TRENDS IN ANIMAL AND PLANT SCIENCES
https://doi.org/10.62324/TAPS/2023.005
www.trendsaps.com; editor@trendsaps.com

REVIEW ARTICLE

A Deep Dive into the Soil Microbiome: Unseen Allies in Enhancing Crop Health and Productivity

Amjad Ali[1], Muhammad Awais[1], Muhammad Tayyab Sadiq[1], Arbaz Hassan[2], *Ali Ammar[2]

[1]Institute of Soil & Environmental Sciences, University of Agriculture Faisalabad, Pakistan
[2]Department of Plant Breeding and Genetics, University of Agriculture Faisalabad, Pakistan
***Corresponding author:** aliammar225@gmail.com

Article History: 23-010 Received: 22-Feb-2023 Revised: 23-Apr-2023 Accepted: 24-May-2023

ABSTRACT

In the face of growing global food demands and environmental challenges, optimizing agricultural productivity while maintaining sustainability is a significant concern. One largely untapped resource lies beneath our feet: the soil microbiome, a complex network of microbial communities. This review aimed to synthesize the current understanding of the soil microbiome and its potential in enhancing crop productivity. We examined the soil microbiome's diverse constituents, their roles in crop health and productivity, and the impact of human interventions. Despite substantial progress in the field, complexities remain due to the inherent diversity of soil microbial communities and the challenges in their study and manipulation. Our analysis reveals the promising potential of soil microbes in augmenting crop yields, disease resistance, and resilience against environmental stressors. Furthermore, the review emphasized that agricultural practices, biofertilizers, biopesticides, and genetic engineering could significantly influence the soil microbiome. While potential risks and ethical considerations exist, particularly in microbial engineering, emerging technologies offer exciting opportunities for microbiome-based crop enhancement. The review underscores the crucial need for continued research in this area, given the potential of the soil microbiome as a game-changer for sustainable agriculture. It also highlights the promising future directions and the emerging techniques in the soil microbiome research.

Key words: Soil Microbiome, Crop Productivity, Sustainable Agriculture, Nutrient Cycling, Disease Suppression, Stress Resistance, Biofertilizers, Biopesticides, Microbe-Plant Interactions, Soil Fertility, Microbial Diversity.

INTRODUCTION

The soil microbiome represents one of the most complex and diverse communities on the planet, influencing an array of processes vital for ecosystem functioning and agricultural productivity (Fierer, 2017). The microbiome, defined as the collective genomic entity of microorganisms in a particular environment, is comprised of a vast assortment of bacteria, archaea, fungi, viruses, and other microbial and eukaryotic species (Thakur and Geisen, 2019). The soil microbiome, in particular, is an intricate ecological network with a central role in regulating soil health and fertility, which is fundamental for crop growth and yield (Bender, *et al.*, 2016).

Agriculture has always depended on the soil microbiome, albeit often unknowingly, due to its importance in nutrient cycling, disease suppression, and modulating plant responses to stressors (Bulgarelli *et al.*, 2013). Modern agricultural practices, such as monoculture cropping and the overuse of chemical fertilizers and pesticides, can alter the soil microbial community's structure and function, often to the detriment of soil health and crop productivity (Lupatini *et al.*, 2017). As such, the sustainable management of soil microbial communities presents an opportunity to enhance agricultural productivity while minimizing environmental impact (abu Haraira et al., 2022).

The diversity of the soil microbiome and its influence on crop health and productivity is an emerging and rapidly expanding field of research (Busby *et al.*, 2017). This is fueled by advancements in next-generation sequencing technologies and bioinformatics, which allow for in-depth exploration of soil microbial diversity and functionality (Trivedi *et al.*, 2020). As we begin to better understand these complex interactions, the potential for

Cite This Article as: Ali A, Awais M, Sadiq MT and Ammar A, 2023. A deep dive into the soil microbiome: unseen allies in enhancing crop health and productivity. Trends in Animal and Plant Sciences 1: 30-36. https://doi.org/10.62324/TAPS/2023.005

harnessing the soil microbiome to support sustainable agricultural practices becomes increasingly clear (AFZAL et al., 2023).

In this review, we delve into the major components of the soil microbiome, its role in crop health and productivity, the impacts of human intervention, and future perspectives in soil microbiome research. Understanding these invisible allies under our feet is a crucial step toward realizing the full potential of sustainable agriculture.

Understanding the Soil Microbiome

The soil microbiome is the embodiment of nature's complexity (I AMJAD et al., 2022). It encompasses a myriad of microorganisms that interact with each other, with plants, and with the soil itself, playing critical roles in ecosystem functioning and stability (Delgado-Baquerizo *et al*., 2018).

A. Major Microbial Components of the Soil (Bacteria, Archaea, Fungi, etc.)

The soil microbiome is a consortium of diverse organisms including bacteria, archaea, fungi, viruses, protozoa, and other eukaryotes (Rillig *et al*., 2019). Bacteria and archaea, the microscopic unicellular prokaryotes, are the most abundant and arguably the most essential components (Ammar et al., 2022). They are key players in nutrient cycling, involved in processes like nitrogen fixation, nitrification, and sulfur and phosphorus transformations (Levy *et al*., 2018).

Fungi also form a significant part of the soil microbiome, with roles in decomposing organic matter and forming mutualistic relationships with plants as mycorrhizae, thereby enhancing plant nutrient uptake (Bonfante and Genre, 2015). Some fungi are pathogenic to plants and can cause diseases, while others protect plants by competing with or directly antagonizing these pathogens (Schlatter *et al*., 2017).

In addition to bacteria, archaea, and fungi, the soil microbiome also includes other less-understood but potentially critical entities such as viruses and protozoa (Bano et al., 2023). These organisms influence soil microbial communities' structure and function through predation and viral lysis, indirectly impacting nutrient cycling and disease suppression (Roux *et al*., 2016).

B. Soil Microbiome Diversity

The soil microbiome is incredibly diverse, arguably more so than any other habitat on Earth. It is estimated that a gram of soil can harbor up to a billion microorganisms belonging to thousands of species (Roesch *et al*., 2007). This immense microbial diversity is a product of the soil's heterogeneous nature, providing a multitude of microhabitats and ecological niches that different organisms can occupy (Fierer and Jackson, 2006).

High microbial diversity often corresponds to improved soil health and function because different microorganisms carry out different functions, contributing to the resilience and stability of the soil ecosystem (Wagg *et al*., 2014). A diverse soil microbiome can also benefit plants by promoting nutrient availability, improving resistance to pathogens, and helping plants tolerate environmental stressors (ALMAS et al., 2023).

C. Factors Influencing Soil Microbiome Composition

Soil microbial communities are shaped by various biotic and abiotic factors. Abiotic factors include soil properties like texture, structure, pH, temperature, and moisture, which directly affect microbial activity and survival (Fierer, 2017). Different microbial groups prefer different soil conditions; for example, acidobacteria are prevalent in acidic soils, while actinobacteria are common in alkaline soils (Lauber *et al*., 2009).

Biotic factors such as plant types also influence the soil microbiome (Ifrah Amjad et al., 2022). Different plant species secrete different root exudates, attracting specific microbial communities—a phenomenon known as the 'rhizosphere effect' (Bulgarelli *et al*., 2013). Further, land management practices, including crop rotation, tillage, and application of fertilizers or pesticides, can also drastically alter soil microbial community composition (Lupatini *et al*., 2017).

Understanding the major components, diversity, and factors influencing the soil microbiome's composition provides critical insights into its role in soil health and agricultural productivity. As we dig deeper into this unseen world, we reveal opportunities to harness the soil microbiome to enhance sustainable agriculture (Ashraf et al., 2022).

Soil Microbiome and Crop Health

An underappreciated facet of agriculture is the crucial role played by the soil microbiome in promoting crop health (BASHIR et al., 2023). The vast microbial network in the soil significantly influences nutrient cycling, plant-microbe interactions, and disease suppression, directly impacting crop productivity (Berendsen, *et al.,* 2012).

A. Role in Nutrient Cycling and Soil Fertility

Soil microorganisms are vital catalysts for biochemical transformations that drive nutrient cycling in the soil-plant system (Bhutta et al., 2023). They decompose organic matter, converting complex compounds into forms readily available to plants (Chaudhry et al., 2022). Bacteria and archaea, for instance, are involved in nitrogen cycling processes, such as nitrogen fixation, nitrification, and denitrification (Levy *et al*., 2018). Soil fungi also play a crucial role in decomposition, particularly of more complex organic compounds like lignin and cellulose (Baldrian, 2017).

Mycorrhizal fungi form symbiotic relationships with the roots of most plant species, enhancing nutrient uptake, particularly of phosphorus, and improving soil structure (Smith and Read, 2008). Similarly, certain bacteria, termed plant growth-promoting rhizobacteria

(PGPR), can enhance plant nutrient uptake and growth by producing plant hormones, solubilizing phosphate, and fixing nitrogen (Backer *et al*., 2018).

B. Microbe-Plant Interactions: Pathogens and Mutualists

The soil microbiome is a complex network of interactions, including those between microbes and plants. These interactions can range from beneficial symbioses to deleterious pathogenic relationships (Fatima, Saeed, Ullah, et al., 2022).

Pathogens in the soil can cause significant crop losses. Some fungi, bacteria, and nematodes are known to cause plant diseases, such as Fusarium wilt, bacterial canker, and root-knot nematode disease, respectively (Mendes *et al*., 2011). Understanding these pathogenic interactions can aid in developing more effective disease management strategies (Imtiaz et al., 2022).

On the other end of the spectrum, many soil microbes engage in beneficial interactions with plants (IQBAL et al., 2023). As mentioned, mycorrhizal fungi and PGPR enhance plant nutrient uptake. Additionally, endophytic bacteria and fungi, which live inside plant tissues without causing harm, can confer benefits to their host plants, such as enhanced tolerance to abiotic stressors and protection against pathogens (Backer *et al*., 2018).

C. Disease Suppression by Beneficial Microbes

Interestingly, certain members of the soil microbiome can suppress plant diseases, offering a biological alternative to chemical pesticides (Khalid & Amjad, 2018a). Some microbes outcompete or antagonize pathogens, produce antimicrobial compounds, or induce systemic resistance in plants, making them more resistant to pathogens (Berendsen, *et al.,* 2012).

Disease-suppressive soils, naturally occurring or induced by certain farming practices, are soils in which specific pathogens cause less damage than expected, thanks to their microbiome composition (Mendes *et al*., 2011). Understanding these systems could pave the way for innovative approaches to plant disease management.

In summary, the soil microbiome's critical roles in nutrient cycling, plant-microbe interactions, and disease suppression underscore its potential in enhancing crop health and productivity. Harnessing these unseen allies could revolutionize sustainable agriculture.

Soil Microbiome and Crop Productivity

The role of the soil microbiome in agriculture extends beyond safeguarding plant health. It exerts direct and indirect influences on crop productivity through mechanisms such as boosting plant growth, augmenting disease resistance, and modulating plant responses to environmental stressors (Zaghum et al., 2021). These interactions emphasize the integral role of soil microbes in agricultural ecosystems (Vandenkoornhuyse *et al*., 2015).

A. Influences on Plant Growth and Yield

Microbial inhabitants of the soil contribute extensively to nutrient cycling, providing a range of essential elements to plants that aid in growth (FATIMA, SAEED, KHALID, et al., 2022). This relationship extends beyond nutrient supply. Microbes like mycorrhizal fungi and plant growth-promoting rhizobacteria (PGPR) interact intimately with plants, encouraging robust growth that can potentially translate to increased crop yield (Backer *et al*., 2018).

Beyond nutrient provision, PGPR and other rhizobacteria impact plant growth through the production of phytohormones like auxins, gibberellins, and cytokinins, further emphasizing their key role in promoting plant development (Glick, 2012). Endophytic microbes, which inhabit plant tissues, represent another microbial community that can promote plant growth and yield through nutrient solubilization, modulation of plant hormones, and alteration of plant metabolic pathways (Hardoim *et al*., 2015).

B. Indirect Effects through Pest and Disease Resistance

The microbiome can also indirectly affect crop productivity by bolstering plant resistance to pests and diseases (Khalid & Amjad, 2018b). Certain beneficial microbes in the soil are known to outcompete or inhibit pathogens, produce antimicrobial substances, or trigger systemic resistance in plants, enhancing their immunity against potential pathogens (Berendsen, *et al.,* 2012).

The potential of endophytes in pest management should not be underestimated (Khalid et al., 2022). Some endophytic bacteria, such as Bacillus thuringiensis, produce toxins that are fatal to many agricultural pests but harmless to humans and most non-target organisms (Bravo *et al*., 2011). Leveraging such biological interactions can reduce reliance on synthetic pesticides, encouraging more sustainable agricultural practices (Khalid, Abdullah, et al., 2021).

C. Modulation of Plant Stress Responses (Drought, Salinity, etc.)

Soil microbes also play a pivotal role in assisting plants to withstand various abiotic stresses, including drought, salinity, extreme temperatures, and heavy metal toxicity (Shahani et al., 2021). Some bacteria and fungi improve plant tolerance to these stresses through various mechanisms, such as osmoprotection, modulation of plant hormone levels, alteration of root architecture, and sequestration or transformation of toxic metals (Yang, *et al.,* 2009).

For example, arbuscular mycorrhizal fungi can enhance plant drought and salinity tolerance by improving water and nutrient uptake, maintaining ion homeostasis, and reducing oxidative damage (Augé, 2001). Likewise, certain PGPR can mitigate the deleterious effects of salt stress in plants by producing osmoprotective compounds, maintaining ion balance, or modifying plant hormonal levels to enhance stress resilience (Egamberdieva *et al*., 2017).

Interestingly, endophytes also play a role in enhancing plant tolerance to abiotic stresses. They may produce protective compounds, alter plant hormone levels, induce changes in gene expression, or modulate plant metabolic pathways to improve the stress tolerance of their host plants (Rodriguez *et al*., 2008).

Taken together, the multifaceted contributions of the soil microbiome in enhancing plant growth and yield, promoting resistance to pests and diseases, and modulating plant stress responses underscore its potential as a powerful tool for improving crop productivity. Leveraging these unseen allies in the soil could unlock new avenues for sustainable agriculture (Hamza et al., 2018).

Human Intervention and the Soil Microbiome

The soil microbiome's composition and function can be profoundly influenced by human interventions, particularly in the context of agriculture. This section will explore the impacts of various agricultural practices on the soil microbiome, the application of biofertilizers and biopesticides, and the potential of genetic engineering to harness soil microbes for crop enhancement (Mustafa et al., 2022).

A. Impacts of Agricultural Practices on Soil Microbiome

Agricultural practices, including crop rotation, tillage, monoculture, use of synthetic fertilizers and pesticides, and irrigation, significantly impact the soil microbiome (Razzaq et al., 2020). While some practices, such as crop rotation and reduced tillage, can enhance microbial diversity and function, others like intensive tillage and excessive use of chemicals can negatively affect microbial communities, compromising soil health and productivity (Francioli *et al*., 2016).

For example, monoculture, a common practice in modern agriculture, has been found to result in a significant reduction in soil microbial diversity, which can decrease soil fertility and productivity over time (Hartmann *et al*., 2015). On the other hand, cover crops and crop rotation practices can increase microbial diversity and soil health, contributing to sustainable agriculture (McDaniel, *et al.,* 2014).

B. The Role of Biofertilizers and Biopesticides

Biofertilizers and biopesticides, derived from beneficial microbes, represent promising alternatives to chemical fertilizers and pesticides. These products can support plant growth and health while mitigating the negative impacts of chemicals on the soil microbiome (Razzaq et al., 2021).

Biofertilizers, such as those containing nitrogen-fixing bacteria or mycorrhizal fungi, can improve plant nutrient uptake, boost crop yield, and enhance soil fertility (Adesemoye, *et al.,* 2009). Similarly, biopesticides, comprising microbes that can inhibit or kill plant pathogens, provide a sustainable approach for pest management with minimal adverse effects on non-target organisms and the environment (Glare *et al*., 2012).

C. Genetic Engineering of Soil Microbes for Crop Enhancement

Recent advances in genetic engineering and synthetic biology provide unprecedented opportunities to manipulate soil microbes for crop enhancement . Through genetic modifications, microbes can be engineered to have enhanced nutrient provision, pathogen inhibition, or stress tolerance abilities, which can in turn improve plant health and productivity (Chen, *et al.,* 2019).

Moreover, microbes can also be engineered to produce beneficial plant compounds or biomolecules that can improve crop traits, such as yield, quality, or resistance to biotic and abiotic stresses. This emerging field, known as plant microbiome engineering, holds immense promise for the future of agriculture (Trivedi *et al*., 2020).

In summary, human interventions, through changes in farming practices, use of bio-based products, and genetic engineering of soil microbes, can significantly impact the soil microbiome. These interventions offer exciting opportunities to harness the power of the soil microbiome to enhance crop productivity sustainably (Kamal et al., 2019).

Challenges and Future Perspectives

Understanding and harnessing the soil microbiome for crop productivity present both exciting opportunities and substantial challenges. This section will discuss the difficulties in studying and manipulating the soil microbiome, potential risks and ethical considerations, emerging techniques in the field, and future directions (Razzaq et al., 2020).

A. Difficulties in Soil Microbiome Study and Manipulation

Studying the soil microbiome is inherently complex due to its incredible diversity and the intricate interactions between microbes and their environment (Fierer, 2017). Additionally, many soil microbes cannot be cultured in the laboratory, which hinders our understanding of their ecology and functions (Stewart, 2012).

Manipulating the soil microbiome for crop enhancement is also challenging. The effects of adding beneficial microbes to soil can be inconsistent, as their survival and functionality are influenced by numerous factors, such as soil type, weather conditions, and the presence of other microbes (Thakur and Geisen, 2019).

B. Potential Risks and Ethical Considerations

The manipulation of soil microbiomes, particularly through genetic engineering, raises potential risks and ethical considerations (Zafar et al., 2020). For instance, engineered microbes may have unintended effects on non-target organisms or disrupt natural microbial communities. They may also transfer engineered genes to other organisms through horizontal gene transfer, with unpredictable consequences (Rovira *et al*., 2019).

C. Emerging Techniques and Approaches in Soil Microbiome Research

Despite these challenges, advances in technologies such as high-throughput sequencing, metagenomics, metatranscriptomics, and bioinformatics are revolutionizing our ability to study soil microbes (Jansson and Baker, 2016). Moreover, synthetic biology and genome editing tools like CRISPR-Cas offer novel ways to manipulate soil microbes for crop enhancement (Huang *et al*., 2020).

D. Future Directions for Enhancing Crop Productivity through Soil Microbiome

In the future, research should focus on understanding the functional traits of soil microbes that contribute to crop productivity, developing reliable methods for microbial community manipulation, and evaluating the long-term impacts of these manipulations on soil health and ecosystem functions (Busby *et al*., 2017).

Moreover, integrating soil microbiome management into conventional farming practices could provide new strategies for sustainable agriculture. This could involve tailoring crop rotation and fertilization strategies to support beneficial microbes, using microbial inoculants or biofertilizers, and genetically engineering crops or microbes for improved interactions (Vorholt *et al*., 2017).

Conclusion

The soil microbiome, often referred to as the 'unseen ally' in agriculture, plays a pivotal role in supporting crop health and productivity. It is a vital participant in nutrient cycling, enhancing soil fertility, and bolstering plant growth. The interaction of soil microbes with plants also aids in suppressing disease, resisting pests, and modulating responses to environmental stresses like drought and salinity.

Human interventions through agricultural practices, biofertilizers and biopesticides usage, and genetic engineering of soil microbes have profound implications for the soil microbiome and its utility in agriculture. Such interventions can help achieve sustainable agricultural systems, augment crop yields, and reduce the reliance on chemical fertilizers and pesticides.

Despite the significant progress made in understanding the soil microbiome and its potential in agriculture, several challenges and complexities remain. The vast diversity and intricate interactions within the soil microbial community necessitate more nuanced study. Technological advancements like metagenomics, synthetic biology, and genome editing are instrumental in driving this research forward.

Further studies are crucial to discern the functional traits of soil microbes contributing to crop productivity, develop reliable methods for manipulating the microbial community, and understand the long-term impacts of these manipulations on soil health and overall ecosystem functions. Such advancements will enable us to more effectively harness the power of the soil microbiome, offering novel strategies for sustainable agriculture and food security in the future (Zafar et al., 2022).

The growing recognition of the soil microbiome's importance underpins its potential as a valuable resource for enhancing crop productivity (Khalid & Amjad, 2018a). Further research in this area, coupled with the development of innovative microbiome-based technologies, holds great promise for the future of agriculture (Khalid, Amjad, et al., 2021). This reinforces the critical need for continued exploration of our 'unseen allies' in the soil, their intricate networks, and their remarkable capacities to sustain and enhance agricultural productivity (Khalid & Amjad, 2018b).

REFERENCES

abu Haraira, A., Ahmad, A., Khalid, M. N., Tariq, M., Nazir, S., & Habib, I. (2022). Enhancing health benefits of tomato by increasing its antioxidant contents through different techniques: A review. Advancements in Life Sciences, 9(2), 131-142.

Adesemoye, A. O., Torbert, H. A. and Kloepper, J. W. (2009). Plant growth-promoting rhizobacteria allow reduced application rates of chemical fertilizers. *Microbial Ecology*, 58(4), 921-929.

Afzal, M., Khalid, M., Imtiaz, M., Nasir, B., Shah, S., Nawaz, M., Nayab, S., Malik, S., Majeed, T., & Maqbool, R. (2023). Selection of drought tolerant wheat genotypes based on mean performance and biplot analysis. Biological and Clinical Sciences Research Journal, 2023(1), 188-188.

Almas, M., Sami, A., Shafiq, M., Bhatti, M., Haider, M., HASHMI, M., & Khalid, M. (2023). Sale price comparison of saggian flower market: a case study. Bulletin of Biological and Allied Sciences Research, 2023(1), 39-39.

Amjad, I., Kashif, M., Akhtar, S., Nazar, M., Latif, A., Sarfraz, S., Shahbaz, U., Ahsan, M., Shamim, F., & Shahzadi, N. (2022). Evaluation of the tolerance of rice (Oryza sativa) for submergence and drought using various yield related stress indices. Biological and Clinical Sciences Research Journal, 2022(1).

Amjad, I., Kashif, M., Dilshad, R., Javed, M. A., Aziz, S., Khalid, M. N., Shakeel, A., Tahir, F., Riaz, M., & Saher, H. (2022). Submergence tolerance regulator, SUB1A: Convergence of submergence and drought response pathways in rice. Journal of Global Innovations in Agricultural Sciences

Ammar, A., Ghafoor, S., Akram, A., Ashraf, W., Akhtar, S., Nawaz, M., Zaghum, M., Khan, M., Aas, M., & Shaheen, A. (2022). Genetic evaluation of indigenous and exotic wheat germplasm based on yield related attributes. Biological and Clinical Sciences Research Journal, 2022(1).

Ashraf, A., Amhed, N., Shahid, M., Zahra, T., Ali, Z., Hassan, A., Awan, A., Batool, S., Raza, M., & Irfan, U. (2022). effect of different media compositions of 2, 4-d, dicamba, and picloram on callus induction in wheat (Triticum aestivum L.). Biological and Clinical Sciences Research Journal, 2022(1).

Augé, R. M. (2001). Water relations, drought and vesicular-arbuscular mycorrhizal symbiosis. *Mycorrhiza*, 11(1), 3-42.

Backer, R., Rokem, J. S., Ilangumaran, G., Lamont, J., Praslickova, D., Ricci, E. and Smith, D. L. (2018). Plant growth-promoting rhizobacteria: context, mechanisms of action, and roadmap to commercialization of biostimulants for sustainable agriculture. *Frontiers in Plant Science*, 9, 1473.

Baldrian, P. (2017). Forest microbiome: diversity, complexity and dynamics. *FEMS Microbiology Reviews*, 41(2), 109-130.

Bano, M., Shakeel, A., Khalid, M. N., Ahmad, N. H., Sharif, M. S., Kanwal, S., Bhutta, M. A., Bibi, A., & Amjad, I. (2023). Estimation of Combining Ability for Within-Boll Yield Components in Upland Cotton (Gossypium hirsutum). Sarhad Journal of Agriculture, 39(1).

Bashir, H., Zafar, S., Rehman, R., Hussain, M., Haris, M., Khalid, M., Awais, M., Sadiq, M., & Amjad, I. (2023). Impact of potentially soil mineralizable nitrogen (PMN) on soil health and crop production. Biological and Agricultural Sciences Research Journal, 2023(1).

Bender, S. F., Wagg, C. and van der Heijden, M. G. (2016). An underground revolution: biodiversity and soil ecological engineering for agricultural sustainability. *Trends in Ecology & Evolution*, 31(6), 440-452.

Berendsen, R. L., Pieterse, C. M. and Bakker, P. A. (2012). The rhizosphere microbiome and plant health. *Trends in Plant Science*, 17(8), 478-486.

Bhutta, M. A., Bibi, A., Ahmad, N. H., Kanwal, S., Amjad, Z., Farooq, U., Khalid, M. N., & Nayab, S. F. (2023). Molecular Mechanisms of Photoinhibition in Plants: A Review. Sarhad Journal of Agriculture, 39(230).

Bonfante, P. and Genre, A. (2015). Arbuscular mycorrhizal dialogues: do you speak 'plantish' or 'fungish'? *Trends in Plant Science*, 20(3), 150-154.

Bravo, A., Likitvivatanavong, S., Gill, S. S. and Soberón, M. (2011). Bacillus thuringiensis: A story of a successful bioinsecticide. *Insect Biochemistry and Molecular Biology*, 41(7), 423-431.

Bulgarelli, D., Schlaeppi, K., Spaepen, S., Ver Loren van Themaat, E. and Schulze-Lefert, P. (2013). Structure and functions of the bacterial microbiota of plants. *Annual Review of Plant Biology*, 64, 807-838.

Busby, P. E., Soman, C., Wagner, M. R., Friesen, M. L., Kremer, J., Bennett, A. and Dangl, J. L. (2017). Research priorities for harnessing plant microbiomes in sustainable agriculture. *PLoS Biology*, 15(3), e2001793.

Chaudhry, U. F., Khalid, M. N., Aziz, S., Amjad, I., Khalid, A., Noor, H., & Sajid, H. B. (2022). Genetic studies in different F2 segregating population for yield and fiber quality traits in cotton (Gossypium hirsutum L.). Journal of Current Opinion in Crop Science, 3(3), 135-151.

Chen, X., Ro, D. K. and Petri, R. (2019). The application of synthetic biology in manipulating plant immunity. *Phytopathology Research*, 1(1), 3.

Delgado-Baquerizo, M., Oliverio, A. M., Brewer, T. E., Benavent-González, A., Eldridge, D. J., Bardgett, R. D. and Fierer, N. (2018). A global atlas of the dominant bacteria found in soil. *Science*, 359(6373), 320-325.

Egamberdieva, D., Wirth, S., Bellingrath-Kimura, S. D., Mishra, J. and Arora, N. K. (2017). Salt-tolerant plant growth promoting rhizobacteria for enhancing crop productivity of saline soils. *Frontiers in Microbiology*, 8, 1897.

Fatima, A., Saeed, A., Khalid, M., Imam, M., Rafique, M., Sharif, M., Iqbal, N., Tipu, A., & Amjad, I. (2022). Genetic studies of f2 population for fiber and yield related attributes in Gossypium hirsutum. Biological and Clinical Sciences Research Journal, 2022(1).

Fatima, A., Saeed, A., Ullah, M., Shah, S., Ijaz, M., Anwar, M., Khaliq, A., Chohan, S., Khalid, M., & Khan, A. (2022). Estimation of gene action for the selection of superior parents and their cross combinations for yield and fiber associated attributes in american cotton (Gossypium hirsutum L.). Biological and Clinical Sciences Research Journal, 2022(1).

Fierer, N. (2017). Embracing the unknown: disentangling the complexities of the soil microbiome. *Nature Reviews Microbiology*, 15(10), 579-590.

Fierer, N. and Jackson, R. B. (2006). The diversity and biogeography of soil bacterial communities. *Proceedings of the National Academy of Sciences*, 103(3), 626-631.

Francioli, D., Schulz, E., Lentendu, G., Wubet, T., Buscot, F. and Reitz, T. (2016). Mineral vs. Organic Amendments: Microbial Community Structure, Activity and Abundance of Agriculturally Relevant Microbes Are Driven by Long-Term Fertilization Strategies. *Frontiers in Microbiology*, 7, 1446.

Glare, T., Caradus, J., Gelernter, W., Jackson, T., Keyhani, N., Köhl, J. and Raupach, M. (2012). Have biopesticides come of age?. *Trends in Biotechnology*, 30(5), 250-258.

Glick, B. R. (2012). Plant growth-promoting bacteria: mechanisms and applications. *Scientifica*, 2012.

Hamza, M., Tahir, M. N., Mustafa, R., Kamal, H., Khan, M. Z., Mansoor, S., Briddon, R. W., & Amin, I. (2018). Identification of a dicot infecting mastrevirus along with alpha-and betasatellite associated with leaf curl disease of spinach (Spinacia oleracea) in Pakistan. Virus Research, 256, 174-182.

Hardoim, P. R., Van Overbeek, L. S., Berg, G., Pirttilä, A. M., Compant, S., Campisano, A. and Sessitsch, A. (2015). The hidden world within plants: ecological and evolutionary considerations for defining functioning of microbial endophytes. *Microbiology and Molecular Biology Reviews*, 79(3), 293-320.

Hartmann, M., Frey, B., Mayer, J., Mäder, P. and Widmer, F. (2015). Distinct soil microbial diversity under long-term organic and conventional farming. *The ISME Journal*, 9(5), 1177-1194.

Huang, H., Luo, R., Chen, H. and Yan, X. (2020). Opportunities and challenges: precision modulation of plant endophytes in the post-metagenomic era. *Frontiers in Microbiology*, 11, 1434.

Imtiaz, M., Shakeel, A., Nasir, B., Khalid, M., & Amjad, I. (2022). Heterotic potential of upland cotton hybrids for earliness and yield related attributes. Biological and Clinical Sciences Research Journal, 2022(1).

Iqbal, J., Khalid, M., Riaz, S., Razaq, A., Shakoor, A., Karim, A., Razzaq, B., Gohar, M., Aqeel, M., & Majeed, T. (2023). dissection of yield and fiber quality traits under drought condition in Gossypium hirsutum L. Biological and Clinical Sciences Research Journal, 2023(1), 330-330.

Jansson, J. K. and Baker, E. S. (2016). A multi-omic future for microbiome studies. *Nature Microbiology*, 1(5), 1-5.

Kamal, H., Minhas, F.-u.-A. A., Farooq, M., Tripathi, D., Hamza, M., Mustafa, R., Khan, M. Z., Mansoor, S., Pappu, H. R., & Amin, I. (2019). In silico prediction and validations of domains involved in Gossypium hirsutum SnRK1 protein interaction with cotton leaf curl Multan betasatellite encoded βC1. Frontiers in Plant Science, 10, 656.

Khalid, M. N., Abdullah, A., Ijaz, Z., Naheed, N., Hamad, A., Sheir, M. A., Shabir, F., Parveen, K., & Khan, M. D. (2021). Application and Potential Use of Advanced Bioinformatics Techniques in Agriculture and Animal Sciences. Ind. J. Pure App. Biosci, 9(3), 237-246.

Khalid, M. N., Amjad, I., Nyain, M. V., Saleem, M. S., Asif, M., Ammar, A., & Rasheed, Z. (2021). A review: tilling technique strategy for cereal crop development. International Journal of Applied Chemical and Biological Sciences, 2(5), 8-15.

Khalid, M., & Amjad, I. (2018a). The application of mutagenesis in plant breeding under climate change. Bulletin of Biological and Allied Sciences Research, 2018(1), 15-15.

Khalid, M., & Amjad, I. (2018b). Study of the genetic diversity of crops in the era of modern plant breeding. Bulletin of Biological and Allied Sciences Research, 2018(1), 14-14.

Khalid, M., Hassan, U., Hanzala, M., Amjad, I., & Hassan, A. (2022). Current situation and prospects of cotton production in Pakistan. Bulletin of Biological and Allied Sciences Research, 2022(1), 27-27.

Lauber, C. L., Hamady, M., Knight, R. and Fierer, N. (2009). Pyrosequencing-based assessment of soil pH as a predictor of soil bacterial community structure at the continental scale. *Applied and Environmental Microbiology*, 75(15), 5111-5120.

Levy, A., Gonzalez, I. S., Mittelviefhaus, M., Clingenpeel, S., Paredes, S. H., Miao, J. and Tringe, S. G. (2018). Genomic features of bacterial adaptation to plants. *Nature Genetics*, 50(1), 138-150.

Lupatini, M., Korthals, G. W., de Hollander, M., Janssens, T. K. S. and Kuramae, E. E. (2017). Soil microbiome is more heterogeneous in organic than in conventional farming system. *Frontiers in Microbiology*, 7, 2064.

McDaniel, M. D., Tiemann, L. K. and Grandy, A. S. (2014). Does agricultural crop diversity enhance soil microbial biomass and organic matter dynamics? A meta-analysis. *Ecological Applications*, 24(3), 560-570.

Mendes, R., Kruijt, M., de Bruijn, I., Dekkers, E., van der Voort, M., Schneider, J. H. and Raaijmakers, J. M. (2011). Deciphering the rhizosphere microbiome for disease-suppressive bacteria. *Science*, 332(6033), 1097-1100.

Mustafa, R., Hamza, M., Rehman, A. U., Kamal, H., Tahir, M. N., Mansoor, S., Scheffler, B. E., Briddon, R. W., & Amin, I. (2022). Asymptomatic populus alba: a tree serving as a reservoir of begomoviruses and associated satellites. Australasian Plant Pathology, 51(6), 577-586.

Razzaq, A., Ali, A., Safdar, L. B., Zafar, M. M., Rui, Y., Shakeel, A., Shaukat, A., Ashraf, M., Gong, W., & Yuan, Y. (2020). Salt stress induces physiochemical alterations in rice grain composition and quality. Journal of food science, 85(1), 14-20.

Razzaq, A., Ali, A., Zafar, M. M., Nawaz, A., Xiaoying, D., Pengtao, L., Qun, G., Ashraf, M., Ren, M., & Gong, W. (2021). Pyramiding of cry toxins and methanol producing genes to increase insect resistance in cotton. GM crops & food, 12(1), 382-395.

Rillig, M. C., Ryo, M., Lehmann, A., Aguilar-Trigueros, C. A., Buchert, S., Wulf, A. and Antunes, P. M. (2019). The role of multiple global change factors in driving soil functions and microbial biodiversity. *Science*, 366(6467), 886-890.

Rodriguez, R. J., Henson, J., Van Volkenburgh, E., Hoy, M., Wright, L., Beckwith, F. and Redman, R. S. (2008). Stress tolerance in plants via habitat-adapted symbiosis. *The ISME Journal*, 2(4), 404-416.

Roesch, L. F., Fulthorpe, R. R., Riva, A., Casella, G., Hadwin, A. K., Kent, A. D. and Triplett, E. W. (2007). Pyrosequencing enumerates and contrasts soil microbial diversity. *The ISME Journal*, 1(4), 283-290.

Roux, S., Enault, F., Hurwitz, B. L. and Sullivan, M. B. (2015). VirSorter: mining viral signal from microbial genomic data. *PeerJ*, 3, e985.

Rovira, A. D., Elliott, L. F. and Cook, R. J. (2019). The impact of cropping systems on rhizosphere organisms affecting plant health. In The Rhizosphere (pp. 389-436). Academic Press.

Schlatter, D., Kinkel, L., Thomashow, L., Weller, D. and Paulitz, T. (2017). Disease suppressive soils: New insights from the soil microbiome. *Phytopathology*, 107(11), 1284-1297.

Shahani, A. A. A., Yeboah, E. O., Nadeem, M., Amjad, I., Ammar, A., Rehman, A. U., Awais, M., & Khalid, M. N. (2021). Cytogenetics, Types and its Application in Crop Improvement. Int. J. Rec. Biotech, 9(1), 9-14.

Smith, S. E. and Read, D. J. (2008). Mycorrhizal Symbiosis. Academic Press, London.

Stewart, E. J. (2012). Growing unculturable bacteria. *Journal of Bacteriology*, 194(16), 4151-4160.

Thakur, M. P. and Geisen, S. (2019). Trophic regulations of the soil microbiome. *Trends in Microbiology*, 27(9), 771-780.

Trivedi, P., Leach, J. E., Tringe, S. G., Sa, T. and Singh, B. K. (2020). Plant–microbiome interactions: from community assembly to plant health. *Nature Reviews Microbiology*, 18(11), 607-621.

Vandenkoornhuyse, P., Quaiser, A., Duhamel, M., Le Van, A. and Dufresne, A. (2015). The importance of the microbiome of the plant holobiont. *New Phytologist*, 206(4), 1196-1206.

Vorholt, J. A., Vogel, C., Carlström, C. I. and Müller, D. B. (2017). Establishing causality: opportunities of synthetic communities for plant microbiome research. *Cell Host & Microbe*, 22(2), 142-155.

Wagg, C., Bender, S. F., Widmer, F. and Van der Heijden, M. G. (2014). Soil biodiversity and soil community composition determine ecosystem multifunctionality. *Proceedings of the National Academy of Sciences*, 111(14), 5266-5270.

Yang, J., Kloepper, J. W. and Ryu, C. M. (2009). Rhizosphere bacteria help plants tolerate abiotic stress. *Trends in Plant Science*, 14(1), 1-4.

Zafar, M. M., Razzaq, A., Farooq, M. A., Rehman, A., Firdous, H., Shakeel, A., Mo, H., & Ren, M. (2020). Insect resistance management in Bacillus thuringiensis cotton by MGPS (multiple genes pyramiding and silencing). Journal of Cotton Research, 3(1), 1-13.

Zafar, M. M., Rehman, A., Razzaq, A., Parvaiz, A., Mustafa, G., Sharif, F., Mo, H., Youlu, Y., Shakeel, A., & Ren, M. (2022). Genome-wide characterization and expression analysis of Erf gene family in cotton. BMC Plant Biology, 22(1), 134.

Zaghum, M., Khalid, M., Zia, M., Gul, M., Amjad, I., & Irfan, M. (2021). Molecular Regulation in Seed Development Influencing the Fiber Growth in Gossypium hirsutum L. Acta scientific agriculture, 5, 15-23.