*(6). https://doi.org/10.1016/j.isci.2020.101223

Hua, L. Q., Yang, S. Q., Xia, Z. F., & Zeng, H. (2023). Application of *Sophora alopecuroides* organic fertilizer changes the rhizosphere microbial community structure of melon plants and increases the fruit sugar content. *Journal of the Science of Food and Agriculture, 103*(1), 164-175. https://doi.org/10.1002/jsfa.12126

Hussain, M. M., Farooqi, Z. U. R., Rasheed, F., & Din, W. M. U. (2022). Role of microorganisms as climate engineers: Mitigation and adaptations to climate change. In *Climate Change and Microbes* (pp. 1-24). Apple Academic Press.

Inubushi, K., & Acquaye, S. (2004). Role of microbial biomass in biogeochemical processes in paddy soil environments. *Soil Science and Plant Nutrition*, *50*(6), 793-805. https://doi.org/10.1080/00380768.2004.10408539

Iqbal, A., He, L., Ali, I., Yuan, P., Khan, A., Hua, Z., Wei, S., & Jiang, L. (2022). Partial substation of organic fertilizer with chemical fertilizer improves soil biochemical attributes, rice yields, and restores bacterial community diversity in a paddy field. *Frontiers in Plant Science*, *13*, 895230. https://doi.org/10.3389/fpls.2022.895230

Iqbal, A., Tang, X., Ali, I., Yuan, P., Khan, R., Khan, Z., Adnan, M., Wei, S., & Jiang, L. (2023). Integrating low levels of organic fertilizer improves soil fertility and rice yields in paddy fields by influencing microbial communities without increasing CH_4 emissions. *Applied Soil Ecology*, *189*, 104951. https://doi.org/10.1016/j.apsoil.2023.104951

Ishfaq, M., Wang, Y., Xu, J., Hassan, M. U., Yuan, H., Liu, L., He, B., Ejaz, I., White, P. J., Cakmak, I., Chen, W.-S., Wu, J., van der Werf, W., Li, C., Zhang, F., & Li, X. (2023). Improvement of nutritional quality of food crops with fertilizer: a global meta-analysis. *Agronomy for Sustainable Development*, *43*(6), 74. https://doi.org/10.1007/s13593-023-00923-7

Jiang, Z., Yang, S., Pang, Q., Xu, Y., Chen, X., Sun, X., Qi, S., & Yu, W. (2021). Biochar improved soil health and mitigated greenhouse gas emission from controlled irrigation paddy field: Insights into microbial diversity. *Journal of Cleaner Production*, *318*, 128595. https://doi.org/10.1016/j.jclepro.2021.128595

John, T., Cordova, K. E., Jackson, C. T., Hernández-Mondragón, A. C., Davids, B. L., Raheja, L., Milić, J. V., & Borges, J. (2023). Engaging Early-Career Scientists in Global Policy-Making. *Angewandte Chemie International Edition*, *62*(34), e202217841. https://doi.org/10.1002/anie.202217841

Kallenbach, C., & Grandy, A. S. (2011). Controls over soil microbial biomass responses to carbon amendments in agricultural systems: A meta-analysis. *Agriculture, Ecosystems & Environment*, *144*(1), 241-252. https://doi.org/10.1016/j.agee.2011.08.020

Khatri, S., Dubey, S., Shivay, Y. S., Jelsbak, L., & Sharma, S. (2023). Organic farming induces changes in bacterial community and disease suppressiveness against fungal phytopathogens. *Applied Soil Ecology, 181*, 104658. https://doi.org/10.1016/j.apsoil.2022.104658

Kim, H., Park, Y. H., Yang, J. E., Kim, H. S., Kim, S. C., Oh, E. J., Moon, J., Cho, W., Shin, W., & Yu, C. (2022). Analysis of major bacteria and diversity of surface soil to discover biomarkers related to soil health. *Toxics*, *10*(3), 117. https://doi.org/10.3390/toxics10030117

Kozjek, K., Manoharan, L., Urich, T., Ahrén, D., & Hedlund, K. (2023). Microbial gene activity in straw residue amendments reveals carbon sequestration mechanisms in agricultural soils. *Soil Biology and Biochemistry, 179,* 108994. https://doi.org/10.1016/j.soilbio.2023.108994

Küfeoğlu, S. (2022). SDG-15: Life on Land. In *Emerging Technologies: Value Creation for Sustainable Development* (pp. 469-486). Cham: Springer International Publishing. https://doi.org/10.1007/978-3-031-07127-0_17

Kumawat, A., Yadav, D., Srivastava, P., Babu, S., Kumar, D., Singh, D., Vishwakarma, D. K., Sharma, V. K., & Madhu, M. (2023). Restoration of agroecosystems with conservation agriculture for food security to achieve sustainable development goals. *Land Degradation & Development, 11,* 34, 3079-3097. https://doi.org/10.1002/ldr.4677

Kurzemann, F. R., Plieger, U., Probst, M., Spiegel, H., Sandén, T., Ros, M., & Insam, H. (2020). Long-term fertilization affects soil microbiota, improves yield and benefits soil. *Agronomy*, *10*(11), 1664. https://doi.org/10.3390/agronomy10111664

Lafaille, N. (2017, January). The development of fertilizer from the early years to today©. In *Proceedings of the 2017 Annual Meeting of the International Plant Propagators' Society 1212* (pp. 213-216). https://doi.org/10.21273/HORTTECH.15.1.0024

Larson, N. B., Oberg, A. L., Adjei, A. A., & Wang, L. (2023). A clinician's guide to bioinformatics for next-generation sequencing. *Journal of Thoracic Oncology*, *18*(2), 143-157. https://doi.org/10.1016/j.jtho.2022.11.006

Latorre-Pérez, A., Villalba-Bermell, P., Pascual, J., & Vilanova, C. (2020). Assembly methods for nanopore-based metagenomic sequencing: a comparative study. *Scientific Reports, 10*(1), 13588. https://doi.org/10.1038/s41598-020-70491-3

Law, S. R., Serrano, A. R., Daguerre, Y., Sundh, J., Schneider, A. N., Stangl, Z. R., Castro, D., Grabherr, M., Näsholm, T., Street, N. R., & Hurry, V. (2022). Metatranscriptomics captures dynamic shifts in mycorrhizal coordination in boreal forests. Proceedings of the National Academy of Sciences, 119(26), e2118852119. https://doi.org/10.1073/pnas.2118852119

Lee, J., Jo, N. Y., Shim, S. Y., Linh, L. T. Y., Kim, S. R., Lee, M. G., & Hwang, S. G. (2023). Effects of Hanwoo (Korean cattle) manure as organic fertilizer on plant growth, feed quality, and soil bacterial community. *Frontiers in Plant Science, 14*, 1135947. https://doi.org/10.3389/fpls.2023.1135947

Lee, J.-Y., Mitchell, H. D., Burnet, M. C., Wu, R., Jenson, S. C., Merkley, E. D., Nakayasu, E. S., Nicora, C. D., Jansson, J. K., Burnum-Johnson, K. E., & Payne, S. H. (2022). Uncovering hidden members and functions of the soil microbiome using de *novo* metaproteomics. *Journal of Proteome Research*, *21*(8), 2023-2035. https://doi.org/10.1021/acs.jproteome.2c00334

Li, N., Sheng, K., Zheng, Q., Hu, D., Zhang, L., Wang, J., & Zhang, W. (2023a). Inoculation with phosphate-solubilizing bacteria alters microbial community and activates soil phosphorus supply to promote maize growth. *Land Degradation & Development*, *34*(3), 777-788. https://doi.org/10.1002/ldr.4494

Li, T., Li, R., Cao, Y., Tao, C., Deng, X., Ou, Y., Liu, H., Shen, Z., & Shen, Q. (2022b). Soil antibiotic abatement associates with the manipulation of soil microbiome via long-term fertilizer application. *Journal of Hazardous Materials, 439*, 129704. https://doi.org/10.1016/j.jhazmat.2022.129704

Li, T., Zhang, Y., He, B., Wu, X., & Du, Y. (2022a). Nitrate loss by runoff in response to rainfall amount category and different combinations of fertilization and cultivation in sloping croplands. *Agricultural Water Management*, *273*, 107916. https://doi.org/10.1016/j.agwat.2022.107916

Li, W. X., Wang, C., Zheng, M. M., Cai, Z. J., Wang, B. R., & Shen, R. F. (2020a). Fertilization strategies affect soil properties and abundance of N-cycling functional genes in an acidic agricultural soil. *Applied Soil Ecology*, *156*, 103704. https://doi.org/10.1016/j.apsoil.2020.103704

Li, Y., Wang, C., Wang, T., Liu, Y., Jia, S., Gao, Y., & Liu, S. (2020b). Effects of different fertilizer treatments on rhizosphere soil microbiome composition and functions. *Land, 9*(9), 329. https://doi.org/10.3390/land9090329

Li, Y., Wang, C., Wu, J., Zhang, Y., Li, Q., Liu, S., & Gao, Y. (2023b). The Effects of Localized Plant–Soil–Microbe Interactions on Soil Nitrogen Cycle in Maize Rhizosphere Soil under Long-Term Fertilizers. *Agronomy*, *13*(8), 2114. https://doi.org/10.3390/agronomy13082114

Lin, Y., Ye, G., Luo, J., Di, H. J., Lindsey, S., Fan, J., Liu, D., & Ding, W. (2021). Long-term organic fertilization regulates the abundance of major nitrogen-cycling-related genes in aggregates from an acidic Ultisol. *Applied Soil Ecology*, *165*, 104014. https://doi.org/10.1016/j.apsoil.2021.104014

Liu, K. L., Han, T. F., Huang, J., Asad, S., Li, D. M., Yu, X. C., Huang, Q. H., Ye, H. C., Hu, H. W., Hu, Z. H., & Zhang, H. M. (2020). Links between potassium of soil aggregates and pH levels in acidic soils under long-term fertilization regimes. *Soil and Tillage Research*, *197*, 104480. https://doi.org/10.1016/j.still.2019.104480

Liu, Y. X., Qin, Y., Chen, T., Lu, M., Qian, X., Guo, X., & Bai, Y. (2021a). A practical guide to amplicon and metagenomic analysis of microbiome data. *Protein & Cell*, *12*(5), 315-330. https://doi.org/10.1007/s13238-020-00724-8

Liu, Y., Lv, Z., Hou, H., Lan, X., Ji, J., & Liu, X. (2021b). Long-term effects of combination of organic and inorganic fertilizer on soil properties and microorganisms in a Quaternary Red Clay. *Plos One*, *16*(12), e0261387. https://doi.org/10.1371/journal.pone.0261387

Liu, Z., Chen, R., Wang, J., Liu, J., Li, M., Lin, X., & Hu, J. (2022). Long-term moderate carbon input benefited arbuscular mycorrhizal fungal community diversity and vitality in a sandy loam soil. *Ecological Indicators*, *136*, 108679. https://doi.org/10.1016/j.ecolind.2022.108679

Lu, Y., Cong, P., Kuang, S., Tang, L., Li, Y., Dong, J., & Song, W. (2022). Long-term excessive application of K2SO4 fertilizer alters bacterial community and functional pathway of tobacco-planting soil. *Frontiers in Plant Science, 13*, 1005303. https://doi.org/10.3389/fpls.2022.1005303

Ma, X., Zhou, Z., Chen, J., Xu, H., Ma, S., Dippold, M. A., & Kuzyakov, Y. (2023). Long-term nitrogen and phosphorus fertilization reveals that phosphorus limitation shapes the microbial community composition and functions in tropical montane forest soil. *Science of the Total Environment*, *854*, 158709. https://doi.org/10.1016/j.scitotenv.2022.158709

Ma, Y., Zhang, H., Wang, D., Guo, X., Yang, T., Xiang, X., Walder, F., & Chu, H. (2021). Differential responses of arbuscular mycorrhizal fungal communities to long-term fertilization in the wheat rhizosphere and root endosphere. *Applied and Environmental Microbiology, 87*(17), e00349-21. https://doi.org/10.1128/AEM.00349-21

Malczynski, M., Zhu, A., Zembower, T., & Qi, C. (2021). Diagnostic performance of Ion 16S metagenomics kit and Ion reporter metagenomics workflow for bacterial pathogen detection in culture-negative clinical specimens from sterile sources. *Diagnostic Microbiology and Infectious Disease, 101*(2), 115451. https://doi.org/10.1016/j.diagmicrobio.2021.115451

Malewski, T., Borowik, P., Olejarski, I., Rutkiewicz, A., Okorski, A., & Oszako, T. (2023). Addition of Organic Matter to Pine Plantations on Agricultural Land Positively Alters the Mycobiome of Agricultural Soils. *Applied Sciences, 13*(9), 5800. https://doi.org/10.3390/app13095800

Maretto, L., Deb, S., Ravi, S., Della Lucia, M. C., Borella, M., Campagna, G., Squartini, A., Concheri, G., Nardi, S., & Stevanato, P. (2023). 16S metabarcoding, total soil DNA content, and functional bacterial genes quantification to characterize soils under long-term organic and conventional farming systems. *Chemical and Biological Technologies in Agriculture*, *10*(1), 78. https://doi.org/10.1186/s40538-023-00450-3

Marić, J., Križanović, K., Riondet, S., Nagarajan, N., & Šikić, M. (2024). Comparative analysis of metagenomic classifiers for long-read sequencing datasets. *BMC Bioinformatics, 25*(1), 15. https://doi.org/10.1186/s12859-024-05634-8

Martello, F., dos Santos, J. S., Silva-Neto, C. M., Cássia-Silva, C., Siqueira, K. N., de Ataíde, M. V. R., Ribeiro, M. C., & Collevatti, R. G. (2023). Landscape structure shapes the diversity of plant reproductive traits in agricultural landscapes in the Brazilian Cerrado. *Agriculture, Ecosystems & Environment*, *341*, 108216. https://doi.org/10.1016/j.agee.2022.108216

May, A., Coelho, L. F., Pedrinho, A., Batista, B. D., Mendes, L. W., Mendes, R., Morandi, M. A. B., Barth, G., Viana, R. S., & Vilela, E. S. D. (2023). The use of indigenous bacterial community as inoculant for plant growth promotion in soybean cultivation. *Archives of Agronomy and Soil Science*, *69*(1), 135-150. https://doi.org/10.1080/03650340.2021.1964017

Mendes, L. W., Raaijmakers, J. M., De Hollander, M., Sepo, E., Gómez Expósito, R., Chiorato, A. F., Mendes, R., Tsai, S. M., & Carrión, V. J. (2023). Impact of the fungal pathogen *Fusarium oxysporum* on the taxonomic and functional diversity of the common bean root microbiome. *Environmental Microbiome, 18*(1), 68. https://doi.org/10.1186/s40793-023-00524-7

Meng, H., Wang, S., Zhang, J., Wang, X., Qiu, C., & Hong, J. (2023). Effects of coal-derived compound fertilizers on soil bacterial community structure in coal mining subsidence areas. *Frontiers in Microbiology, 14*, 1187572. https://doi.org/10.3389/fmicb.2023.1187572

Menzies Pluer, E. G., Schneider, R. L., Morreale, S. J., Liebig, M. A., Li, J., Li, C. X., & Walter, M. T. (2020). Returning degraded soils to productivity: an examination of the potential of coarse woody amendments for improved water retention and nutrient holding capacity. *Water, Air, & Soil Pollution, 231*, 1-14. https://doi.org/10.1007/s11270-019-4380-x

Meunier, R., & Bayır, S. (2021). Metagenomics approaches in microbial ecology and research for sustainable agriculture. *TATuP-Zeitschrift Für Technikfolgenabschätzung in Theorie Und Praxis*, *30*(2), 24-29. https://doi.org/10.14512/tatup.30.2.24

Mukherjee, A., & Reddy, M. S. (2020). Metatranscriptomics: an approach for retrieving novel eukaryotic genes from polluted and related environments. *3 Biotech, 10*(2), 71. https://doi.org/10.1007/s13205-020-2057-1

Mukhles, M. B., Rahman, M. M., Rana, M. R., Huda, N., Ferdous, J., Rahman, F., Rafi, M. H., & Biswas, S. K. (2022). Effect of pesticides on nitrification activity and its interaction with chemical fertilizer and manure in long-term paddy soils. *Chemosphere, 304,* 135379. https://doi.org/10.1016/j.chemosphere.2022.135379

Mustafa, G., Hayat, N., & Alotaibi, B. A. (2023). How and why to prevent over fertilization to get sustainable crop production. In *Sustainable Plant Nutrition* (pp. 339-354). Academic Press. https://doi.org/10.1016/B978-0-443-18675-2.00019-5

Nguyen, S. H., Nguyen, D. N., Nguyen Thu, N., Pham, H. H., Phan, H. A., & Dao, C. D. (2023). Current Soil Degradation Assessment in the Thua Thien Hue Province, Vietnam, by Multi-Criteria Analysis and GIS Technology. *Sustainability, 15*(19), 14276. https://doi.org/10.3390/su151914276

Notario, E., Visci, G., Fosso, B., Gissi, C., Tanaskovic, N., Rescigno, M., Marzano, M., & Pesole, G. (2023). Amplicon-Based Microbiome Profiling: From Second-to Third-Generation Sequencing for Higher Taxonomic Resolution. *Genes*, *14*(8), 1567. https://doi.org/10.3390/genes14081567

Nwachukwu, B. C., & Babalola, O. O. (2022). Metagenomics: A tool for exploring key microbiome with the potentials for improving sustainable agriculture. *Frontiers in Sustainable Food Systems, 6,* 886987. https://doi.org/10.3389/fsufs.2022.886987

Özbolat, O., Sánchez-Navarro, V., Zornoza, R., Egea-Cortines, M., Cuartero, J., Ros, M., Pascual, J. A., Boix-Fayos, C., Almagro, M., de Vente, J., Díaz-Pereira, E., & Martínez-Mena, M. (2023). Long-term adoption of reduced tillage and green manure improves soil physicochemical properties and increases the abundance of beneficial bacteria in a Mediterranean rainfed almond orchard. *Geoderma, 429*, 116218. https://doi.org/10.1016/j.geoderma.2022.116218

Pande, P. M., Azarbad, H., Tremblay, J., St-Arnaud, M., & Yergeau, E. (2023). Metatranscriptomic response of the wheat holobiont to decreasing soil water content. *ISME Communications, 3*(1), 30. https://doi.org/10.1038/s43705-023-00235-7

Ponge, J. F. (2015). The soil as an ecosystem. *Biology and Fertility of Soils*, *51*, 645-648. https://doi.org/10.1007/s00374-015-1016-1

Poveda, J. (2022). Effect of volatile and non-volatile metabolites from *Leptosphaeria maculans* on tomato calli under abiotic stresses. *Plant Stress, 3*, 100054. https://doi.org/10.1016/j.stress.2021.100054

Qaisrani, M. M., Zaheer, A., Mirza, M. S., Naqqash, T., Qaisrani, T. B., Hanif, M. K., Rasool, G., Malik, K. A., Ullah, S., Jamal, M. S., Mirza, Z., Karim, S., & Rasool, M. (2019). A comparative study of bacterial diversity based on culturable and culture-independent techniques in the rhizosphere of maize (*Zea mays* L.). *Saudi Journal of Biological Sciences*, *26*(7), 1344-1351. https://doi.org/10.1016/j.sjbs.2019.03.010

Qian, X. B., Chen, T., Xu, Y. P., Chen, L., Sun, F. X., Lu, M. P., & Liu, Y. X. (2020). A guide to human microbiome research: study design, sample collection, and bioinformatics analysis. *Chinese Medical Journal, 133*(15), 1844-1855.

Qiu, Q., Xiang, D., Li, Q., Wang, H., Wan, Y., Wu, Q., Ye, X., Jiang, L., Fan, Y., Liu, B., Liu, Y., Li, H., & Liu, C. (2023). Interkingdom multi-omics analysis reveals the effects of nitrogen application on growth and rhizosphere microbial community of Tartary buckwheat. *Frontiers in Microbiology*, *14*. https://doi.org/10.3389%2Ffmicb.2023.1240029

Russel, D. A., & Williams, G. G. (1977). History of chemical fertilizer development. *Soil Science Society of America Journal*, *41*(2), 260-265. https://doi.org/10.2136/sssaj1977.03615995004100020020x

Saqib, M., Yasin, R., & Akhtar, J. (2020). Inorganic Fertilizers: Necessity to Achieve Global Zero Hunger Target. *Zero Hunger*, 414-424. https://doi.org/10.1007/978-3-319-95675-6_29

Saunders, O. E., Fortuna, A. M., Harrison, J. H., Cogger, C. G., Whitefield, E., & Green, T. (2012). Gaseous nitrogen and bacterial responses to raw and digested dairy manure applications in incubated soil. *Environmental Science & Technology*, *46*(21), 11684-11692. https://doi.org/10.1021/es301754s

Semenov, M. V., Krasnov, G. S., Semenov, V. M., & van Bruggen, A. H. (2020). Long-term fertilization rather than plant species shapes rhizosphere and bulk soil prokaryotic communities in agroecosystems. *Applied Soil Ecology, 154*, 103641. https://doi.org/10.1016/j.apsoil.2020.103641

Serrano-Silva, N., & Calderon-Ezquerro, M. C. (2018). Metagenomic survey of bacterial diversity in the atmosphere of Mexico City using different sampling methods. *Environmental Pollution, 235*, 20-29. https://doi.org/10.1016/j.envpol.2017.12.035

Sessou, P., Keisam, S., Gagara, M., Komagbe, G., Farougou, S., Mahillon, J., & Jeyaram, K. (2023). Comparative analyses of the bacterial communities present in the spontaneously fermented milk products of Northeast India and West Africa. *Frontiers in Microbiology, 14.* https://doi.org/10.3389%2Ffmicb.2023.1166518

Shahmohamadloo, R. S., Febria, C. M., Fraser, E. D., & Sibley, P. K. (2022). The sustainable agriculture imperative: A perspective on the need for an agrosystem approach to meet the United Nations Sustainable Development Goals by 2030. *Integrated Environmental Assessment and Management, 18*(5), 1199-1205. https://doi.org/10.1002/ieam.4558

Sharma, L. K., Zaeen, A., & Bali, S. (2022). Growing potatoes. In L. K. Sharma, A. Zaeen, & S. Bali (Eds.), *Insect Pests of Potato (Second Edition): Global Perspectives on Biology and Management* (pp. 7-14). Insect Pests of Potato. https://doi.org/10.1016/B978-0-12-821237-0.00025-1

Shen, F., Yang, L., Zhang, L., Guo, M., Huang, H., & Zhou, C. (2023). Quantifying the direct effects of long-term dynamic land use intensity on vegetation change and its interacted effects with economic development and climate change in Jiangsu, China. *Journal of Environmental Management*, *325*, 116562. https://doi.org/10.1016/j.jenvman.2022.116562

Shi, W., Zhao, H. Y., Chen, Y., Wang, J. S., Han, B., Li, C. P., Lu, J. Y., & Zhang, L. M. (2021). Organic manure rather than phosphorus fertilization primarily determined asymbiotic nitrogen fixation rate and the stability of diazotrophic community in an upland red soil. *Agriculture, Ecosystems & Environment*, *319*, 107535. https://doi.org/10.1016/j.agee.2021.107535

Tang, S., Ma, Q., Marsden, K. A., Chadwick, D. R., Luo, Y., Kuzyakov, Y., Wu, L., & Jones, D. L. (2023). Microbial community succession in soil is mainly driven by carbon and nitrogen contents rather than phosphorus and sulphur contents. *Soil Biology and Biochemistry*, *180*, 109019. https://doi.org/10.1016/j.soilbio.2023.109019

Tang, T., Sun, X., Liu, Q., Dong, Y., & Zha, M. (2023). Treatment with organic manure inoculated with a biocontrol agent induces soil bacterial communities to inhibit tomato *Fusarium* wilt disease. *Frontiers in Microbiology, 13*, 1006878. https://doi.org/10.3389/fmicb.2022.1006878

Tartaglia, M., Ranauda, M. A., Falzarano, A., Maisto, M., Postiglione, A., Prigioniero, A., Scarano, P., Zuzolo, D., Sciarrillo, R., & Guarino, C. (2023). Metatranscriptomics of pastures under drought stress show a rhizospheric meta-organism reshape.

Rhizosphere, 26, 100687. https://doi.org/10.1016/j.rhisph.2023.100687

Taş, N., de Jong, A. E., Li, Y., Trubl, G., Xue, Y., & Dove, N. C. (2021). Metagenomic tools in microbial ecology research. *Current Opinion in Biotechnology, 67*, 184-191. https://doi.org/10.1016/j.copbio.2021.01.019

Thompson Jr, W. R. (1992). Importance of water solubility in phosphate fertilizers. In *Proceedings of the Annual Meeting Fertilizer Industry Round Table (USA)*.

Tian, L., Zhang, F., Zhang, L., Gao, X., & Feng, B. (2023). Use of metagenomics and metabolomics to quantify changes in rhizosphere soil microbial function in response to mulching regimes. *Land Degradation & Development, 34*(10), 3033-3048. https://doi.org/10.1002/ldr.4666

Toole, D. R., Zhao, J., Martens-Habbena, W., & Strauss, S. L. (2021). Bacterial functional prediction tools detect but underestimate metabolic diversity compared to shotgun metagenomics in southwest Florida soils. *Applied Soil Ecology*, *168*, 104129. https://doi.org/10.1016/j.apsoil.2021.104129

United Nations. (2023). Sustainable Development Goals Report 2023. United Nations. Retrieved January 7, 2024, from https://sdgs.un.org/goals

Verma, B. C., Pramanik, P., & Bhaduri, D. (2020). Organic fertilizers for sustainable soil and environmental management. *Nutrient Dynamics for Sustainable Crop Production*, 289-313. https://doi.org/10.1007/978-981-13-8660-2_10

Wang, B., Wang, X., Wang, Z., Zhu, K., & Wu, W. (2023). Comparative metagenomic analysis reveals rhizosphere microbial community composition and functions help protect grapevines against salt stress. *Frontiers in Microbiology*, *14*, 1102547. https://doi.org/10.3389/fmicb.2023.1102547

Wang, L., & Xiong, X. (2022). Long-Term Organic Manure Application Alters Urease Activity and Ureolytic Microflora Structure in Agricultural Soils. *Agronomy, 12*(12), 3018. https://doi.org/10.3390/agronomy12123018

Wang, S., Ai, J., Cui, P., Zhu, Y., Wu, H., & Zhang, W. (2020). Diagnostic value and clinical application of next-generation sequencing for infections in immunosuppressed patients with corticosteroid therapy. *Annals of Translational Medicine*, *8*(5), 227. https://doi.org/10.21037%2Fatm.2020.01.30

Wang, W., Yang, S., Zhang, A., & Yang, Z. (2021). Synthesis of a slow-release fertilizer composite derived from waste straw that improves water retention and agricultural yield. *Science of the Total Environment, 768*, 144978. https://doi.org/10.1016/j.scitotenv.2021.144978

Wang, Z. J., Yue, F. J., Wang, Y. C., Qin, C. Q., Ding, H., Xue, L. L., & Li, S. L. (2022). The effect of heavy rainfall events on nitrogen patterns in agricultural surface and underground streams and the implications for karst water quality protection. *Agricultural Water Management*, *266*, 107600. https://doi.org/10.1016/j.agwat.2022.107600

Wei, W., Cao, J., Wu, X. C., Cheng, L. P., Shen, X. N., Sha, W., & Sun, Q. (2023b). Diagnostic performance of metagenomic next-generation sequencing in non-tuberculous mycobacterial pulmonary disease when applied to clinical practice. *Infection*, *51*(2), 397-405. https://doi.org/10.1007/s15010-022-01890-z

Wei, Z., Sixi, Z., Xiuqing, Y., Guodong, X., Baichun, W., & Baojing, G. (2023a). Arbuscular mycorrhizal fungi alter rhizosphere bacterial community characteristics to improve Cr tolerance of Acorus calamus. *Ecotoxicology and Environmental Safety*, *253*, 114652. https://doi.org/10.1016/j.ecoenv.2023.114652

Wenhui, Z., Zucong, C., Lichu, Y., & He, Z. (2007). Effects of the long-term application of inorganic fertilizers on microbial community diversity in rice-planting red soil as studied by using PCR-DGGE. *Acta Ecologica Sinica*, *27*(10), 4011-4018. https://doi.org/10.1016/S1872-2032(07)60084-5

Wijitkosum, S. (2018). Fuzzy AHP for drought risk assessment in Lam Ta Kong watershed, the north-eastern region of Thailand. *Soil and Water Research, 13*(4), 218-225. https://doi.org/10.17221/158/2017-swr

Williams, A., Birt, H. W., Raghavendra, A., & Dennis, P. G. (2023). Cropping system diversification influences soil microbial diversity in subtropical dryland farming systems. *Microbial Ecology*, *85*(4), 1473-1484. https://doi.org/10.1007/s00248-022-02074-w

Windisch, S., Sommermann, L., Babin, D., Chowdhury, S. P., Grosch, R., Moradtalab, N., Walker, F., Höglinger, B., El-Hasan, A., Armbruster, W., Nesme, J., Sørensen, S. J., Schellenberg, I., Geistlinger, J., Smalla, K., Rothballer, M., Ludewig, U., & Neumann, G. (2021). Impact of long-term organic and mineral fertilization on rhizosphere metabolites, root–microbial interactions and plant health of lettuce. *Frontiers in Microbiology*, *11*, 597745. https://doi.org/10.3389/fmicb.2020.597745

Wolsing, M., & Priemé, A. (2004). Observation of high seasonal variation in community structure of denitrifying bacteria in arable soil receiving artificial fertilizer and cattle manure by determining T-RFLP of *nir* gene fragments. *FEMS Microbiology Ecology*, *48*(2), 261-271. https://doi.org/10.1016/j.femsec.2004.02.002

Woo, S. L., De Filippis, F., Zotti, M., Vandenberg, A., Hucl, P., & Bonanomi, G. (2022). Pea-wheat rotation affects soil microbiota diversity, community structure, and soilborne pathogens. *Microorganisms, 10*(2), 370. https://doi.org/10.3390/microorganisms10020370

Wyszkowska, J., Borowik, A., & Kucharski, J. (2022). The role of grass compost and *Zea Mays* in alleviating toxic effects of tetracycline on the soil bacteria community. *International Journal of Environmental Research and Public Health, 19*(12), 7357. https://doi.org/10.3390/ijerph19127357

Xiang, L., Harindintwali, J. D., Wang, F., Bian, Y., Zhao, Z., Wang, Z., Wang, Y., Mei, Z., Jiang, X., Schaffer, A., & Xing, B. (2023). Manure-and straw-derived biochars reduce the ecological risk of PBDE and promote nitrogen cycling by shaping microbiomes in PBDE-contaminated soil. *Chemosphere*, *312*, 137262. https://doi.org/10.1016/j.chemosphere.2022.137262

Xu, G., Zhang, L., Liu, X., Guan, F., Xu, Y., Yue, H., Huang, J.-Q., Chen, J., Wu, N., & Tian, J. (2022). Combined assembly of long and short sequencing reads improve the efficiency of exploring the soil metagenome. *BMC Genomics, 23*(1), 37. https://doi.org/10.1186/s12864-021-08260-3

Xu, J., Si, L., Zhang, X., Cao, K., & Wang, J. (2023b). Various green manure-fertilizer combinations affect the soil microbial community and function in immature red soil. *Frontiers in Microbiology*, 14. https://doi.org/10.3389%2Ffmicb.2023.1255056

Xu, P., Gao, Y., Cui, Z., Wu, B., Yan, B., Wang, Y., Wen, M., Wang, H., Ma, X., & Wen, Z. (2023a). Application of Organic Fertilizers Optimizes Water Consumption Characteristics and Improves Seed Yield of Oilseed Flax in Semi-Arid Areas of the Loess Plateau. *Agronomy, 13*(7), 1755. https://doi.org/10.3390/agronomy13071755

Yamazaki, S., Mardani-korrani, H., Kaida, R., Ochiai, K., Kobayashi, M., Nagano, A. J., Fujii, Y., Sugiyama, A., & Aoki, Y. (2021). Field multi-omics analysis reveals a close association between bacterial communities and mineral properties in the soybean rhizosphere. *Scientific Reports*, *11*(1), 8878. https://doi.org/10.1038/s41598-021-87384-8

Yang, J., He, J., Jia, L., & Gu, H. (2023b). Integrating metagenomics and metabolomics to study the response of microbiota in black soil degradation. *Science of The Total Environment*, *899*, 165486. https://doi.org/10.1016/j.scitotenv.2023.165486

Yang, K., Wang, X., Hou, R., Lu, C., Fan, Z., Li, J., Wang, S., Xu, Y., Shen, Q., Friman, V. P., & Wei, Z. (2023a). Rhizosphere phage communities drive soil suppressiveness to bacterial wilt disease. *Microbiome*, *11*(1), 1-18. https://doi.org/10.1186/s40168-023-01463-8

Yu, H., Ling, N., Wang, T., Zhu, C., Wang, Y., Wang, S., & Gao, Q. (2019). Responses of soil biological traits and bacterial communities to nitrogen fertilization mediate maize yields across three soil types. *Soil and Tillage Research*, *185*, 61-69. https://doi.org/10.1016/j.still.2018.08.017

Zhang, C., Zhao, X., Liang, A., Li, Y., Song, Q., Li, X., Li, D., & Hou, N. (2023a). Insight into the soil aggregate-mediated restoration mechanism of degraded black soil via biochar addition: Emphasizing the driving role of core microbial communities and nutrient cycling. *Environmental Research, 228,* 115895. https://doi.org/10.1016/j.envres.2023.115895

Zhang, H., Luo, G., Wang, Y., Fei, J., Xiangmin, R., Peng, J., Tian, C., & Zhang, Y. (2023b). Crop rotation-driven change in physicochemical properties regulates microbial diversity, dominant components, and community complexity in paddy soils. *Agriculture, Ecosystems & Environment, 343*, 108278. https://doi.org/10.1016/j.agee.2022.108278

Zhang, H., Wang, X., Li, Y., & Ding, W. (2022a). Effect of long-term fertilization on bacterial community in a sandy loam soil and its relation to organic carbon accumulation. In *E3S Web of Conferences* (Vol. 338, p. 01007). EDP Sciences. https://doi.org/10.1051/e3sconf/202233801007

Zhang, X., Feng, J., Su, X., Lei, Y., Wu, W., & Cheng, X. (2020). Next generation sequencing reveals a synchronous trilateral lung adenocarcinoma case with distinct driver alterations of EGFR 19 deletion or EGFR 20 Insertion or EZR-ROS1 fusion. *OncoTargets and Therapy*, 12667-12671. https://doi.org/10.2147/OTT.S283617

Zhang, Z., Zhang, Q., Cui, H., Li, Y., Xu, N., Lu, T., Chen, J., Penuelas, J., Hu, B., & Qian, H. (2022b). Composition identification and functional verification of bacterial community in disease-suppressive soils by machine learning. *Environmental Microbiology*, *24*(8), 3405-3419. https://doi.org/10.1111/1462-2920.15902

Zhao, G., Wu, K., An, T., Wen, L., Zi, S., Fan, Z., Zhou, F., Ouyang, C., Yang, Y., Wu, B., & Fullen, M. A. (2023). Integrated analysis of changes in soil microbiota and metabolites following long-term fertilization in a subtropical maize-wheat agroecosystem. *Pedosphere,* *33*(3), 521-533. https://doi.org/10.1016/j.pedsph.2022.06.055

Zhao, S., Zhang, C., Mu, J., Zhang, H., Yao, W., Ding, X., Ding, J., & Chang, Y. (2020). All-in-one sequencing: An improved library preparation method for cost-effective and high-throughput next-generation sequencing. *Plant Methods*, *16*(1), 1-14. https://doi.org/10.1186/s13007-020-00615-3

Zhao, Y., Rodić, N., Liaskos, M., Assimopoulou, A. N., Lalaymia, I., & Declerck, S. (2024). Effects of fungal endophytes and arbuscular mycorrhizal fungi on growth of *Echium vulgare* and alkannin/shikonin and their derivatives production in roots. *Fungal Biology,* *128*(1), 1607-1615. https://doi.org/10.1016/j.funbio.2023.12.004

Zheng, Q., Zhang, S., Liang, J., Chen, Y., & Ye, W. (2023). The Impact of Cultural Memory and Cultural Identity in the Brand Value of Agricultural Heritage: A Moderated Mediation Model. *Behavioral Sciences*, *13*(2), 79. https://doi.org/10.3390/bs13020079

Zhou, W., Kang, L., Duan, H., Qiao, S., Tao, L., Chen, Z., & Huang, Y. (2021). A virtual sequencer reveals the dephasing patterns in error-correction code DNA sequencing. *National Science Review*, *8*(5), nwaa227. https://doi.org/10.1093/nsr/nwaa227

Zhou, Y., Zhang, J., Xu, L., Nadeem, M. Y., Li, W., Jiang, Y., Ding, Y., Liu, Z., & Li, G. (2022). Long-term fertilizer postponing promotes soil organic carbon sequestration in paddy soils by accelerating lignin degradation and increasing microbial necromass. *Soil Biology and Biochemistry*, *175*, 108839. https://doi.org/10.1016/j.soilbio.2022.108839

Zhu, L., Huang, C., Li, W., Wu, W., Tang, Z., Tian, Y., & Xi, B. (2023a). Ammonia assimilation is key for the preservation of nitrogen during industrial-scale composting of chicken manure. *Waste Management,* *170*, 50-61. https://doi.org/10.1016/j.wasman.2023.07.028

Zhu, L., Li, W., Huang, C., Tian, Y., & Xi, B. (2023b). Functional redundancy is the key mechanism used by microorganisms for nitrogen and sulfur metabolism during manure composting. *Science of The Total Environment,* 169389. https://doi.org/10.1016/j.scitotenv.2023.169389