Microorganisms in the Integration of Environmental Sciences and Field Crop Diseases: A Comprehensive Perspective on Plant Health and Sustainable Production

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AkiNik Publications ®
New Delhi

Published By: AkiNik Publications

AkiNik Publications
169, C-11, Sector - 3,
Rohini, Delhi-110085, India
Toll Free (India) – 18001234070
Phone No.: 9711224068, 9911215212
Website: www.akinik.com
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Publication Year: 2026

Edition: 1st

Pages: 113

Paperback ISBN: 978-93-7150-340-2

E-book ISBN: 978-93-7150-747-9

Book DOI: https://doi.org/10.22271/ed.book.3529

Price: ₹ 555/-

Registration Details

- Printing Press License No.: F.1 (A-4) press 2016
- Trade Mark Registered Under
  - Class 16 (Regd. No.: 5070429)
  - Class 35 (Regd. No.: 5070426)
  - Class 41 (Regd. No.: 5070427)
  - Class 42 (Regd. No.: 5070428)

Abstract

Microorganisms are vital to the healthy functioning of the planet. Their intricate interactions with ecosystems and each other maintain soil health and fertility, influence the health of plants, animals, and humans, enable the remediation of polluted environments, and sustain the production and quality of food, feed, and fiber. These aspects are particularly relevant in the context of emerging pathogens and climate change. However, the microbiology of field-crop diseases and the simultaneous study of soil, plant, and environment have rarely been undertaken from an integrated viewpoint. This multidisciplinary and comprehensive synthesis highlights the integrated role of microorganisms in environmental sciences and field-crop diseases, focuses on their implications for plant health and sustainable production, and delineates future directions.

Microbial action is crucial for nutrient management and the biological control of crop diseases. Biological methods of improving soil health and restoring pollution-damaged ecosystems are growing in importance. In addition, pathogen detection and disease-monitoring systems play essential roles in the management of emerging diseases. A concept of integrated disease management (IDM) is proposed whereby the ecological knowledge of disease systems is incorporated with cultural practices, aiming to minimize chemical inputs while maintaining disease control. Furthermore, approaches using novel technologies like synthetic biology, microbiological engineering, artificial intelligence, and big data are evaluated.

Contents

Chapter - 1

Introduction to Microorganisms and Sustainable Agriculture

Microorganisms play a crucial role in functioning of agro-ecosystems and are intricately related with sustainable production systems. Agricultural microbiology has made tremendous progress during the past century, shaping the modern agriculture through useful applications. However, various factors are jeopardizing the production and productivity of agro-ecosystems, especially in field crops, as is evidenced by declining soil health and fertility, rising incidence of field crop diseases, and growing resistance to fungicides and bactericides. The regulatory authorities are also emphasizing the reduction of synthetic chemical inputs in integrated disease management. Microorganisms, being the most abundant and diverse living organisms in nature and existing in close association with higher plants, play a pivotal role in disease management. Microbial interactions, particularly those involving plant-associated microorganisms with potential beneficial effects, should be systematically studied. Omics tools are generating huge sequence data, giving an idea of the diversity and basic functions of microbial communities. Nevertheless, more focused research is needed to harness the intricate association among microorganisms and crop plants to improve disease resistance and alleviate other environmental stresses.

Microbial diversity and community structure in all major crop diseases and the influence of weather parameters on disease incidence should be investigated to develop predictive disease models and integrated microbial-based disease management. Practical environmental microbiology is being developed to understand and utilize microbial communities for natural degradation of environmental pollutants, including herbicides and pesticides. The combined application of novel detection methods and remote-sensing technologies is expected to improve pathogen detection, disease monitoring, and early warning systems for integrated disease management. The potential of disease-resistant cultivars, biological-control agents, and biopesticides is being harnessed, and their integration with other IDM components is being emphasized [1, 2, 3].

Role of microorganisms in agro-ecosystems

Microorganisms are vital components of all terrestrial and aquatic ecosystems with essential socio-economic and ecological roles. They are implicated in the recycling of nutrients within the environment, are involved in the biogeochemical cycling of important elements such as carbon and nitrogen needed for life, and play key roles in such processes as the breakdown of organic matter, mobilization of essential nutrients, detoxification of xenobiotics, and biological control of diseases. Interest in beneficial or helpful microbes has often led to increased understanding of plant and animal diseases; the marketing and production of antibiotics, vaccines, and other therapeutic agents; the production of many fermented foods; the use of nitrogen-fixing bacteria in crop-livestock management; and the biotechnological applications of microbes in the production of enzymes, amino acids, alcohols, vitamins, and organic acids.

Agriculture is the most altered ecosystem on Earth and has the greatest impact on the environment, affecting soil, water, and atmospheric systems. Inputs of synthetic chemical fertilizers and pesticides have enabled tremendous increases in crop yields, but at great cost to human health and environmental quality. These and other agricultural practices have also greatly altered the biodiversity of soil and water ecosystems, leading to considerable losses in species and genetic diversity of many important organisms. The maintenance of a healthy environment and enhancement of agricultural production have become top priority issues facing the world today. Sustainable plant and animal production using reduced chemicals has gained momentum in recent years, with major policies promoting less polluting, less chemistry-oriented, and more environmentally friendly practices. [4, 5, 6]

Historical development of agricultural microbiology

The history of agricultural microbiology is a tale comprising doctrine promulgated by leaders of the past and meritocratic action by players in the field advancing through headwinds to provide humanity with an increased understanding of the microbial world. It is replete with key inventions that have led not only to the present-day lifestyle but also to human survival in the future.

Equipped with powerful microscopes designed by Van Leeuwenhoek in the 18th century, the scientists of that time perceived microbes through an entirely different prism. While they were the first to unveil the door to the microbial world and recognized the significance of these organisms by outlining disease causation and food spoilage, their efforts remained largely unheralded. Their contributions provided the platform for a drastic change to take place in all major sectors, including agriculture and related fields.

The subsequent decade heralded gigantic steps in the understanding of soil biological processes. These pioneering contributions in microbiology were made by scientists such as Pasteur, Koch, Winogradsky, Beijerinck, and Hesseltine. However, although knowledge concerning microbial activity was accumulating, contributions of the topic with respect to crop production and disease management was rather limited. [3, 7, 8, 9]

Microbial diversity in agricultural environments

Is remarkable and complex, yet it remains under-explored in comparison with other habitats. The diversity of microorganisms found associated with different components of the agro-ecosystem contributes significantly to the sustainability of the product systems. Microbial communities of the soil, rhizosphere, phyllosphere, bulk leaf tissue, and other plant tissues are influenced by factors such as the nature of the habitat, type of management practices, climatic and edaphic conditions, frequency of crop rotations, kind of crop grown, and their geographical location and distribution. Understanding the diversity of microorganisms in relationship with their structure and function in a phyco-eco-physiological perspective is essential for host-microbe mutualistic relationships and healthier interactions within the environment. Sustaining healthy Soil-Plant-Microbe systems, while refining the understanding of spatio-temporal diversity of the involved key microbial players, is essential for improving system management and crop yield. The fate of these players under changing environmental conditions must also be taken into consideration.

Microbial diversity colonizing plant viruses in the selected chief cultivated vegetation is also crucial to the sustainability of the agricultural ecosystems. A considerable number of bacteria, fungi, and viruses depend on a considerable assortment of plants both for survival and for food quality. Recent research highlights the importance of these pathogens for the control of bio-chains in the higher ecosystem. In addition to primary producers, plants also serve as host for large and diverse groups of viruses that induce a wide range of symptoms and syndromes. The recycling of culture-associated wastes can contribute to organic soil fertility management and hypocotyl pigmentations and serve as bioenergy sources. Numerous naturally occurring solid wastes in various agro-ecological zones, mainly in developing countries, are recycled through bio-chemico microbial processes, appreciably enhancing their conversion into bio-energy. [3, 10, 11]

Microorganisms and sustainable production systems

Research outcomes described above conclude that microorganisms are vital to agriculture and the implementation of sustainable production systems. This section defines microorganisms and presents their significance in developing sustainable production systems in different agro-ecosystems.

Whether beneficial, neutral, or pathogenic, microorganisms are a large and irreplaceable part of the agro-ecosystem. Their functions and reactions are essential for efficient energy flow and nutrient cycling, as well as for maintaining overall soil health and ecosystem stability. Microflora present in the soil, rhizosphere, phyllosphere, roots, and other plant parts directly contribute to sustainable agriculture through biological nitrogen fixation, the solubilization of phosphorus and potassium, the control of diseases, composting waste recycling, and more. Microbiology can also modulate a variety of soil properties. A better understanding of microorganism-related topics is essential to anticipate, control, and reduce field-crop disease losses. Techniques and knowledge that will help decrease input costs while maintaining or increasing soil health and crop productivity for a growing population must be established. Ongoing research is needed in a number of fields of agricultural microbiology. [12, 13, 14]

Future directions in environmental and plant microbiology

Further research priorities for environmental and plant microbiology include an improved understanding of the role of microorganisms as a source of natural products, especially rare and medically important compounds; advanced molecular biology tools to address gene functions in environmental and plant-associated microorganisms; a deeper understanding of the ecological roles of phages, viromes, viruses and protozoa in environment; the biology of the abundant and ubiquitous, yet poorly understood, Fungi; the functioning of terrestrial, moorland, estuary and coastal ecosystems; natural microbial degradation pathways for heavily polluted areas (e.g. plastic, oil, metals, etc.); and microbial contributions to remediations under different climates. Development and field testing of rapid field detection of plant-pathogenic nematodes would also be of great value, as these nematodes are responsible for substantial yield losses in a variety of crops.

New directions in metabolic modelling, combined with single-cell sequencing techniques, are shifting metabolic modelling from laboratory-based semicontinuous cultures to environmental habitats under different conditions. Advances in artificial intelligence and machine learning promise to unlock a multitude of applications for precision agriculture. The prospects in synthetic biology and biotechnologies can pave the way for future applications in plant and environment microbiome, where modifying the association between microbes and plants could be a promising approach in producing 'healthy food for healthy people'. [15, 16, 17]

Chapter - 2

Soil Microbiology and Ecosystem Function

Soil is the habitat for heterogeneous microbial communities that fulfill vital roles in terrestrial ecosystems. Global microbial populations are typically estimated to reach 106 cells g−1, while local abundance in bulk soil ranges from a few tens to hundreds of million cells g−1. These microbial communities include bacteria, actinobacteria, fungi, and unicellular eukaryotes such as algae and protozoa, which interact in intricate ways and contribute to the cycling and exchange of nutrients, energy flows, organic matter decomposition, soil formation, soil aggregation, and fertility.

The various metabolic pathways of the soil microbiome allow the transformation of inorganic and organic compounds, thus either recycling or degrading diverse substrates and compounds from the environment, including recalcitrant synthetic molecules. The disturbance of microbial communities either through natural or anthropogenic activities can, moreover, affect their functional diversity and ecological potential, leading to severe changes in ecosystem function; during mass mortality events or the introduction of extreme conditions, specific keystone or core microbes can be responsible for maintaining soil functioning. For these reasons, the ecology and dynamics of soil microbial communities should be considered microbial biodiversity indicators of ecosystem health. Such indicators can then be applied to assess the effects of land-use change on soil microbial community structure and on microbial-mediated processes of nutrient cycling and organic matter decomposition, helping improve understanding of the interplay between biodiversity, ecosystem functioning, and resilience. [18, 19, 20]

Soil microbial communities

A recent meta-analysis evaluated soil microbial community structure on the basis of characteristics from 14,429 16S rRNA gene amplicon sequencing datasets across 2733 studies. Soil properties (texture, pH, organic carbon, etc.), plant characteristics (vegetation types, plant productivity, etc.), climate (temperature and precipitation) and other factors influenced the relative abundances of major bacterial phyla. The model predicted that Soil Microbial Community Structure (SMCS) could be affected by soil pH, total nitrogen, sand, silt, annual mean temperature and yearly precipitation, and that microbial communities would be more stable in temperate forest, temperate grassland and tundra than in tropical seasonal forest, tropical grassland and cropland. In addition, higher total nitrogen concentration and lower sand content would enhance soil microbial community stability.

Soil health is the capacity of the soil to function as a vital living ecosystem that sustains plants, animals, and humans, Digital Soil and Microbial Biodiversity Maps are products generated from soil information contained within Soil Grids and Microbiomes. The distribution of these datasets can be linked to ecosystem predictions. Despite progress in informative study design and experimental data collection, the understanding of soil biodiversity remains abstract and disconnected from many ecological paradigms. Careful selection and inclusion of data collation strategies and metadata fields will allow coherent analyses linking to evolutionary ecology and modern ecology concepts. [21, 22, 23]

Nutrient cycling and decomposition

Soil microorganisms drive nutrient cycling, organic matter decomposition, and humus formation, and in doing so support primary productivity and ecosystem functioning. Key biological processes include the mineralization and immobilization of nutrients, nitrogen fixation and denitrification, and the decomposition of organic matter. Soil microorganisms are best characterized as heterotrophic decomposers that mediate the turnover of complex organic substrates into simple microbial products, thereby accelerating nutrient cycling and ultimately returning nutrients to the plant pool. The decay of necromass from microbial metabolism sustains other soil biota, including soil invertebrates, and is a major source of resistant organic material (soil humic substances). Because they are sensitive to soil perturbation, changes in microbial community structure and diversity are increasingly recognized as indicators of soil quality or health.

While soil microbial communities are highly diverse, research has typically focused on broader groups of organisms as drivers of ecosystem services. Indeed, a wealth of experimental evidence supports the hypothesis that soil microbial diversity is also positively related to nutrient cycling and the decomposer function. However, linking species richness to a specific function in an ecosystem remains an elusive challenge. Current evidence indicates that microbial community composition, as opposed to diversity, may be a more informative indicator of ecosystem change, with changes in evenness and the relative abundance of key taxa or groups of functions providing the strongest relationship with overall ecosystem functioning. Given that species and functional richness can change independently, these results emphasize the importance of distinguishing between biodiversity measures when predicting the soil ecosystem consequences of disturbance. [19, 24, 25]

Microbial indicators of soil health

The importance of soil microorganisms is increasingly recognized in understanding soil health and fertility. Soil microorganisms represent important breeding resources for crop production and ecosystem stability. Their response to agriculture, forest, and grazing land management often determines whether soil serves as a source or sink of atmospheric greenhouse gases.

In healthy soils, microbes fulfill key roles in recycling and transforming organic and inorganic matter so that nutrients are readily taken up by plants. Changes to the physical, chemical, or biological properties of soil all have an impact on soil biota. Consequently, soil-borne pathogens and disease-suppressive microbes can cause severe economic problems and limit plant growth. Microbial communities are therefore key indicators of soil health due to their functional diversity and rapid responsiveness to management practices. Integrating molecular and soil microbiological approaches can provide a detailed understanding of microbial community changes in response to land-use changes and management options, and support the development of science-based management strategies to both preserve soil ecology and optimize human activity. [18, 26, 27]

Soil biodiversity and resilience

Soil biodiversity supports functioning and resilience of soil microbiomes but has been less clearly associated with general soil health than microbial activity and community structure. Microbial community structure has been linked to a range of soil ecosystem functions and services within specific regions and land uses, but evidence from other data-rich regions corroborating this relationship is limited. Linking soil functional turnover with soil microbial α- and β-diversity across contrasting sites and soil property gradients provides new insight into the relevance of β-diversity for ecosystem functioning in diverse environments and highlights the need to understand the microbial community structure of soils throughout the world.

Increased management intensity of natural and semi-natural ecosystems can lead to biodiversity loss, yet the effects of such loss on the functioning and stability of soil biodiversity are poorly understood. Certain properties of soil bacterial and fungal communities—as well as microbial functional turnover—are known to be more sensitive to loss of β-diversity than change in α-diversity alone. In ecosystems suffering primary production loss, phylogenetic and functional redundancy in the bacterial community is present, the spatial variability in response patterns is higher for bacteria than for fungi, and the underlying mechanism involved in the response of soil microbial communities remains poorly understood. Changes in community composition due to natural or anthropogenic influences may therefore threaten nutritional cycling and thus long-term soil health [28].

Impact of land management on soil microbes

Land management practices influence the structure and functioning of soil microbial communities, which are critical for soil health and ecosystem services. Changes in soil physicochemical properties such as temperature, pH, moisture content, nutrient status, and organic matter alter specific microbial communities, resulting in variations in community composition, metabolic activity, biodiversity, and functional profiles.

Land use and management practices shape soil microbial communities and wastewater application influences the composition of bacterial communities. Drainage affects the abundance of nitrogen-cycling microbes. In forest soils, soil characteristics, parent material, and climate significantly influence microbial community composition and diversity. Short management periods can result in shifts in microbial community composition and affect community diversity. The impact of organic amendment on the bacterial community appears to be stronger than that of different synanthropic plants at arid sites. [29, 30, 31, 32]

Chapter - 3

Rhizosphere Microbiology

Microbial communities inhabiting the soil surrounding roots (the rhizosphere) are fundamentally important for plant nutrition, health, and development. The interaction of the root with a wide variety of resident or transient microorganisms shape the function of the surrounding rhizosphere ecosystem, and the capability of the root to attract beneficial microbiota is key. Among these, plant-growth-promoting rhizobacteria (PGPR) are a class of pervasively studied bacteria, and are recognized for their capacity to enhance plant health and yield. Root exudates serve as a major signal that shape the composition of root-associated microbiota, and serve as a key source of energy for microbes in the rhizosphere. The delicate balance of positive and negative interactions among resident root-associated microbes can be engineered through manipulation of root exudation, use of inoculates and microbiome editing practices. Rhizosphere microbiota shape plant health through mechanisms that, in addition to providing direct nutritional benefits, help plants cope with biotic or abiotic stresses and diseases.

Roots interact with the microbial community present in the soil by secreting various compounds and forming intimate associations with rhizobial species. The area of soil that surrounds roots and is influenced by these secretions is called the rhizosphere. Microorganisms in the rhizosphere gain energy and nutritional sources through root exudation. Rhizosphere microorganisms can also alleviate biotic and abiotic stresses of host plants by producing metabolites and hormones, thereby stimulating plant growth and promoting yield. The plant-microbe interaction in the rhizosphere region is often beneficial to both partners. For example, some plant-growth-promoting rhizobacteria (PGPR) are known to promote plant growth, increase yield and improve disease resistance. These beneficial microorganisms are frequently used as bio-inoculants to enhance the growth and yield of economically important crops. [33, 34, 35]

Root-microbe interactions

Root exudates released into the soil by plant roots play an important role in mobilizing microbial populations that can modify the rhizosphere by regulating their growth and inducing resistance in plants against biotic or abiotic stresses. Operate through signaling molecules in root exudates that are recognized by microorganisms, making communication between the root and the microbiome essential for optimization of plant health and productivity. PGPR inhabiting the rhizosphere are well known for their ability to enhance plant growth via various mechanisms, including nitrogen fixation, phosphate solubilization, and production of phytohormones. For an optimal response, however, these microbes must exist in functional units with the plant. Novel concepts such as rhizosphere microbiome engineering and use of consortia have recently been proposed in order to successfully utilize the rhizosphere for enhancing plant health, defense, and productivity.

With intensive agriculture, quantity has been emphasized over quality, resulting in a greater incidence of disease, deficiency, and reduced productivity. Maintenance of plant health by optimizing root-microbe interactions that can improve plant vigor and resistance to stress appears to be a practical approach for sustainable crop production under deteriorating conditions. Root-microbe interactions could be developed for integrating microbial biotechnology into disease management systems by enriching the root zone with appropriate beneficial microbes. [36, 37, 38]

Plant growth-promoting rhizobacteria (PGPR)

Root-microbe interactions are crucial to the health and productivity of plants. Enhance plant growth and health by improving stress tolerance, nutrient availability, and resistance to pathogens. PGPR influence plant growth by making nutrients more available and by directly affecting plant metabolism through a variety of mechanisms, including the synthesis of phytohormones or other metabolites that stimulate growth. The roles of root exudates as sources of carbon and energy for PGPR, as signals influencing rhizosphere colonization, and as mediators of plant-microbe interactions are recognized. Engineering the rhizosphere microbiome through the application of PGPR or other beneficial microorganisms may improve plant growth and reduce the incidence and severity of disease. The beneficial effects of PGPR on host plants are attributable to changes in the composition and activity of the rhizosphere microbiome, which can be shaped through inoculation.

The presence of a healthy and diverse microbiome within the rhizosphere usually contributes to plant health by enhancing growth, development, yield, and nutrients uptake. The presence of PGPR may be one factor determining the composition of the entire rhizobiome associated with a plant species; however, the composition of the rhizobiome is not only determined by the inoculated PGPR but also by other environmental factors. PGPR cultures containing a single or a few selected strains have consistently been shown to effectively enhance plant health. However, the real-life rhizosphere microbiome is a complex community, and one-time inoculation with only a few PGPR elements, although beneficial, may not have a lasting beneficial effect. Additionally, the effect of a PGPR attack on host plants depends not only on the strength and timing of the attack but also on the ecological interactions among different lineages of PGPR present in the rhizosphere community. Initiatives aimed at discovering PGPR capable of activating microbiome-induced systemic resistance could improve the management of fungal diseases in monocot plants [39, 40, 41, 42].

Root exudates and microbial signaling

Microbial life thrives around the root in the rhizosphere zone where root exudates comprise simple sugars, organic acids, and complex proteins. These exudates function as nutritional strategy for the microflora community in the rhizosphere ecosystem. However, recent reports have documented important fine-tuning aspects in regulating structure and functional diversity in the rhizoplane and endophytic microflora and also for local levels of soilborne pathogens. Yet the fine-tuning bit in the attractive quality of different C sources or C-amino and/or C-protein mixtures for promoting root elongation and root-associated microbial growth of extensive testmicrobiome remains elusive. In this context, it is noteworthy that screening is still absent, even for coupling between root-exudation profile and rhizosphere health-disease threshold concept.

Secretion-associated enzymes including polysaccharide lyases, pectin lyases, and others are involved in the biosynthesis or turnover of exudate components; the corresponding transcript patterns, the regulation of these enzymes at post-transcriptional status, and the circadian regulation of root exudation still remain to be particularly addressed in the field, despite being exciting research areas. As also reiterated by recent reports, the high-survival-requirement microbial signals recognized by different receptors are identified to be vital for the exchange of information between root-associated bacteria and their root hosts for modulating plant physiology and modulating the outcome of plant-microbe interactions. [43, 44, 45, 46]11111111

Rhizosphere microbiome engineering

Understanding microbial communities in the rhizosphere—root-associated soils—is critical for sustaining plant health. The selection of beneficial microbes, engineering of root-exudate signaling, and microbial community assembly for natural disease suppression offer avenues for harnessing rhizosphere microbes through their remodeling and enhancement.

Root exudates supply carbon and energy to the resident microbial community, allowing complex and sometimes subtle root-microbe interactions to develop, but we are only beginning to understand their total significance. That complexity opens new engineering opportunities, including synthetic microbial consortia and microbiome modulation to enhance protection against disease. The field is poised for merging omics with microbiome-remodeling approaches to increase plant health and productivity. [47, 48, 49]

Role in plant health and productivity

Microorganisms play a fundamental role in crop health and sustainable production. Importantly, plant-microbe interactions contribute to the production of healthy crops with minimal chemical inputs. The link between health, productivity, and nutrient availability is particularly salient. Microorganisms enhance nutrient supply through biological fixation, solubilization, and mineralization, enabling higher yield and better quality with lower fertilizer use compared to non-treated control plants. Microorganisms also establish a variety of symbiotic relations with crops—particularly, mycorrhizal fungi, nitrogen-fixing bacteria, and plant growth-promoting microbes. Employing disease-suppressive microbial communities or bioagents protects against crop diseases, yielding crops with lowered pest control measures. The adoption of disease-suppressive approaches enhances both environmental health and plant health.

The understanding of microbial systems underlying disease epidemiology guides the application of disease management strategies. Concepts such as the disease triangle, disease cycle, microbial antagonism, and competition form the ecological basis of integrated disease management (IDM). The integration of biological disease control with other cultural practices enhances the prospects of disease-free crop production. IDM reduces chemical pesticide use, enabling the production of commercially valuable food with enhanced health benefits. Bioremediation utilizes microbial metabolic capabilities for the breakdown of pollutants and toxins, and biosensors exploit microbial biosynthetic pathways for extracting metabolites following chemical exposure. Metabolic and biochemical processes are also called for in waste recycling, and directed microbial activity aids in composting and controlled degradation. [50, 51, 52, 50, 51, 52, 50, 51, 52]

Chapter - 4

Phyllosphere and Endophytic Microorganisms

Leaves are among the most highly exposed parts of plants, necessitating constant protection against biotic and abiotic stresses. Environmental conditions capable of altering the leaf surface can also modulate the phyllosphere microbial community composition, and the distribution of microbial species can differ qualitatively or quantitatively in relation to leaf age and plant developmental stage. The leaf surface is colonized mainly by epiphytes but also by endophytes. Some endophytes that semantically colonize the internal tissues of plants can establish symbiotic relations. Endophytic microorganisms have gained interest for application in biotechnology, as they can enhance the resistance of host plants to diseases. Such resistance mechanisms vary for different microbial taxa and include the production of antimicrobial compounds, increased plant defense responses, and the establishment of beneficial associations with other protective microorganisms located in the plant rhizosphere or phyllosphere.

The microbial community inhabiting the leaf surface, referred to as the phyllosphere, contributes to plant protection, mainly through competition for space and nutrients as well as the production of metabolites harmful to other organisms. However, the establishment of these microbial species varies with environmental conditions. Changes in the leaf surface morphology, physiology, or chemical composition can create a more suitable microhabitat for some species than for others. Phytopathogenic fungi may also benefit from alterations in the leaf surface caused by infection. For these reasons, identifying the leaf-surface microbial composition and demonstrating the possible beneficial actions of its members is a basic requirement for exploring phyllosphere microorganisms in applied research.

Microbial communities on leaf surfaces

The aerial parts of plants are colonized by phyllospheric microorganisms that can be pathogenic, saprophytic, or symbionts. Although the aboveground parts of plants, especially leaf surfaces, are usually considered hostile environments because of exposure to high insolation, temperature, and moisture fluctuations, they nevertheless support a spectrum of diverse and complex communities comprised of bacteria, fungi, algae, yeasts, and protozoa. The leaves are subject to moisture from dew, rain, clouds, and mist. Leaf surface conditions also vary with movement in wind, clouds, fogs, photoperiod, dew, and precipitation, making it favorable for colonization and growth of microorganisms. Rain falling on leaves, coupled with rain splash, may deposit materials that can serve as energy and carbon sources for the microbial community.

The presence of diverse accessary communities on the leaf surface of plants has been linked to plant health. In addition to increasing the use efficiency of nitrogen-based fertilizers in crops, a considerable body of work has consistently shown that various endophytes can enhance growth, induce systemic tolerance to various abiotic and biotic stresses, improve yield and quality, and provide various other benefits. They can also suppress diseases of economically important crops, but less frequently than other traditional biocontrol agents, including Pseudomonas, Bacillus, and Trichoderma-based products. The fermentation techniques of endophytes are bullishly used for large-scale production. A few commercial preparations based on endophytes have either been marketed or are under development. Induced systemic disease resistance by leaf-clearing fungus as a biological control agent was prominently demonstrated in mulberry.

Endophytes and plant symbiosis

The terminal portion of a plant leaf, often involved in photosynthesis and transpiration, is known as the saprobic phyllosphere because of its moist and warm environment. Fungi and bacteria colonizing leaves can proliferate widely and form abundant, richly varied populations. Though potentially pathogenic, phyllosphere microorganisms are mainly saprobic, recycling nutrients and cellulose, while some bacteria enhance leaf prominence. Endophytes—fungi or bacteria that colonize otherwise healthy plant tissue—may cause minimal or no damage. Leaf endophytes improve host photosynthetic capacity, promote plant growth, confer tolerance to abiotic stress, induce protective substances, and assist plant defenses against phytopathogens via mechanisms such as niche occupation, toxin/parasitic metabolite production, competitive inhibition, and phytohormone production. Additionally, plant colonization by certain basidiomycetous epiphytic fungi enhances resistance against bacterial and fungal infections.

AUBURN, University of, LASER- A Techno-Ecological Synthesis Report on the Fungal Kingdom, 2020. Endophyte-plant symbiosis encompasses interactions between endophytes and plants, with the former colonizing plant internal tissues without causing disease or harm, and operating mainly in the leaf, stem, and root. Most described leaf endophytes belong to the Ascomycota group. Their colonization may improve several physiological functions of host plants, including photosynthesis, biomass increase, and tolerance to stressors such as drought, salinity, and heavy metals, as well as diseases caused by biotic and abiotic agents. The principal mechanisms of biological control mediation comprise competition for space and resources, toxin production, and phytohormone synthesis, and specially target fungi, bacteria, nematodes, and insects. Leaf endophytes from persistently resistant cultivars are promising candidates for bioprotective products against existence-related infections [53, 54, 55].

Benefits of endophytic colonization

Plant endophytes are defined as non-pathogenic microorganisms that colonize living plant tissue without causing any immediate deleterious effects. Endophytes can live in different plant compartments such as leaves, stems or roots and can be exchanged from one plant to another via root or leaves/fruits; they are isolated from all plant species and recognized as important components of the plant holobiont, reflecting the wide-ranging interactions between plants and endophytes.

Numerous studies have documented the diverse benefits conferred by plant endophytes to host plants. These include growth promotion; active defense against phytopathogens; alleviation of abiotic stress (abiotic stress is the imposed on plants due to external environmental factors that are not conducive for growth and development); enhanced nutritional and medicinal qualities; and biotechnological applications since some endophytes produce various bioactive compounds such as alkaloids and terpenoids.

Most of the beneficial effects reported for the endophytic colonization are due to three actions: - endophytes improve growth directly by producing bioactive compounds and/or phytohormones, increasing nutrient acquisition, enhancing photosynthesis and stimulating germination, among others; - provide systemic resistance to pathogens via activation of the plant immune system through signal molecules, protection via direct action (e.g. degradation of secondary metabolites), as well as induced resistance; and/or - promote mitigation to abiotic stress through the production of antifreeze proteins, osmoregulatory solutes or phytohormones such as abscisic acid (ABA) that reversibly adjust physiological processes. [56, 57, 58]

Disease suppression mechanisms

A diversity of microorganisms colonize plant tissues without causing any symptoms of disease. Many of these interactions have beneficial outcomes for the host and are summarized as beneficial functions:

1) The colonization of the plant has no adverse effect on growth or development.
2) The beneficial microorganism is detected within the plant.
3) Production of metabolites such as growth hormones, vitamins, or pheromones that stimulate growth.
4) Improvement in nutritional characteristics of the host.
5) Assistance in photosynthetic activities.
6) Production of compounds such as antifungal substances, enzymes, antibiotics, and signaling molecules.
7) Induction of host defense response.

8) Protection from biotic and abiotic stress.
9) Increased resilience to heat or cold.
10) Enhancement of disease resistance or tolerance.

Beneficial endophytic fungi have been isolated from several plant species and shown to exert various protective functions. They can colonize and survive inside the plant without causing disease symptoms, and have been detected in roots, stems, leaves, flowers, and seeds. Colonization of plants by endophytic fungi has been shown to protect plants from pathogens through several proposed mechanisms:

1) Competition for ecological niches and nutrient media.
2) Synthesis of antibiotics.
3) Induction of systemic resistance responses at the whole-plant level.

The variety of antifungal metabolites produced by these endophytes is enormous and ranges from low-molecular-weight antibiotics to secondary metabolites. Induction of systemic resistance response in the plant has been implicated in the disease suppression role of endophytes. Priming or triggering the defense metabolism in the plant leads to faster and enhanced accumulation of defense-related compounds, which confer protection against subsequent infection [59, 60, 56, 61].

Biotechnological applications of endophytes

Bacterial and fungal endophytes are plant symbionts that grow within the plant tissue without causing wilting or other visible deleterious effects. Both contribute to the protection of the host plant from stress, especially biotic and abiotic stressors. In addition to their contributions to the overall health of the host, promote growth and enhance yield, and thus have great importance in agriculture. Various potential applications of endophytic microorganisms in biotechnology have been recognized. Endophytes are of great interest for bioprospecting because these microbes are usually specialized to live with certain plant species and can produce plant-specific and bioactive compounds. Assays for pharmaceutical and agricultural industry applications have detected a wide-spectrum production of bioactive metabolites such as antimicrobial, antioxidant, antitumoral, anticoagulant, allelochemicals, and nematicidal compounds; metabolites involved in chlorophyll biosynthesis; and enzymes (e.g., chitinase, β-glucanase, and protease) with the potential to control various plant pathogens and pests. The industrial implementations of such metabolites have a high commercial value.

Other valuable aspects include the potential to apply colonized plants in phytoremediation and bioremediation, the enhancement of growth and quality traits in various crops, such as tomato, cucumber, pepper, and jute, and the mitigation of various stresses in different crops (drought, salinity, flooding, metal stress). Genetic modifications of endophytic bacteria with a wide range of functions have been reported recently, with applications to promoting growth and improving tolerance/resistance against diverse biotic and abiotic stresses in plants [62, 63, 64, 35].

Chapter - 5

Plant Pathogenic Microorganisms

Microorganisms cause multiple plant ailments, commonly bacterial, fungal, oomycete, nematode, phytoplasma, or viral. For each group, principal illness-causing agents are listed and factors enabling prevalence in specific environments are identified with a focus on the biology of the pathogen. Such knowledge is essential for the development of culture- and weather-based warning systems, biofeedback systems, integrated resistance management programs, and other strategies for effective control.

Fungi cause the widest range of plant diseases. Major fungal pathogens include species of Fusarium, Phytophthora, Alternaria, Colletotrichum, Cercospora, Sclerotinia, Helminthosporium, Pythium, and Rhizoctonia. Oomycete pathogens include species of Phytophthora and Pythium. Virus diseases important in economically important crops are caused by potyviruses and begomoviruses. Bacteria, particularly species of Xanthomonas, Ralstonia, Erwinia, and Pseudomonas, are responsible for many severe bacterial infections. Plant-parasitic nematodes such as Meloidogyne spp., Heterodera spp., Pratylenchus spp., and Globodera spp. cause diseases of economic significance in various crops. Recent research has uncovered various new phytoplasma diseases including those associated with papaya, pineapple, banana, guava, and other hosts [65, 66, 67].

Bacterial plant pathogens

Bacterial pathogens infecting field crops include species from 24 genera. Members of these genera can affect different crops; however, a subset of genera is primarily responsible for diseases on specific field crops. The occurrence of complete information on the biology and epidemiology of disease in cultivated plants depends on the importance of the diseases. Furthermore, certain pathogens play a key role in infection and distribution, often combining the presence of known “corynebacteria,” “coryneform bacteria,” and “pseudomonads” that cause different types of cankers. Pathogen management depends on knowledge of the pathogen and disease. Environmental conditions at the time of infection, growth of susceptible varieties, and pathogen biology influence the severity of diseases.

Plant pathogenic fungi, oomycetes, bacteria, viruses, nematodes, and phytoplasmas are common to field crops. Among the agents, 44 genera of bacteria are known to infect cultivated plants, causing major economic losses and damage to food security and safety. The principal genera infecting vegetables are identified and their distribution presented. Additionally, the biology of type species of three economically important genera-Clavibacter, Ralstonia, and Xanthomonas-has been summarized to advance knowledge and understanding of diseases. [68, 69, 70, 71]

Fungal and oomycete pathogens

The former group is represented by ascomycetes, basidiomycetes, and deuteromycetes. The ascomycetes comprise many saprobes and large numbers of important plant and animal pathogens. The basidiomycetes are largely terrestrial, including most of the familiar mushroom fungi of contacting with N-containing compounds and acting on diverse substrates. The more economically important basidiomycetes are those attacking the roots or stems of woody trees and shrubs, especially in forests. The deuteromycetes are a large, heterogeneous assemblage of fungi whose relationships are not clearly established with any one of the other three divisions in mycology and thus are included in this separate division. They include many significant plant pathogens. Important fungal and bacterial pathogens of sunflower and potential determinants of disease incidence and severity in India have been elucidated based on knowledge of the biology and epidemiology of diseases associated with these pathogens.

Oomycetes (also known as water molds) are unicellular eukaryotic microorganisms and morphologically resemble fungi. They are propagated through flagellated asexual zoospores and reproduce sexually through the formation of oospores. They are responsible for some major plant diseases such as downy mildew, white rust, and late blights of potato and tomato. Some are also used for biological control of weeds, particularly azolla. However, others cause diseases and kill fish and amphibians. Oomycetes have been associated as important plant-pathogenic microorganisms causing significant economic losses. Oomycetes share similarities and differences with true fungi. Though these organisms are adapted to life in water, many members are pathogenic and infect their terrestrial hosts.

Viral plant diseases

Viruses infecting agricultural plants have attracted much interest from researchers due to their impacts not just on crops and horticultural plants but also on natural plant communities. However, only a few viruses have been utilized for the biological control of crop diseases. The introduction and spread of viruses should be prevented in order to ensure quality and quantity of produce. Viruses reproduce in living host cells with very limited subsystems; they depend on the host's metabolism for the biosynthesis of their components and are mainly responsible for packaging these into progeny virions. An understanding of the structure, functions and interactions of the viral proteins and the virus genome leads to a better understanding of the biology of viruses and provides fundamental knowledge for developing detection systems and control measures.

Viruses belong to different families that are composed of single-stranded or double-stranded RNA or DNA. The virus particle consists of at least a core of nucleic acids (DNA or RNA) protected by a protein coat (capsid). The capsid is composed of capsomers, which are formed by monomer units of the capsid protein. The classification of viruses is based on various criteria, including the type of nucleic acid, type of capsid symmetry, method of transmission, type of host, site of infection, and biological properties of the virus. In nature, viruses infect not only plants but also bacteria, fungi, insects, and animals. [72, 73, 74]

Nematodes and phytoplasmas

Plant-parasitic nematodes affect all plant parts. They utilize oral spear-like structures to penetrate host tissues, elicit root galls, induce syncytia, and establish ecto- and endoparasitic lifestyles. Nematodes-colonized plants have stunted growth, reduced quality and yield, and eventually die. Phytoplasmas are non-culturable cell wall-less prokaryotes that inhabit the phloem of plants and are transmitted by sap-sucking hemipteran insects. Phytoplasma-infected plants show stunted growth, yellowing, decolorization, reddening, and leaf curl. Phytoplasmas manipulate host plant development and physiology to their advantage. Symptoms may resemble other biotic or abiotic diseases, and diagnosis needs molecular tools or specific insect vectors.

Plant-parasitic nematodes reduce crop health and yield. Root knot nematodes of the genus Meloidogyne and the cyst nematodes Heterodera and Globodera are the most damaging. Plants infected by the root-knot nematode M. incognita exhibit root galls, resulting in stunted growth and yield loss. The reniform nematodes of the genus Rotylenchulus find hosts in a large number of families, and Rotylenchulus reniformis is a serious pest of cotton and other crops. Phytoplasmas cannot be cultured in artificial media but are transmitted by leafhoppers, planthoppers, and other hemipterans; many aphid and treehopper species can also transmit phytoplasmas. [75, 76, 77]

Epidemiology of crop diseases

Plant pathogenic microorganisms can be classified into bacterial, fungal, oomycete, viral, nematode, and phytoplasmal groups. In recent years, increasing emphasis has been placed on studying these pathogens in relation to the diseases they cause on agricultural crops, emphasizing their diagnosis and management. Epidemiology research has sought to elucidate the factors leading to the emergence of diseases and the role played by the biology of the pathogens in the development of the diseases. Epidemiology clearly influences Management strategies and the knowledge of these aspects should guide the control of diseases.

Diseases are caused by the interaction of susceptible plants, virulent pathogens, and environmental conditions conducive to infection. Understanding the biology of the pathogens and conducting targeted field studies is essential for predicting outbreaks and recommending preventive measures. Pathogen biology is linked to the timing and quantity of inoculum available in the field and can influence both the development and severity of diseases. The presence of virulence factors, such as toxins and enzymes, can also condition the relative weight of the inoculum and the environmental conditions in the development of the disease. [78, 79, 80]

Chapter - 6

Microbial Ecology of Crop Disease Systems

Plant diseases arise from the complex interplay among hosts, pathogens, and the environment, represented in the disease triangle. These three components are also part of a larger ecosystem, where pathogen behavior is modulated by other microbes, including potential antagonists. Disease severity can therefore be influenced by competition between microbes, and manipulation of the microbiome offers new avenues for disease management. Microbial activity can also augment disease prediction, yet outbreaks are also determined by climatic factors, including pests and diseases in association with changing climate, as diseases are often most severe in complicated seasons. Knowledge of the underlying principles permits the development of predictive disease models.

The disease triangle illustrates the interaction among host, pathogens, and environment. Microbial ecology examines the interaction among individuals in a community and explores temporal and spatial changes in community composition. Biotic interactions greatly impact microbial community composition in the context of disease and can modulate epidemiological dynamics. Disease severity can be altered by additional microbial communities present with pathogens in infected hosts. Microbial community composition in the rhizosphere and foliar surfaces has been shown to correlate with subsequent disease severity in a number of pathosystems. [81, 82, 83]

Disease triangle and microbial interactions

The disease triangle describes the static biotic components of the complex environment of a disease: susceptible host, pathogen capable of causing disease, and favourable environmental conditions (temperature, relative humidity, moisture, and other parameters).

Understanding the interactions among members of the disease triangle is a prerequisite for developing integrated disease management strategies that can effectively utilize ecological principles for disease regulation. Any factor that can affect disease incidence/severity will also have an effect on the composition and diversity of the microbial community associated with the plant. These microorganisms can compete for nutrients and space with pathogens while secreting bioactive compounds that may inhibit pathogen growth or activity.

Disruption of the microbial community can favour the outbreak of a disease, as observed in the early 1990s during a sorghum downy mildew outbreak in southern Mali, where the introduction of a new pathotype, together with land-use changes, was highlighted as a major cause of the epidemic. Field observations on leaves infected with powdery mildew showed a significant reduction in the total bacterial and fungal populations, suggesting the sensitivity of these organisms to the presence of the pathogen. Similarly, studies on the evolution of germinous assemblies during Coffea canephora Fusarium disease observed a reduction in bacterioplankton abundance and diversity in infected plants.

Hence, introduction of any pathogen into the ecosystem will certainly create modifications in the community involved, mainly through crosstalk, which occurs mutually from healthy to infected plants and vice versa. Analysis of edge effects on the total microbial community structure in coffee plantations revealed that some bacterial groups frequently associated with coffee plants were negatively affected when growing near the border of a native forest. Additionally, reductions in species richness and evenness of fungi associated with C. canephora trees were attributed to changes in environmental factors induced by the transition between the coffee plantation and the native forest. These findings suggest that modification of environmental conditions may govern the assembly of bacterial and fungal communities. [84, 85, 86]

Microbial competition and antagonism

The three components of the disease triangle - pathogen, host, and environment - must all be considered when assessing the potential for disease. Bacteria and fungi compete with pathogens for available resources and space through physical and chemical interactions, and over time, these relationships shape the structure of diseased or healthy microbiota. For example, small-molecule signalling from the root and root microbiome can modulate make-make, make-break and break-break interactions, thereby directly regulating disease severity. Populations with the potential for antagonism can alleviate stress induced during illness, and Cornell University has identified a range of microorganisms that tend to suppress disease. Notably, abundant environmental microbes modulate salinity in the declining storage roots of diseased elm trees. Environmental factors, including temperature, moisture, soil type, and fertilisation, can also impact diseases—notably through precipitation and surface humidity, which are considered crucial for disease initiation and the balance within plant-pathogen systems. Predictive models supported by big data enhance understanding of the impacts of these environmental factors on outbreaks. [87, 88, 89]

Microbiome influence on disease severity

The collective composition of the microbiome influences host health and plays an essential role in pathogen attack outcome. The disease triangle—pathogen, plant, and environment—describes suitable conditions for an outbreak. Microbial community composition impacts disease severity through direct competition, resource consumption, and metabolite production. Healthy plants with specific microbiota may either facilitate or antagonize disease establishment, making it crucial to manipulate the microbiome to counteract diseases.

The onset and severity of crop diseases are affected not only by the virulence of the pathogen but also by the composition of the microbial community present in the plant. Microorganisms contribute to biological determinants involved in the disease triangle, specifically those associated with the host plant. Thus, while the presence of a virulent pathogen is essential, environmental conditions conducive for foliar, stem, or root infection and disease establishment are equally crucial. Recent approaches in disease control suggest that seedlings with specific beneficial microbial communities may increase disease resistance. Factors such as host health and the role of beneficial indigenous microorganisms in disease initiation, establishment, severity, and post-disease recovery are being investigated, along with the microbial processes involved. [90, 91, 92]

Environmental drivers of disease outbreaks

The occurrence of epidemics within a crop disease system relies on three interrelated factors: the pathogens, the host crop and its environment, the physical state of the environment, and also on human practices degree that favour these factors. However, groupings of various other competing or antagonising major groups such as bacteria, fungi, and nematodes can also influence the crop disease process by either favouring or preventing the outbreak of the disease. Such influences can either serve to reduce the risk of disease within a healthy host crop or help it to recover quickly or even destroy the pathogens within the host crop.

Nevertheless, once the primary centre of origin of the pathogens favourable in terms of concentration, virulence, and pathogenicity of the pathogens is present, with the suitable environmental factors exerting the necessary cumulative stress on the primary host crop, the crop is in the process of achieving a level of disease severity or loss finally, even with the full support of the competing group or groups of antagonistic organisms, disease may progress towards considerably catastrophic levels. Thus, a careful study of the system under consideration enables researchers and practitioners to prepare predictive models that warn at an early stage of a potential epidemic and help in the development of an appropriate management strategy.

Predictive disease modeling

Approaches harness the data from several aspects of a disease system: crop yield response, weather, disease risk, and disease epidemiology into a single framework, providing a real-time, quantitative basis for decision support, erosion prediction, and reduction of economic losses. The collection and integration of this information require the sustained input of many research scientists, including those investigating the processes by which soil and on-plant microbes and disease pathogens interact. Disease-triangle theory predicts that plant diseases develop when a susceptible host plant, virulent pathogen, and suitable environmental conditions occur in the same place at the same time. In practice, combinations of these components can create conditions in which disease is improbable, unlikely, possible, or probable. For many diseases, the most dependable predictions are probabilistic rather than deterministic. Fulfilling M. A. Z. M. Mezek's assertion that “predictive microbiology is applicable to all microorganisms acting on food products, agricultural commodity and soil, no matter what the quality and characteristic of their product," probablistic disease prediction has been the goal of many research groups.

Chapter - 7

Biological Control and Beneficial Microorganisms

Principles of biological control are based on the use of living organisms for the prevention, suppression, or mitigation of diseases. Biological control of crop diseases has the potential to lessen the reliance on chemical pesticides, thus benefiting human and animal health as well as the environment. Numerous fungi and bacteria with antagonistic activity against plant pathogens have been identified and studied for their use as biological control agents.

Antagonistic fungi include those belonging to the Hyphomycetes, Ascomycetes, and Basidiomycetes classes, and their mechanisms of action can involve competition for space and nutrients, production of toxins, mycoparasitism, induction of systemic resistance in plants, and bioremediation of the pathogens' by-products. Antagonistic bacteria mainly belong to the genera Bacillus, Pseudomonas, and Serratia. These can produce a wide variety of biocontrol compounds, including antibiotics, hydrogen cyanide, various biosurfactants, and volatile organic compounds. Furthermore, they are capable of promoting plant health and vigor, provide multiple-benefit services against different pathogens, and can be commercialized as consortia. Several commercial products based on biological control of crop diseases are currently available, and these are considered effective and environmentally benign whenever used within a relevant integrated disease management framework. [93, 94, 95]

Principles of biological disease control

Biological control measures considered effective can be employed in a number of ways: as soil amendments, by foliar applications, wherein the agents directly contact the pathogen, or in management strategies that promote the colonization of plant surfaces by antagonistic microorganisms. For fungal pathogens, biological disease control is mostly based on the application of fungal antagonists, due to their mode of nutrition. For bacteria, both yeasts and actinomycetes have been the subject of study, in some cases with promising results. Some of the commercially available biocontrol products based on fungi or bacteria were first recognized as potential biocontrol agents in either palms or other hosts. The mechanisms involved in biological disease control have been well summarized, and some of the knowledge has already been applied in commercial products that are now used in the field. These products can be used alone or in combination within the confines of an integrated disease management strategy.

The plant surface is colonized by a number of microorganisms; fungi dominate the community, comprising the majority of the fungal species that have been detected through culture-independent methods. Fungi with the capacity to suppress the development of leaf blast disease have been found. Such foliar antagonists are frequently applied as a preventive measure. Products marketed as “biofungicides” are now available, mostly based on fungal antagonists that can compete for the same niche or produce substances which are toxic to the target pathogen. A few products based on bacteria have also been put on the market, although the effects of such applications have been, at best, inconsistent. [96, 97, 98]

Antagonistic fungi and bacteria

Numerous fungi and bacteria possess the ability to thwart pathogens and pest populations, often on targeted host plants. These microorganisms can be harnessed in biocontrol strategies aimed at decreasing the use of chemicals in plant protection, enhancing residue-free produce, and adhering to organic farming and sustainability mandates. Several biocontrol agents are undergoing commercial production or are being used in the market.

A diverse array of Bacillus species can hinder the growth of fungi, bacteria, and nematodes. Bacillus subtilis and Bacillus cereus are registered in multiple countries for biological control. Within the genus Trichoderma, T. virens and T. harzianum are the most broadly utilized. Four isolates continue to receive regulatory evaluation in the EU for controlling fungal pathogens on fruits, vegetables, and ornamentals.

Trichoderma-bacteria combinations can also confer greater pest repellent effects than individual agents. Other fungal genera engaged in biological control include Clonostachys, Myrothecium, Lecanicillium, Ampelomyces, and Pseudogymnoascus; among yeast, Aureobasidium pullulans has been widely commercialized. Many of these organisms produce multiple secondary metabolites implicated in biological control. In addition, some beetle symbionts of the genus Sphingobacterium exhibit antibacterial activities against plant pathogens. [99, 100, 101]

Mechanisms of biocontrol

Biological control can be defined as the use of living organisms to control plant diseases. Disease-suppressive organisms may be either indigenous or introduced. Many forms of biological control actually involve a combination of biological, physical, and chemical processes of disease suppression. Suppression of soilborne pathogens by suppression of the propagules is accentuated during root colonization of the pathogen by other more virulent soilborne pathogens acting faster than the pathogen of concern. Therefore, native disease-suppressor microorganisms should be selected for each pathogen of concern.

In disease supression, antagonistic fungi or bacteria confer some level of suppression but by themselves do not confer euphoric disease control. The most common forms of biological control are antagonism, mycoparasitism, competition for nutrients and space, hyperparasitism, and antibiosis. The control conducted by a living organism may be diluted or rerouted into pathogenic processes, termed opportunism. Bio-control can also be regarded as system immunity induced by an active agent, leading to enhanced defence mechanisms of host plants against disease. Other forms of control, not represented by active compound synthesis, such as regulation or induction of host fruit developmental stages, may also be considered. The production of a biological control agent for disease management is not sufficient; these agents need to be incorporated into field trials. In this assessment, the potential for improving disease control using Biocontrol was determined and combined into a table that presents the potential and realized biocontrol of the disease. [102, 103, 67]

Commercial biocontrol products

Principles of biological disease control stipulate that antagonistic species should be naturally present and adapted to the crop-disease system, exhibit high antagonistic potential, exert limited post-application toxicity, and achieve a ubiquitous population distribution. Biocontrol-active products must be eco-friendly, non-toxic to beneficial organisms, and operate in synergy with other management methods to avoid forcing pathogens towards more aggressive forms. Fungal antagonists account for most commercial products, notably Trichoderma species, which invade plant tissues and trigger protective systemic responses. Bacterial biocontrol agents, especially species in the genera Pseudomonas and Bacillus, occupy different ecological niches, suppress diseases through diverse mechanisms, and are less sensitive to chemical treatments. Bacteriophage biopesticides have yielded encouraging results, primarily against bacterial blights and wilts. Nevertheless, options for practical implementation are limited.

Diverse mechanisms mediate biological control, enabling different product categories. Mycoparasitic or endophytic activity can suppress saprophytic growth of soilborne pathogens or biotrophy of endophytes. Antibiosis, competition for resources and space, secretion of non-host-specific lytic enzymes, and induction of plant defenses can deter epiphytic pathogens. Bacteria that enhance TER in and around the root zone contribute indirectly to disease control. Products incorporating dual, multi-site, or multi-target antagonists have shown added value in controlling plant health. Microbial biopesticides can be integrated into integrated disease management programs, while microbial fertilizers-living inoculants added with nutrients or organic carriers-facilitate nutrient assimilation to support growth, health, and productivity. [104, 105, 106, 107]

Integration into disease management programs

Biological control of plant-pathogenic microorganisms is an integral component of an integrated disease management program. Commercial products that consist of antagonistic microorganisms provide protection against a range of diseases, including several traditionally ascribed to specific pathogens, and their effectiveness has been demonstrated repeatedly in both laboratory and field. These organisms must be integrated into management programmes if their full potential is to be realised.

Replacements of deadly fumigants and conventional fungicides in soil diseases have been a major driving force behind the development of biocontrol products. Other product categories have emerged more recently. For example, surrogate protection and bioamplification are concepts currently being evaluated. Surrogates encompass antagonists applied preventively that do not kill or deter pathogens but occupy niches, thereby limiting host access. Surrogates may compete with pathogens for space and nutrients, but their production of bioactive metabolites and interaction with the fungal microbiome are also crucial. Bioamplification is synonymous with a microbiome reshaped by local soil conditions, such as Pythium-inoculated onion, in which Pythium has no impact, yet disease severity increases if early-growth natural-equipment pulses are prevented. The next driver of biocontrol research is likely to be the establishment of permeable biomes. The basic principle is that pre-saturated permeable zones of a crop disease system can be protected by biocontrol agents and are excluded from infection, while adjacent zones remain free of biocontrol applications. [108, 109, 110, 108, 109, 110]

Chapter - 8

Microorganisms in Nutrient Management

Availability of nutrients is known to be an important requirement for maintaining and enhancing yield and quality of field crops. Microorganisms play a crucial role in providing nutrients in an eco-friendly manner in an agriculture-dominated ecosystem. Some prokaryotes, especially those belonging to the family Rhizobiaceae and the genera Azotobacter and Clostridium are known to undertake biological nitrogen fixation, while members of genera Pseudomonas, Bacillus, Mycobacterium, and Achromobacter are explored for biological degradation of urea. Mycorrhizae play a significant role in enhancing phosphorus and potassium availability.

These forms of nutrient supply, when supplemented with chemical fertilizers, have been shown to enhance nutrient use efficiency (NUE) that is derived as kilogram of grain produced per kilogram of fertilizer used. Application of P-solubilizing bacteria (PSB) along with NK fertilizers had recorded increased yield in paddy fields. Field studies have shown that addition of nitrogen-fixing and Phosphate Solubilizing Micromonospora spp. together with potassium-solubilizing microbes results in enhanced yield of jute and up to 15% higher yield of coconut. Field studies with microbial consortia have revealed that microbial combinations significantly improve soil microbial diversity and induce long-lasting beneficial effect on yield with superior quality of produce. In addition, the above additions are capable of meeting around 60% crop nutrient requirement of basal fertilizers without compromising yield and quality of produce, and promoted environment-friendly sustainable crop production with better quality of produce.

Nitrogen-fixing microorganisms

The efficiency of nitrogen fertilizers can be mitigated through the use of beneficial microorganisms. A variety of nitrogen-fixing microorganisms, both symbiotic and free-living, can increase the supply of nitrogen in soils. The use of genetically modified or engineered strains of rhizobia has not yet gained commercial acceptance. Several new approaches, such as the use of diazotrophic plant associations, transgenic plants or microbial consortia, have shown promise for enhancing nitrogen efficiency during field trials or in pot experiments. However, most of these reports are preliminary and require further research and development before commercialization.

Biofertilizers based on diazotrophic microorganisms have gained preferential attention, especially due to their role in achieving increased crop yield and quality. The application of diazotrophic N2-fixing microorganisms such as Azotobacter and/or Azospirillum has been shown to increase both plant growth and yield either alone or in consortia with other beneficial microorganisms like mycorrhizal fungi or phosphate solubilizing bacteria. However, the application of diazotrophic biofertilizers is generally being pursued on the basis of N-balances and yield increase only. Moreover, the degree of N-benefit derived from biofertilizers has almost been neglected and it is well known that the availability of N is of supreme importance to plants in the early phases of growth for achieving better growth and yield. [111, 112, 113, 111, 112, 113]

Phosphorus- and potassium-solubilizing microbes

In addition to fulfillment of nitrogen requirements, optimal crop production also depends upon phosphorus (P) and potassium (K), the two macro-nutrients, in sufficient quantities. Phosphorus is the second most critical nutrient for plants after nitrogen. Large amounts of phosphorus remain fixed in soil where it is not available to plants, which leads to inefficient use of chemical fertilizers. Mycorrhiza and phosphate solubilizing microbes help in making phosphorus available to plants. Still, there is a need for more detailed work on the specific strains useful to particular crops and regions to develop truly multispecies inocula and consortia of microorganisms that can supplement chemical P-fertilizers for sustainable agriculture. Numerous organisms, including several species of bacteria, fungi, algae, Archaea, actinomycetes, and viruses, solubilize potassium-bound forms of K from soil and rocks and render it available for plants. Bacteria belonging to the genera Microbacterium, Pseudomonas, Rhizobium, and Bacillus have been reported for their solubilizing ability. Fungal genera, such as Penicillium, Aspergillus, and Periconia, have also been shown to solubilize K.

These microbes are of immense importance for sustainable agriculture and are increasingly used to develop bio-inoculants. Application of a consortium of P- and K-solubilizing bacteria positively regulates functional microbial communities in groundnut rhizosphere soil, regulates nutrient uptake, and improves pod yield. Likewise, the three-way combination of mycorrhizal and P- and K-solubilizing inoculation improves leaf nutrient levels, the photosynthetic process, agronomic efficiency, and crop yield of blackgram. Can thus increase nutrient-use efficiency and contribute to sustainability of agriculture and food security.

Mycorrhizal associations

Mycorrhizal association occurs between fungal hyphae and plant roots. Mycorrhizal fungi increase nutrient (N, P, K, Zn) uptake through their vast hyphal network in exchange for C from plants. Mycorrhizal and P-solubilising microorganisms mitigate P deficiency and enhance yield and quality. Mycorrhizae are involved in promoting host tolerance to abiotic stresses (salt, drought, heavy metals) and biotic stresses (diseases). Application of functional mycorrhizal and P-solubilising microorganisms through spraying or soil application in association with crop production greatly affects growth, pest resistance, yield, and quality.

Soil microbial consortia, including nitrogen-fixing, phosphorus-solubilising, potassium-solubilising, mycorrhizal, and plant-beneficial fungi and bacteria, influence grain yield and nutritional quality of various crops. Foliar application of non-pathogenic mycorrhizal fungi reduces disease incidence in crops. Adequate supply of NPKNR and balanced use of organic and inorganic fertiliser improve plant health, nutrient status, and powdery mildew disease management and also enhance the yield and quality of crops like squash. These traits aid in an eco-friendly approach to crop nutrient management and plant disease control. [114, 115, 116, 114, 115, 116]

Microbial consortia for nutrient efficiency

Microbial consortia are increasingly recognized as essential in meeting the nutrient demands of cultivated crops and improving crop quality. Under challenging environmental conditions, deploying combinations of multiple microorganisms rather than single strains enhances microbial functionality in nutrient cycling processes and provides complementary benefits to plant growth and yield. Research evidence indicates that co-inoculation with diverse Nand P-solubilizing microorganisms can improve plant growth and productivity beyond single-species inoculation. Nitrogen-fixing plus phosphate- and/or potassium-solubilizing microorganisms can support cotton yield and lint quality. Incorporating multi-species inocula containing N2-fixers and arbuscular mycorrhizal fungi into crop management can improve nutrient uptake and seed oil content. Integrated application of N2-fixing bacteria, phosphate-solubilizing bacteria, and plant growth-promoting fungi can enhance plant growth and yield of crops like lentils, peas, and chickpeas.

Apart from N and P, potassium-solubilizing microorganisms are promising inoculants that also contribute to crop growth. Potassium-solubilizing bacteria, when applied together with other beneficial microorganisms or co-inoculated with certain crops, can improve yield and quality of cardamom, coriander, moringa, peanuts, and sugarcane. The functions of microbial consortia involving N2-fixing and P-solubilizing bacteria are further extended when they associate with mycorrhizae. [117, 118, 119]

Impacts on crop yield and quality

Nitrogen-fixing, phosphorus-solubilizing, potassium-solubilizing and mycorrhizal fungi constitute functional groups contributing to soil nutrient availability that support crop yield improvement. Besides, co-inoculation of various microbial genera create microbial consortia that provide synergistic benefits to plants, improving yield and enhancing quality parameters. Such microbial consortia are commercialized to enhance nutrient use efficiency in different crops. In addition to these single benefits, phosphate solubilizers and nitrogen fixers act as ameliorating agents during metal stress in plants by reducing accumulated metals, which not only favor plant growth but also enhance yield.

Financed by an external carbon source and using organic waste as growth medium, some bacteria and fungi also increase carbon and nutrients in the soil, resulting in enhanced yield and quality of the product. Similarly, assisted phytoremediation, which uses specific microbial strains with plants, helps in removal of heavy mental compounds, contributing significantly to environmental remediation while enhancing quality yield. Several microbial-derived biostimulants are reported to improve the quality of both fruit- and seed-bearing crops by reducing the concentration of both nitrate and heavy metals. These wholesome aspects of microbial-based strategy in agriculture highlight the importance of integrated innovative approach in achieving sustainability in production. [120, 121, 122, 123]

Chapter - 9

Environmental Microbiology and Pollution

In the last few decades, pollution has emerged as a major global concern negatively affecting the environment and human health. Microorganisms, due to their metabolic versatility, play a pivotal role in the biodegradation of various organic and inorganic pollutants from the environment. They accelerate the breakdown of xenobiotic compounds by using them as carbon and energy sources. Chemical fertilizers and pesticides are often used in agriculture to boost crop yield, but part of these chemicals leaches into soil and water bodies, leading to environmental pollution. Fungi and bacteria can remodel or degrade these chemicals into less toxic products. Metal-tolerant bacteria can alter the oxidation-state of metals and aid their bioremediation. The relation of microbes with environmental pollution as well as the application of microorganisms in environmental monitoring and management of polluted sites is discussed here.

Microbial decomposition of various pollutants presents a viable alternative to conventional chemical removal. Bacteria and fungi are employed in the bioremediation of chemical compounds such as hydrocarbons, chlorinated solvents, explosives and pesticides. The capability of microorganisms to utilize various organic matters and inorganic metal-tolerating properties have conferred them with enormous potential in removing pollution and restoring the environment. The discharge of heavy metals, plastics, pesticides and other pollutants has also collected considerable attention. Metal-tolerant or metal-accumulating strains have been isolated, characterized and applied in the bioremediation of polluted environments. [124, 125, 126, 127]

Microbial degradation of pollutants

Microorganisms have an invaluable role in the cycling of nutrients in polluted agro-ecosystems subjected to anthropogenic activities and in the detoxification of environmental pollutants, thus curbing their harmful effects on ecosystems. Environmental microbiology aims to understand these processes and uses microbial or plant-microbial systems for bioremediation and restoration of contaminated sites. Increasing concentrations of heavy metals in the environment due to rapid industrial development affect the microbiological make-up of the pollutant-affected areas. The presence of heavy metals may hinder microbial functions while tolerant microbes persist, establishing a different community structure. Microorganisms capable of degrading pesticides and herbicides play an important part in alleviating pesticide-induced soil disturbances and in bioremediation approaches for polluted sites.

And the use of microbial or plant-microbial processes for bioremediation have gained considerable attention in recent decades. Such approaches, along with studies on genetically modified organisms promising to alleviate pollution, also support waste recycling in agriculture by alternative methods. Such explorations and developments are particularly relevant in less developed countries striving for rapid growth. The co-cycling of multiple anthropogenic pollutants by microorganisms has received more consideration only recently. Consequently, an increasing number of new reports focus on the interplay between heavy metals and organic micropollutants. Being eco-friendly, microbial processes, either using naturally or engineered microorganisms, appear to be an ideal choice for addressing increasing pollution levels. [128, 129, 130, 131]

Bioremediation strategies

Terrestrial and aquatic ecosystems rely on microorganisms to maintain a balance of biological processes. For example, the ability of microbes to degrade a wide range of pollution is essential for the implementation of natural attenuation. Pollutants result from human activities and frequently exceed the capacity of microbial populations to degrade them. Therefore, in these situations, microbial communities that promote electrode processes of interest in geoelectrical bioremediation systems should be used. In addition to degrading microcontaminants, microorganisms can also regain their viability in the presence of high concentrations of metals and compounds toxic to other organisms. Through several technical approaches, certain groups of microorganisms can degrade or store heavy metals, or even degrade hazardous substances such as pesticides and herbicides.

Biodegradation allows the removal of hydrocarbons and many other extraordinary structures. The complete bioremediation of an ecosystem affected by pollutants takes years. Strategies to accelerate these processes are called biostimulation and bioaugmentation, where nutrients or specific microorganisms are applied to increase biodegradation rates. Microbial detection for screening of degradation has gained much attention. Environmental pollution has had important repercussions on human health, soil, and fresh water quality, and has severely damaged the ecosystem. Therefore, monitoring the state of pollution becomes very important. Some microorganisms develop resistance to environmentally polluted conditions and can be used as bioindicators to assess the level of contamination.

Bacteria and fungi, and especially fungi, have a great capacity to live in environments contaminated by insecticides, herbicides, or industrial and medicinal wastes and have been tested for either the detoxification or alteration of those substances. These bioremediation studies using supercritical fluids or biological materials have gained much interest due to the benefits associated with “green chemistry.” For example, different strains of purple non-sulfur bacteria have been studied for the degradation of various wastewaters, as well as yellow-green algae. [132, 133, 134]

Heavy metal tolerance and transformation

Microorganisms in the Integrated Role between Environmental Sciences and Field Crop Diseases Real and potential pollution of heavy metals is one of the most serious environmental stresses facing the world. Their heavy metal content, even when very low, can have deleterious effects on human, animal, and plant health. Contaminants belonging to this group are toxic, with no mineralogically stable form in the environment. Among their physicochemical characteristics, they are nonbiodegradable and can persist for long periods, passing from one environmental compartment to another. A variety of biological and chemical methods have been explored for the bioremediation of heavy metal-polluted environments, based on the ability of different halophilic and moderate halophilic microorganisms to tolerate and absorb heavy metals, and the detoxifying effect by salt-adapted bacteria on salt and heavy-metal contaminated agricultural soils and crop growth.

Accumulating evidence shows that several bacterial species are able to tolerate high concentrations of cadmium, nickel, lead, cobalt, and mercury; knowledge about their metabolic pathways is also increasing. Tolerance mechanisms include membrane transport, intracellular accumulation by specific nanocomponents, complexation with proteins and other biomolecules, valence reduction, and intracellular enzyme formation. Some processes are antimicrobial, whereas others involve transformation of the metal that is less harmful to organisms. Algae can also carry out bioremediation of heavy-metal-contaminated wastewater and soils, not only reducing metal levels but also reducing the toxicity of the effluents. The combination of different approaches, using transgenic plants and improving the efficiency of the microorganisms' metabolic activity consequently decrease heavy-metal content in the soil-feeding water-environmental organisms system because these means complement each other. [135, 136, 137, 138, 135, 136, 137, 138]

Pesticide and herbicide degradation

Microorganisms capable of degrading organic pollutants can be harnessed for bioremediation, a strategy with promising results in controlled laboratory settings. Many natural microbes, however, contribute to the detoxification of organochlorine compounds while growing on other carbon sources. Bacillus, Clostridium, Pseudomonas, and Acinetobacter species display high tolerance to different pesticides but lack effective degradation ability. Isolated strains with high pesticide tolerance will be grouped into consortia for enhanced detoxification. Pesticides can also inhibit Quorum Sensing (QS) in bacteria, leading to reduced bioluminescence. A QS-biosensor coupled with pesticide degradation was used to screen and isolate a Pseudomonad strain capable of degrading endosulfan. The strain showed pesticide degradation in mono- and co-cultures and decreased endosulfan-induced bioluminescence in a Vibrio fischeri biosensor. Root colonization and endosulfan degradation were also monitored during the initial stage of tomato plant growth.

Development of intelligent biosensors that detect herbicides within an appropriate concentration range during biosensing when immobilized on electrochemical nanocomposite platforms is a key aspect of biosensing technology with a very low detection limit and very good selectivity. Thus, there is a central demand for modified carbon electrodes with an electro-active hybrid film containing palladium using phosphomolybdic acid (H3[PMo12O40]· n H2O), which acts as a particulate carrier for the enzyme, that resolve conflicting requirements for very high turnover rates and a detection limit in the range of nano-molar concentrations of organic pollutants. Microbial degradation of phenolics, such as benzoic, salicylic, and p-hydroxybenzoic acids, was examined under aerobic conditions in batch mode using pure and mixed cultures of Arthrobacter, Terbacillus, Brevibacterium, and Rhodococcus. The acclimatized mixed culture was able to remove 71% of benzoic, 64% of salicylic, and 43% of p-hydroxybenzoic acids, each present at an initial concentration of 1.5 g l-1. [139, 140, 141, 142]

Microbial indicators of environmental contamination

Environmental quality monitoring requires sensitive indicators for detecting pollution and assessing ecosystem health. Microorganisms represent ideal monitoring tools because they are often the first to respond to environmental changes, can be sensitive to subtle variations in the environment, and respond quickly to shifts in environmental quality. Bacteria, fungi, and eukaryotic microbial communities are frequently used in pollution monitoring programs and qualitative models have been developed for various pollutant sources and indices. Microbial indicators of organic pollution intensity are available for lakes, rivers, and sediments. Soil microbial indicators have also been defined. Fungi and bacteria have emerged as major indicators of heavy metal pollution.

Several assays based on growth inhibition, metabolic and enzymatic activities, biomass composition, community structure, community diversity, and community-function response are often used to assess microbial toxicity bioassays. These assays help elucidate metabolic activity, structural integrity, and community biodiversity sensitivity to a particular pollutant gradient. Microbial bioassays can detect contamination of water and sediments in order to prioritize site remediation. Soil microorganisms are increasingly used for assessing soil quality as well as soil health monitoring. Microbial bioassays have proved to be effective indicators for water, soil, and sediment contamination risk assessment. [143, 144, 145, 146]

Chapter - 10

Climate Change and Microbial Dynamics

Microbial responses to climate change represent an active field of investigation with implications for climate-smart agriculture. Temperature directly influences microbial processes; modulations in the rates of mesophilic and psychrophilic organisms will affect rates of carbon cycling, soil organic matter decomposition, and consequent emissions of carbon dioxide and methane. Changes in drought and salinity will influence microbial group structure and metabolic pathways involved in soil carbon-mineral interactions and carbon cycling; microbes will also play a role in ecosystem resilience and adaptation to climate change. Correlations between changes in microbial biodiversity and alterations in specific soil properties can serve as an early warning of change, including microbial indicators of soil health.

Microbial communities with the potential to alter some soil properties have been identified, with the appropriate diversity of specialized strains attractive for microbial consortia to sustain soil health in arid and semiarid regions and assist in climate-smart agriculture. Integration of microbial processes into predictive climate or productivity models must account for the multiple pathways influencing greenhouse gas emissions. Despite a host of recognized short-term and long-term predictors of microbial community composition, microbial processes contributing to changed decomposition under extreme weather events remain poorly understood. Concern has been expressed that predicted ecosystem sensitivities to climate drivers may be insufficiently addressed in risk assessments. Studies have assessed microbial diversity dynamics, functional gene abundance, and community assembly processes in response to natural simulated climate change over 12 years.

Effects of temperature on microbial activity

Soil microbial activity responds to variations in temperature, exhibiting heightened respiration during warm months that can lead to significant carbon release. The modeled temperature sensitivity of soil carbon respiration indicates that elevated atmospheric temperatures will enhance soil carbon releases, thereby exacerbating enhanced greenhouse gas-related effects. High ambient temperatures weaken soil microbial metabolic capacity. Such temperature-related changes in microbial activity can have consequences for nutrient availability and cycling. Soil organic carbon and nitrogen concentrations decline with increased temperature, although nitrogen losses appear to stabilize at higher temperatures owing to the implicit temperature sensitivity of degradation of soil organic carbon. Enzyme responses and litter decay rates exhibit predictable shifts in response to climate change, accounting for altered biochemical controls on microbial activity. Short-term changes increase substrate availability, which subsequently declines and yields longer-term decreases in enzyme activities beyond the temporal window of the fertilization treatment. As in other groups, microbial biomass accumulation and physiological responses to short-term temperature change depend on initial temperature and mask the inherent sensitivity of the present community. Precise predictions remain elusive, despite improved understanding.

In soil carbon cycling, temperature exerts direct control through the Arrhenius effect on microbial metabolism and controls the biochemical quality of pulverized litter through litter decay rates and the activities of extracellular enzymes. Temperature-mediated changes in litter- and soil-derived carbon fuel soil respiration and co-vary with soil temperature. Microbial activity, derived primarily from litter and soil organic carbon in turn, drives temperature responses of both ammonium and nitrate. The mineralization of litter carbon appears to act as a brake on nitrogen mineralization. The coupling of microbial activity to substrate quality has important implications for ecosystem responses to climate change in terms of nutrient availability, the importance of different litter types, and the influences of altered precipitation and resulting shifts in litter dynamics on ecosystem functioning. [147, 148, 149, 150, 147, 148, 149]

Soil carbon cycling and greenhouse gases

As global temperatures rise, a multitude of negative impacts are being observed that affect the development and productivity of agro-ecosystems. Changes in temperature, rainfall patterns, frequency of extreme weather events such as droughts and floods, and the occurrence of soil salinization or acidification will drastically impact soil biological processes that influence carbon pools, hydrocarbon production by soil organisms, and soil fertility. Soil microorganisms play a central role in enabling soils to function as carbon sinks because they comprise a large part of the organic carbon cycle.

Carbon dioxide (CO_2) and methane (CH_4) account for about 95% of greenhouse gases. Therefore, it is essential to understand how soil carbon pools and soil microbial processes contribute to the production and consumption of the two gases. Plants absorb carbon dioxide produced by fossil fuels and other human activities during photosynthesis and sequester it as organic carbon in the soil, from where it can continue to serve as a source of carbon for soil organisms. However, the fixation of atmospheric carbon must be accompanied by a corresponding reduction in the rates of return of carbon to the atmosphere and, for this reason, more organic matter must remain immobilized as soil organic matter than is mineralized through soil respiration. Respiration balances decomposition with accumulation in carbon-rich environments in an inverted pyramid of pools. If soil organisms are replaced by more-thermophilic species, or if the populations of methanogenic and methanotrophic bacteria are altered for some reason, Carbon dioxide and methane production may be greatly increased. Elevated nitrogen deposition resulting from the combustion of fossil fuels can also have a major impact on soil carbon cycling in terrestrial ecosystems. [151, 152, 153]

Drought and salinity effects on microbes

Prolonged dry periods followed by excessive precipitation may create drought conditions, limiting microbial activity and abundance. Drought disrupts soil structure, reducing aeration and inactivation of microbes. Soil salinity adversely affects microbial growth, inhibiting hydrolytic and exoenzymatic activities, yet halophilic bacteria thrive.

Prolonged stress induces community succession and reduced enzyme activity. Drought retards growth and alters relative abundance of microbial and archaeal communities in the rhizosphere. Drought modifies seed-borne fungal pathogens by favouring Aspergillus Mucor, and inducing a shift from true to false powdery mildew in wheat.

Soils are the origin and collective habitat for all microorganisms, with textural, chemical and spatial variations influencing composition, numbers, distribution and activity. Understanding the mechanism of soil microorganism metabolism around crop roots is crucial for developing effective microbial agents to mitigate drought, improve soil quality and relieve soil ecological damage. Arbuscular mycorrhizae are important for increasing the drought tolerance of plants. Microbial activity is also constantly changing; nutrients subsequently maintained in the soil cause long-term changes to microbial activity and community structure. Technology based on human intervention can also improve microbial activity and nutrient cycling to help plants adapt to drought. However, drought can induce Rhizobium death. Extreme drought can reduce soil urease activity, while moderate drought considerably inhibits soil enzyme activity. Temperature effects on soil microbial processes and global warming modelling approaches indicate that increasing temperature and associated shifts in rainfall amount can directly influence the growth and distribution patterns of Rhizobia in global soil regions and identify the future physiological response of Rhizobium populations in Toxcacao. [154, 155, 156, 157]

Microbial adaptation to climate stress

While temperature influences microbial activity and community structure, its effect on soil reaction and moisture has a greater impact on microbial community composition. Soil microbial communities support carbon cycling essential for greenhouse-gas concentrations, with temperature stimulating above—as below—ground production; subsequent decomposition increases carbon-dioxide stocks, while higher nitrogen concentration accelerates carbon loss and promotes methane output. Drought stress induces changes in soil bacterial communities, genera positively correlated with moisture supporting the degradation of complex polymers, whereas enrichment with Actinobacteria is crucial for soil restoration. Salinity alters soil microbial activity and reduces organic-matter mineralization; however, tolerant communities can restore soil quality. Microbial adaptive mechanisms to local conditions provide valuable information about climate-smart agriculture and future scenarios that facilitate the development of extensivity-based exploitation methods.

Microbial attributes outline soil response to climate change, with increased metabolic activity and biomass leading to elevated carbon-dioxide production. Drought stress alters soil bacterial communities by decreasing diversity and richness, while selected taxa positively correlated with soil moisture support the degradation of complex organic polymers. Nitrogen-removal processes are promoted by fungal-bacterial interactions. Salinity severely impacts soil microbial activity and organic-matter mineralization but tolerant microbial communities can restore soil quality. Actinobacterial abundance, positively correlated with salinity, is useful for managing recycling-based extreme-salt remediation. Temperature affects soil response to large-scale pool burning; microbial loss through warming-induced dosage employs metagenomics to reveal symbiotic and pathogenic Mycobacterium abundance. [158, 159, 160, 161]

Role in climate-smart agriculture

A detailed understanding of microorganisms, particularly soil microorganisms, is essential for implementing climate-smart agricultural practices. Soil microbes play crucial roles in decomposing soil organic matter, nutrient cycling, the mutualistic interactions of arbuscular mycorrhizal fungi, and the metabolic activity of soil—especially in terms of mineralization and nitrification processes. These processes are significant for carbon cycling in the soil and can help mitigate greenhouse gas emissions, including carbon dioxide and nitrous oxide. Soil microbial communities, including prokaryotes and eukaryotes, are inherently sensitive to changes in climate or climatic variables such as temperature, moisture, and salinity; their composition and functional dynamics can therefore predict potential disturbances to the soil's capacity to support plant growth. Additionally, microorganisms are important for developing practical solutions in response to climate change, enabling crops to cope with aridity or submergence.

The response of soil microorganisms to climatic variables determines not only soil functioning but also the potential to mitigate climate change through greenhouse gas exchange. In this context, changes in microbial parameters of soil carbon cycling have often been used to assess the efficacy of different cropping systems in terms of greenhouse gas emissions. Soil-climate models that incorporate microbial-mediated carbon and nitrogen dynamics are in most cases more accurate than those based merely on deterministic or empirical relations. Soil microbes and microbial processes are also critical for the implementation of climate-smart agriculture. [162, 163, 164, 165]

Chapter - 11

Molecular Tools in Environmental and Plant Microbiology

Molecular approaches using nucleic acid tools enable crop pathogens to be detected and quantified through PCR and qPCR techniques. Metagenomic analyses are employed for studying environmental samples such as soil, compost, sewage, and water, while the investigation of microbial community profiles in plant disease systems relies on microbiome sequencing. Transcriptomics and proteomics are further aspects used to monitor responses induced by the interaction of plants with their environment, including rhizospheric and phyllospheric microorganisms. Bioinformatic tools help to process sequence data. Molecular tools also aid in studying electromicrobiology, denitrification, biocontrol, and chemical degradation. In plant disease systems, they are used for crop-pathogen diagnostics.

Detection and quantification of specific pathogens are critical for disease epidemiology and management. Early warnings can minimize disease impact. Various rapid detection techniques have been developed based on the principle of PCR to identify the DNA of pathogens in infected tissues, nematodes, and insects. Biosensors have been designed for detecting pathogens and toxins, while satellite images of crop canopies can estimate the severity of some diseases surveillance is important for decision-making in disease management. An effective information system should combine detection, monitoring, and forecasting functions. Remote sensing technologies could detect, monitor, and estimate the severity of plant disease outbreaks. [166, 167, 168, 169]

PCR and qPCR applications

Polymerase chain reaction (PCR) and quantitative PCR (qPCR) play central roles in the detection of microbes in the environment as well as in diseases of agricultural crops. The versatility of classic and multiplex PCR enables the rapid and sensitive detection of known pathogens using specific primers. It also enables the addition of diverse fluorescent probes to detect and monitor plant pathogens under field conditions. Specialized PCR systems have been developed to detect low-abundance pathogens or to detect and quantify bacteria in complex and diverse systems.

PCR amplification and detection systems display the potential for high-throughput and user-friendly suitability in the monitoring of crop pathogens, carrying advantages such as speed, high sensitivity, and scalability for multiplexing assays. Owing to the increasing availability of in-depth pathogen genome sequences, the construction of specific probes for newly detected viruses and for more widespread classes of pathogens has become straightforward. Combination with near-real-time or rapid reaction sequencing systems is likely to allow the detection of more pathogens in lesser time frames. qPCR has enabled improvement in the precision of pathogen quantification, and the recently released qPCR eco systems provide added advantages of portability, reduced cost, and ease of operation. Development of field-friendly qPCR-based detection systems for all check diseases of important crops, particularly under high- and low-risk disease conditions, is thus a priority for integrated disease management.

Metagenomics and microbiome analysis

Are essential components of modern microbial ecology that involve sampling microbial communities or individual components of those communities without the cultivation of populations. Metagenomics involves direct extraction of genetic material from assembled communities, resulting in taxonomic and metabolic characterization. Specific taxa may be studied using PCR amplification and sequencing of appropriate genetic regions, allowing quantification of the amplicon, but coverage can also be deeper using shotgun approaches or amplification of entire metagenomes. Data generated via these technologies is often profiled using bioinformatics analysis pipelines that analyze sequences to assign taxonomic classification, identify functional genes, metagenomic typing, generate ecological indexes, perform assembly profiling, and integrate host- microbial interaction information. These methods can analyze the interactions among many components of microbial communities and the drivers responsible.

High-throughput sequencing can be used beneath the waxy cuticle or specialized structures in both leaves and stems to generate rich metagenomic data and sequence references for healthy and diseased tissues. Some tools make use of marker genes located in single organisms as natural tags, addressing a specific group or species represented by a few probes that are not cross-amplified by other potential primers. Pyrosequencing opened new possibilities for culture-independent investigation of the phyllosphere microbiome, and diverse sampling strategies related to spatial, temporal, and seasonal changes have been combined with small subunit (SSU) rRNA pyrosequencing to characterize the variability in the community structure. [170, 171, 172, 170, 171, 172]

Transcriptomics and proteomics

The expression profiles of active and inactive microbial communities can be assessed using transcriptomics and proteomics. Different nucleic acid tracer approaches target specific members of these communities, such as rRNA or rRNA-derived nucleotides using RT-qPCR, while real-time proteomic analysis can be conducted using TMT labels. The use of functional messenger RNA (mRNA) profiles (iTRAQ-proteomics) demonstrates the ability to quantify and characterize transcript expression levels in Soil Meta Proximity Ligation Sequencing (SoMetaPLS). metatranscriptomic and metaproteomic profiling of active microbial communities in specific soil layers along the vertical soil profile at the Nanjing Grassland Ecosystem Research Station reveals that these profiles elucidate the microbial driving processes and community assembly mechanisms.

The shrinkage of soil microorganisms under environmental changes may provide a stress backup to ensure the stability of the soil microbial community. CLP elicits systemic defense responses at both transcript and metabolite levels in Japanese cedar. A comprehensive understanding of plant bacterial-fungal networks involved in the P-deficiency response can be achieved through integrated metabolomic, transcriptomic, and microbial-monitored metagenomic analyses.

Artificial Smart Environment (ASE) enables highly efficient microbial community reconstruction by regulating the environmental parameters of the environment. These approaches provide deeper insights into the dynamics of the plant phyllosphere and its microbial components. What remains poorly understood is how other aspects of the microbial ecology influence crop health and behaviour and how big data support precision decline soil proposal with the help of machine learning and AI. [173, 174, 175]

Bioinformatics for microbial ecology

Bioinformatics tools and resources developed through genome sequencing projects can be applied to environmental and plant microbiology research, and find wide-ranging applications, including in novel microbial isolation, functional trait prediction and evolutionary analyses, disease diagnostics, and design of targeted probes for detection of specific microorganisms in environmental samples. Metagenomics is an emerging field that utilizes high-throughput sequencing of environmental samples to study microbial community composition and function through bioinformatics. Advancement of knowledge of niche differentiation in complex environments, together with transcriptomic and proteomic techniques, can provide deeper understanding of microbial ecology. Significant talent gaps in bioinformatics are hindering further adoption of these powerful techniques.

Over the past century, research on the ecology of microorganisms in natural and engineered environments has become dominated by discovery-oriented metagenomics. The combination of sequencing and bioinformatics currently enables the culture-independent study of the majority of microorganisms in a given microbial community based on ‘-omic’ signatures and gDNA sequence depth. Predicting RNA and protein profiles based on predictive genome content promises to remove certain bottlenecks in culturing broader diversity of microorganisms. Population genomics, together with transcriptomics and proteomics, thereby facilitate targeted laboratory cultivation for further, preferably targeted, testing of the role or function of previously detected taxa in environmental processes in the wild situation. [176, 177, 178]

Molecular diagnostics of crop pathogens

Rapidly accurate detection, identification, and monitoring of plant pathogens is crucial for integrated crop protection in a changing climate. Nucleic acid-based techniques offer great promise in this regard, providing rapid, sensitive, and specific identification of pathogens directly from infected plants and plant products or from plant debris and the environment using very small amounts of infected tissues. Such techniques include polymerase chain reaction (PCR) and quantitative PCR (qPCR), which detect and amplify specific nucleic acid regions. Use of multiplex, nested multiplex, real-time, and reverse-transcription approaches increases efficiency, sensitivity, and specificity. While conventional PCR and its variants still dominate, metagenomics and other high-throughput sequencing techniques are revolutionizing environmental and taxonomic pathogen identification. Synthesis of PCR primers used for the detection of several important fungal and oomycetous plant pathogens is also presented.

Advanced and high-throughput monitoring technologies, such as biosensors, remote-sensing satellites, and unmanned aerial vehicles integrated with artificial intelligence, facilitate comprehensive monitoring of crop health and disease records at the national level. Rapid detection-based pathogen monitoring and early-warning systems are promising for assisting sustainable crop-introduction and protection strategies. Molecular tools establish an integrated approach for prompt diagnosis, hourly disease monitoring, and consequent action planning.

Chapter - 12

Microbial-Based Disease Diagnostics and Monitoring

For sustainable agriculture, knowledge-based pest management is essential, supported by precise infection monitoring and detection tools for pathogens and pest damage. Microorganisms provide the means for preliminary monitoring, early detection, severity evaluation, and early warning system development. In some instances, green and brown algae, trainable to sense specific compounds, are employed in bioreceptive systems. Beyond classical systems, reinforced endogenous plant immune responses, upon disease identification, is an additional monitoring method developed with great impact for subsequent damage evaluation. Interest in decision-support systems for management tactics and strategy remains high.

Accurate, easy-to-use detection systems are required to identify crop pathogens rapidly and accurately, and to instantly confirm symptoms or the presence of specific antigens or metabolites. In particular, field-deployable systems with fast turnaround times will empower farmers to make real-time treatment decisions. Such systems reduce the incidence of misdiagnosis and excessive chemical application. Rapid and precise assays are essential for detecting emerging infections or managing plant virus diseases. Real-time detection and precise quantification are achieved using biosensors based on specific nucleic-acid hybridization and/or antibodies immobilized onto nanostructured transducers. Quantitative real-time polymerase chain reaction systems fulfilling the requirements of cost-effectiveness, specificity for end-users, and high throughput are valuable for the rapid identification of economically important viruses of major crops. [179, 180, 181, 179, 180, 181]

Rapid pathogen detection systems

Are combination of nucleic acid amplification with different detection platforms. Plant pathogens can be rapidly detected using PCR-based techniques that amplify DNA or cDNA in an exponential manner so that transformations on detection can be avoided. Nucleic acid amplification techniques (NAATs) allow sensitive identification of single microbial cells or minute amounts of nucleic acids extracted from infected tissues. Detection is usually carried out on agarose or polyacrylamide- gels, but electrophoresis is not always necessary, for example with a fluorimeter. Other detection methods like reverse transcriptase fluorescence-based detection have been developed.

Biosensors are an attractive alternative to conventional approaches for rapidly and efficiently detecting plant pathogens. Biosensors are coupled with amplification mechanism to improve the detection limits. A variety of nanomaterials have been used to label sensors, which combined the merits of conventional detection methods and biosensors. Nanomaterials, usually in the size range of 1-100 nm, possess biochemical properties unlike those of analogues that are either smaller or larger in size. They offer high reactivity, sensitivity and Electron confinement effect collapse capability. Nanobiological sensors are biosensor techniques that have opened new horizons for biosensing with distinct advantages such as good reproducibility, a high ratio of surface film to voltage, reliability and low manufacturing cost. These qualities have facilitated the detection of various plant viruses and their components, as well as related diseases. Nanomaterials are expected to play an important role in pathogen detection systems.

Remote sensing provides a means of detecting unseen properties of the plant canopy. Fungi can infect normal appearing foliage but symptoms may not be visible to the naked eye until long after the infection has occurred. These often unrecognizable infections can, however, be detected by multispectral, hyperspectral, thermal, or laser scanner remote sensors. Sensing of infection through leaf temperature and stomatal conductance may provide the best opportunity for classification. Such approaches and other studies may lead to a system for detecting an infection and its associated progressive rate. [182, 183, 184]

Biosensors and field diagnostics

In the search for sustainable solutions to manage agricultural crop pathogens, rapid detection and monitoring tools have enormous potential. Sensory devices such as biosensors, integrated with nanotechnology, have emerged as powerful candidates for detecting plant diseases caused by biotic stressors such as viruses, bacteria, fungi, nematodes and protozoa. Biosensors are a kind of electronic tongue, made safe and cheap, that have shown susceptibility to disease-causing agents by responding appropriately to the chemicals secreted by pathogens or plant tissues. Detection of these signals can be achieved through field sensors. Other devices include hand-held kits, biosensors, biochips and androids, which analyze disease severity based on physiological changes of the host plant, predictions through models and signatures identified during the uptake stage of the pathogen. Remote sensing can also be relied upon for monitoring plant disease development. Active and passive sensors through imaging with different wavelengths can offer information about the infection stage. Attempts using remote sensing signals in modelling disease development and yield loss have shown promising results. Currently, disease monitoring systems based on remote sensing are becoming popular in combination with spatial data.

Risk assessment enables early warning of crop disease outbreaks, which in turn helps in decision-making for deploying and monitoring of control measures over larger areas. These warning systems are based on observations of disease occurrence on disease monitoring networks and on prevailing infection conditions, recognised from weather factors, for different pathogens. Such early warning systems, integrated with decision support tools linked to the weather-smart approach, can empower farmers to take timely action against field crop diseases. Integrated-disease-warning systems show promise for greater use and connectivity in digital platforms. [185, 186, 187, 188]

Remote sensing and disease monitoring

Remote sensing constitutes the systematic acquisition of information regarding a particular area, employing sensors and imaging devices installed in aircraft or spacecraft. An array of instrument types, including thermal infrared, optical/visible microwave, radar, and multispectral sensors, has been utilized to monitor agricultural lands over the past 30 years. On the basis of atmospheric correction, soil moisture, and vegetation index estimation, advanced multispectral remote sensing techniques may assist in characterizing leaf area and above-ground biomass in broad-acre crops. Consequently, the quantification of plant growth over the growing season, the identification of water deficit patterns or heat stress, and the mapping of spatial texture of crop stands can all be addressed using modern remote sensing capabilities.

Remote-sensing techniques also enable recognition of apparent damage caused by a disease; early warning systems incorporate disease susceptibility to fertilization and micronutrient deficiency. Through the political, social, and economic implications of remote sensing, it is necessary to consider aspects of improved prediction from greater ecological detail for successful integration with social sciences. Sensor systems suitable for wide-area monitoring of crops, including hyperspectral imaging from the AISA Eagle 1, canopy temperature monitoring for detecting heat stress, thermal infrared remote sensing, and integrated pest risk forecasting systems for input to early warning systems are increasingly available. Synthesis of phenological, spatial, and apparent damage information with models of host-population interaction using detection thresholds has the potential to further enhance the investment in these activities. [189, 190, 191]

Early warning systems

Pathogenic threats to crops increase with climatic fluctuations, creating the need for disease monitoring and early warning systems. Remote sensing plays a vital role at different operational levels in identifying hotspots and predicting epidemic trends. The reconnaissance of affected areas and the identification of the spatial extent of infections within those areas require ground-based inspections. Monitoring is essential for successful integrated disease management programs, and effective decision support systems integrate such information. Disease warning systems, tools that incorporate monitored data into threshold values to generate alerts, are particularly useful.

Remote sensing offers quantitative data on the current status of crops at a regional or larger scale. Disease warning systems combine remote sensing data with crop growth and disease development simulation models, enabling the issuance of spatially explicit and temporally dynamic risk predictions. Two distinct spatial domains (i.e. local, regional) possess different requirements for remote sensing monitoring. Crop- specific symptom expression, spatial extent of infection, host and environmental interaction, and land use management influence the appropriate level of resolution. At the local scale, symptomatic crop monitoring based on aerial or satellite- borne multispectral imagery can support regional and local management. [192, 193, 194, 195]

Decision-support tools

The rapid identification of plant pathogens, their associated symptoms, and weather conditions favorable for disease outbreak is critical for improving farmers' decision-making and curtailing crop losses. Disease monitoring, prediction, and forecast systems are key components of integrated disease management (IDM) programs. Several systems and tools have been developed in this context for diverse applications, ranging from pathogen detection to schedule-based monitoring and predictive systems.

Plant-disease early warning systems are non-instrumented and instrumented systems that provide warnings based on data. Non-instrumented systems utilize historical evidence of disease occurrence, crop-pathogen phenology, weather data, and farmers and field assistants and are helpful for crops like paddy, potato, rice, and sugarcane. On the other hand, instrumented systems have information and communication technology and sensing technologies to help support farmers' field options. Integrated biosensors for different crops and crop pathogens have also been developed and deployed for real-time pathogen detection and monitoring. [196, 197, 198]

Chapter - 13

Integrated Disease Management and Microbial Approaches

Integrated Disease Management (IDM) emphasizes the exploitation of diverse knowledge systems for sustainable risk management. Knowledgeable disease management strategies protect crops from pathogens while reducing reliance on synthetic agrochemicals. Research on the interplay between microbes and IDM principles can strengthen IDM frameworks alongside health-based approaches.

Microorganisms are integrated into IDM via cultural strategies (niche modification through agrotechniques, feedback from natural enemies and diversity within resources, introduction of resistant/tolerant host varieties), reduction of APIs (affinity manipulation) and environmental conditions promoting pathogen proliferation. Additionally, supporting biopesticides fit into the IDM strategy. Reducing disease risk with cultivated biodiversity fusion will motivate farmers to combine crops in a plant association-disease relationship model. Consensual fungicides are feasible when monitoring mechanisms predict pathogen appearance. IDM rules help restrict pathogen resistance development to biocontrol agents, and integrated RNA-silencing pathogens pose less risk to human health. [199, 200, 201]

Concepts of integrated disease management (IDM)

Integrated disease management (IDM) comprises both general concepts and processes that consider disease a component of the agro-ecosystem, thus necessitating integration of all available options to minimize the impact of disease on crop production. Microorganisms, with their diverse ecological functions, can be incorporated into IDM concepts through their integration with other disease management practices and their ability to reduce chemical inputs, manage resistance, and address environmental and human health concerns. The disease triangle describes the interrelation among host, pathogen, and environment, providing insight into the inclusion of microorganisms in IDM as modulators of biological processes regulating disease severity. The host-microbiome interaction plays an important role in plant health and resistance, imparting disease tolerance through microbiome-mediated mechanisms. Influencing abiotic and biotic factors of disease with microorganisms, such as through engineering an antagonistic soil microbiome of the growing season preceding disease outbreaks, can minimize severity. Additionally, physiological and chemical signals of the host during pest-pathogen-host interaction can modulate antagonist activity and enhance IDM. Furthermore, proper grew choice reduces pathogen inoculum potential, while disease prevention reduces the use of active ingredients against pathogen development. Overall, these strategies contribute to a better understanding of IDM to mitigate the impact of diseases on crop yield. [200, 202, 199, 203]

Microbial integration with cultural practices

Integrated disease management (IDM) combines biological, physical, and chemical controls with cultural practices such as varietal resistance, soil health management, and nutrient and water supply. Microorganisms interact with these practices in diverse ways that can increase their effectiveness and sustainability. These interactions can be classified according to whether the cultural practice is aimed primarily at pathogen suppression or enhancement of host resistance or tolerance.

Cultural practices based on chemical reduction of disease can be coupled with biological control to use fewer pesticides, mitigating potential negative effects on human and animal health, the environment, and the economy. The addition of biocontrol agents before or during host colonization shifts early-symptom severity to a less damaging stage in certain pathosystems, and combinations of soil solarization and biological control for wilts in several regions increase the potential for biocontrol adoption. However, closer examination reveals that in several of these combinations the biocontrol agents had no significant effect on disease suppression. Potential negative interactions between approved biological and chemical controls can also influence IDM success; such risks warrant further study.

Cultural practices also enhance host resistance and tolerance. Induction of systemic resistance is the main outcome in these interactions, with root-feeding nematodes, mycorrhizal fungi, and PGPR facilitating growth and nutrition during disease development and contributing to mitigation of diseases such as downy mildew and blights. Induced resistance and biological control can also act in tandem; arbuscular mycorrhizae increase the production of jasmonic acid, supporting beneficial soil fungi and decreasing disease severity in agricultural systems. [78, 204, 205]

Reduced chemical input strategies

Crop protection programs based exclusively on synthetic pesticides are increasingly deemed unsustainable. Applications of these chemicals not only have direct implications on non-target organisms, including beneficial microbes and insects, they can also contribute to increases in pesticide resistance in pathogen populations. The resultant risks outweigh benefits in many cases. Exploration of reduced-chemical-input strategies becomes imperative, especially for economically important diseases for which crop resistance and cultural measures cannot provide adequate alternative control. Examples include the integration of microbial approaches with diverse cultural practice strategies, including cover crop rotations, crop diversity and intercropping, soil nutrition management, delaying planting dates, and novel product use, plus early detection of disease outbreaks as part of the IDM strategy or decision support systems.

Microbial research is critical to underpinning proposals for reduced chemical use. Pathogen detection systems and rapid biosensors that identify outbreaks prior to disease appearance can reduce dependence on prophylactic disease control measures. Knowledge of crop-associated microbes opens new opportunities for breaking the resistance of pathogens with high residual virulence after chemical treatments. Microbial disruption of the multiphase disease cycle affords direct substitution for chemical control, especially for diseases of high incidence that drive widespread chemical use. The need for continuous pesticide applications can be curtailed through identification of antagonistic microbial groups in the crop environment and their enhancement. Crop sensitivity and virulence of the most aggressive pathogens can be reduced as part of integrated resistance management plans. [206, 207, 208]

Resistance management

Integrated Disease Management (IDM) principles recommend the use of resistant varieties in combination with other disease management practices to minimize the selection pressure on pathogen populations. Development of resistance in cultivars through breeding is a long-term strategy, but breeding programs take time, especially for durable resistance. Resistance-breaking pathotypes often develop under disease pandemics; for instance, targeted deployment of the Major Gene for downy mildew resistance in pearl millet led to the evolution of the new physiological races like S1R1, S1R2, S1R3, and S2R2 of the pathogen. Localized release of resistant varieties in combination with susceptible ones can give better results. However, reduced-chemical-input IDM strategies that integrate the deployment of resistant varieties with popular, widely grown, and highly susceptible varieties with GPS-based farm management techniques to anticipate disease development across the entire area can minimize disease impact without creating selection pressure for virulence in the pathogen, e.g., towards bacterial blight and sheath blight of rice.

Development of resistant sources and cultivation of resistant cultivars in suitable cultivable areas with less destructive strains may minimize the selection pressure on virulence in the pathogen. Resource-conserving cultural practices together with resistant varieties are helpful in combating the disease without a heavy expenditure on chemicals. However, just like the use of broiler chicken on a large scale with no reserve, farmers rely exclusively on a few resistant sources, which are then rapidly broken down. Many of the resistance genes in pearl millet have broken down as a result of such exclusive use across large areas without precaution. Therefore, for diseases with high probability of incidence, it is important to identify and characterize a broad spectrum of resistance sources and reserve these in the germplasm collection. [209, 210, 211]

Sustainable crop protection systems

To ensure sustainable agriculture production with healthy crops, integrated disease management (IDM) systems following the principles of integrated pest management (IPM) must be developed for major diseases affecting field crops. The introduction of beneficial microorganisms for the control of crop diseases via biological disease control or generated resistance has been recognized as a major component of IDM systems. Microorganisms and their interactions with pathogens are increasingly integrated into disease management strategies, sharing an equivalent role with agro-ecosystem management practices that minimize the pressure of crop pathogens in the environment. Competitive microorganisms with similar ecological niches as pathogens have been used successfully for disease suppression. However, their application has suffered setbacks because of complex environmental conditions that are not addressed in any stage of the development. Recent developments have shown how microbiome structures drive disease incidence and severity. Microbiome engineering is now possible to minimize disease occurrence; however, the relation between disease outbreaks and environment is not yet well established.

The introduction of microorganisms for managing crop diseases is a promising approach that requires considerable research. Collaboration among different scientific fields will allow the subtleties of disease systems with multiple and structured microbial interactions to be understood and exploited for crop protection. Such research will provide farmers with user-friendly information and decision-support tools based on the better conditions for effective biological disease control to improve overall disease management by integrating microbial and traditional practices, thus minimizing the selectivity and effects of agro-chemicals on the environment. [212, 67, 213]

Chapter - 14

Waste Recycling and Agricultural Microbiology

Composting processes and agricultural waste biodegradation foster a circular economy and yield environmental benefits. Microbial recycling underpins composting and waste treatment. A growing research database supports biomass valorization for energy and biofuels, alongside biogas production and residual digestate utilization. Such recycling mitigates pollution, improves fertility, reduces dependence on fossil fuels, and reinforces a sustainable circular economy. Additionally, biotechnological approaches to waste valorization promote environmental benefits.

Microorganisms are crucial for the breakdown and recycling of organic material. Their activity generates compost, a rich organic fertilizer. Non-hazardous organic agricultural waste can be recycled through composting or anaerobic digestion. Various composting strategies allow rapid and efficient compost production, with effects on the final product. A large amount of organic waste generated under different agricultural conditions facilitates research on developing different composting materials for environmental- and crop-production-related benefits. Compost reduces fertilizer demand and promotes soil health and fertility.

Anaerobic digestion and subsequent utilization of bioenergy through biomass are intensively investigated. Biogas can provide a viable energy alternative and contribute to carbon-neutral development as a local energy source. The residual digestate generated by biogas production may be suitable for use in fertigation. Using digestate can also improve the environmental performance of crop production and recycling in a closed-loop system in an increasing-value circular economy. The potential combined use of agricultural waste for both biogas and biocomposite product development seems encouraging. [214, 215, 216, 217]

Composting and microbial processes

Composting is a natural biological process, of physiological importance in biological and environmental sciences, during which organic matter is preserved with the action of prokaryotes and fungal microorganisms. Composing seeks to obtain material with product quality. It has been adopted as a waste management strategy for reducing the pressure on landfills and been a proposed alternative for preventing environmental degradation. Microorganisms play a key role in the biodegradation of agricultural waste, as well as in bioenergy and biogas production and in the sustainability of the bioeconomy and circular economy. Their participation in the recycling of over 100 raw materials of different chemical composition and characteristics, from a diverse range of sources, has been reported. Composing is usually employed as waste management strategy for avoiding environmental pollution and protecting human health and the health of living beings.

Composting is generally recognized as a strategy for waste recycling and achieving carbon neutrality. Micro-organisms are crucial for the success of composting processes not only during waste biodegradation, but also during methane-production from anaerobic digestion of biogas generation and in the detoxification of effluents contaminated with persistent organochlorine and organophosphorous compounds. Microbial processes are also important for maintaining land productivity and protecting ecosystem functions from microbial communities that are affected by several factors associated with climate change. [218, 219, 220, 221]

Agricultural waste biodegradation

Biodegradation of agricultural waste relies on the activity of fungal, bacterial, and actinomycete populations and their enzymes. Many fungi and bacteria play a decisive role in the decomposition process under controlled conditions. Moreover, the improvement of the environment creates a better microbial habitat due to the addition of nutrients during thedevelopment of the composting process.

Agricultural production generates a large amount of biomass that can be converted into useful products, such as biogas and compost. The use of natural biotechnological processes by microorganisms opens the door to a circular economy in agriculture, with the aim of improving agricultural wastes and production with positive environmental and economic effects.

Biogas production from residual biomass (cereals and oilseeds) in Eastern Europe could cover about 25% of the electricity demanded in these countries, while biogas plants for bioenergy production have recently increased in Germany, the USA, and Sweden. Biogas production can take place in unused fields. The production of microbial protein from agricultural wastes is also gaining attention. Compared with classical plant production, the use of biogas fermentation allows a higher protein yield due to the faster growth of the microorganisms. [222, 223, 224]

Bioenergy and biogas production

The conversion of agricultural wastes into bioenergy sources via composting represents one of the best examples of recycling in soil-environmental microbiology since it exploits the ability of microorganisms to oxidize toxic organic matter to harmless products.

Sugarcane bagasse, straw, coffee pulp, palm oil empty fruit bunch, molasses after biosugar production, aseptic apple pulp waste, and others are residual products from agricultural activities. These organic wastes, when mixed in adequate proportions, can produce compost; the biodegradation process involves complex interactions between microorganisms and is affected by C/N ratio, temperature, moisture, pH and aeration. The successful inoculation and the control of important microorganisms like Clostridium are essential factors for the optimization of the biodegradation process. Proper composting will generate a product that will benefit soil health by enhancing carbon content, utilization of nutrients, and production of humates.

Digestion of wastes by anaerobic microorganisms under controlled conditions generates biogas. The gaseous fuel can be used in several different ways: for running either freight and mass transport vehicles; for producing electric energy and heat in biogenerating sets; for driving motors that pump irrigation water; or for heating. Biogas plants can be established in rural areas as a family enterprise. Such plants supply energy for the families with a demand for 5 to 15 m3 of biogas per day, reducing fuelwood need considerably and resulting in improved health condition for the family. Waste treatment through biomethanization is an important step in the CIRCULAR ECONOMY, contributing to economic gain for processing industries. In this framework the production and use of biogas is an important strategy to reduce the production of greenhouse gases and convert waste into a renewable resource which can help reversing the depletion of fossil fuels in a sustainable manner. [225, 226, 227]

Circular economy in agriculture

The circular economy strives to minimize waste and make the most of resources. Current farming practices generate significant waste streams—such as animal manure and crop residues—that create economic burdens for farmers and contribute to pollution. Examples include the persistence of crop residues and livestock waste causing environmental pollution problems. Garbage offers potential as a resource in waste recycling, particularly in production composting. Waste recycling reduces the total requirement for inorganic fertilizers, improves soil quality and structure, reduces water pollution, and increases carbon sequestration. Biogas production can be linked to the circular economy and rendered available as an empirical technology.

Industry developments have incorporated the establishment of composting production and microbial recycling to complement traditional technology. Microorganisms provide technical solutions for recycling plant farmland-produced wastes, returning nutrients to the soil. These sustainable systems recycle agricultural and forest waste by using microbial populations for environmental purification, natural resource availability, nutrient recycling, waste reduction, ecological environment improvement, and circular economy promotion. The microbiological capacity for recycling organic resources, especially organic waste and crop residues, can be used to tackle environmental pollution problems; promote the additive manufacturing industry; stimulate and safeguard public health; and develop a circular economy.

Information from microbiological studies of agricultural waste recycling can support the national direction of agricultural waste composting technology, involving livestock and poultry manure treatment and resource utilization. The successful development of composting technology leads production and consumption into a transition stage, where the quality of compost can be guaranteed with safety. A healthy agriculture can be constructed by gradually promoting the application of compost in production practice, efficiently reducing residual waste nutrients from livestock and poultry harvest after feeding, and re-modifying micro-ecological balance characteristics during use. [228, 229, 230]

Environmental benefits of microbial recycling

Considerable attention has been given to sustainable waste management through recycling and reuse of organic waste in recent years as part of the circular economy model. Biodegradation of organic waste in landfills without proper management leads to greenhouse gas emissions. Organic wastes either recycled in the form of compost have several beneficial effects on soil fertility, which in turn contributes to nutrient supply for crops. Microbial recycling of agricultural residues, spent mushroom substrate, coconut coir dust, water hyacinth, and other organic wastes reduces environmental hazards associated with their accumulation and through composting improves their nutrient status. Bioenergy/biogas production through anaerobic digestion reduces the cost of fertilizing crops as bio-fertilizers can be produced along with energy from biogas plants. Bioremediation processes using microbes are employed in managing polluted environments; bioremediation with native microbes in contaminated areas with proper management plays an important role in nutrient cycling in microorganisms. Compositing can be successfully utilized for the treatment of organic matter mixed with heavy metals, or pesticides.

Increased fertilizer input into farming systems has noticeably accelerated food production. However, the overuse of synthetic fertilizers can deteriorate the environment, leading to several physiological problems in crops, such as decreased resistance to pest and disease, increased incidence of physiological disorder during storage, lowered nutritional value, and possible health hazards. Regular application of chemical fertilizer creates a nutrient imbalance that becomes a danger for sustainable agriculture. Intensification of agriculture has also led to severe depletion of organic matter in soil. Integrated and organic farming systems rely on the application of organic sources of nutrients like compost, vermicompost, and on the natural ability of soil to sustain crop productivity. Hence it is essential to invent and develop different waste recycling methods, such as composting, in order to replenish soil fertility and improve crop yield and quality. [231, 232, 233]

Chapter - 15

Socio-Economic, Policy, and Regulatory Aspects

Regulatory frameworks support the use of microbes in crop protection, complementing and amplifying their roles in nutrient management and bioremediation. Biological products, based on beneficial microorganisms, are effective and essential components of integrated disease management in crops. Proper regulation attracts investment, and more products are expected to reach markets, increasing farmers' knowledge and confidence for adoption and application. However, the influence of farmers on policy is often weak, intermediaries play a crucial role in introducing new solutions, and higher prices are a barrier for less prosperous producers. Enkeeping and promoting these products offers significant opportunities for sustainable plant production. The successful adoption and use of beneficial microorganisms also depend on biosafety considerations, technology transfer, economic viability, and the establishment of well-defined and transparent protocols that help farmers understand the associated benefits.

The importance of natural recycling processes in crop production, associated with plant health, is evident through ecological, socio-economic, and climatic considerations. Controlled biological decomposition of organic material, microbial degradation of most organic waste, production of biogas and biosolids, and transformation of dropped or waste products of economic processes into nutrients are steps towards a circular economy, where recycling minimizes the use of natural resources and therefore pollution of air, soil, and water. Products such as air, drinking water, and food and feed for human and animal health cannot be recycled, but mycorrhizal fungi, phrensimunium, and actinobacterial brooming of leaves on comminuting trees should be promoted to ensure food security and health, stress-free environment, and ecosystem sustainability in the context of present and future climate change. [234, 235, 236, 237]

Regulation of microbial products

In the past, there have been few regulatory issues in applying fungi, bacteria, yeast, and viruses. Most biosafe cultures producing enzymes, growth hormones, vitamins, and organic acids might need regulatory approval only when produced at high levels. However, increasing awareness of genetically modified microorganisms and their potential risks has raised concerns. Genetically modified (GM) microorganisms used in bioremediation, agriculture, and the production of enzymes and metabolites require careful consideration. National regulatory bodies, such as the Risk Assessment and Management Committee in India or the Environmental Protection Agency in the USA, can study the potential risks associated with widespread, uncontrolled use.

Safety assessment of microbial agents or products should focus on three interrelated aspects: toxicological evaluation of the agent, exposure assessment, and risk characterization. Assessment entails evaluating the product's stability, ability to grow and survive in the environment, and potential pathogenicity. For example, the likelihood of microbial fermentation by a specific organism during food production is limited, and the product's fate in the food chain must be defined. Transgenic microorganisms contain specific modifications that should be thoroughly studied. For example, the AMT gene from Bacillus licheniformis, which confers resistance to ampicillin, or the transgenic microbe Pseudomonas syringae containing the crop pathogen psx toxin gene, should not be allowed to escape into the environment. Biosensors for genetically altered organisms are urgently needed, as are remote-sensing-based detection methods for environmental contamination with manmade chemicals and monitoring natural ecosystems for early warning of microbial outbreaks associated with climate variability. [238, 239, 240]

Biosafety and environmental risk

Biosafety assurance while using different microbial strategies needs special concern and would require a proper clearance from regulatory authorities as the use of living organism directly related human health, environmental, and biosecurity issues. Depending on the regulatory framework, scientists and industrialists will have to choose their candidate species and the techniques of manufacturing products containing living organisms. Novel products ready to use and Industrial preparation of BMGs, PGPR, Trichoderma and Mycorrhiza Point/ Policy action BMG products for controlling and disease management and improving nutrient supply and growth of major crops are under development. It needs to either accelerate the regional technology transfer through interdisciplinary approaches by involving different departments or build close partnership with National/International Network. High-scoring products generated with niche information, biosafety and environmental risk checked point of view should be scaled up with industry partner support.

Research on emergent issues such as suppression of viral diseases in plants, biocontrol of non-pathogenic fungi, environmental bio-remediation by fungi, PGP role of algae/arbuscular mycorrhizal fungi combined with other microbes in plant growth and development offers great promise and demand for major sustained investment by policy makers to provide beneficial product for improving present agricultural input system and production. Though new products are developed to narrow down chemical impact to environment in crop protection still these chemical are either used continuously or in combination to productively manage the diseases due to varietal susceptibility and non-availability of effective products. Effective multidisciplinary research on need-based, targeted diseases with knowledge-based community for practical scaling up and farmer-friendly field-testing thereby creating bio-safe support to various crop protection strategies on long term basis. [241, 242, 243]

Farmer adoption and technology transfer

The understanding of crop diseases and their management is influenced by advances in science. When new information is made available, farmers must change outdated practices based on old information, either because they are no longer effective or no longer sustainable. If applied, the new concepts hold the potential to save money and ensure greater harvests. An understanding of how neighbouring crops as well as weeds affect disease risk and crop vigour may provide farmers with a newstrategy for managing these problems.

Generally, diseases are more severe when crops are closely spaced than when they are widely spaced. Rows of wheat sown in wide furrows or strips through barley, grass, or pea also suffer less infection than control crops. The encouraging result holds for different diseases, in different seasons, in different areas, and even across continents, suggesting that crop management based on neighbouring risks is especially promising.

In many cases, new treatments for diseases may appear riskier than the old. Past success should not discourage exploraton of these new methods. For all crop-disease pairs where biological control has been attempted, beneficial microbes have reduced disease severity. Important experimental work in the area of defence induction must now be applied across the full flowering stage of attacked crops. The market for disease-free plants appears to be sorely underestimated by growers. Biology-based services that prevent or treat crop diseases need promotion. Farmer participation is necessary for the successful development of all such technology, by generating local confidence and funding research. [244, 245, 246]

Economic benefits of microbial technologies

The application of microorganisms in sustainable disease management and plant health support can be a critical factor for successful, profitable crop husbandry within a changing global agricultural landscape. Disease prevention will reduce chemical inputs, and yield increases by disease-resistant and healthier plants will produce direct financial benefits for farmers. Ensuring the connection between scientific discovery of novel microbial products and the delivery of sustainable solutions to the full range of crop disease systems are key questions for the research community. However, recent advances in biotechnology, economic and regulatory support for product development, and need-driven selection of disease targets now mean that resources can be invested not only in finding new biocontrol organisms, but also in viroid and pathogenic nematode control, crop resistance induction, and predictive disease modelling.

Simultaneously, successful biocontrol now treats many important crops worldwide, with commercial products developed for additional targets. Recognition by the World Bank of the contribution of biological control to sustainable smallholder farming motivates support for bringing new products out of the laboratory and into safe and effective disease management packages. Integrating biological disease control within chemical disease management products, systems, and management will reduce reliance on inputs and prolong their effectiveness, ensuring economic profitability of microbial approaches. [67, 103, 247]

Policy frameworks for sustainable agriculture

Regulatory frameworks governing microbial products focus on biosafety, with comprehensive strategies necessary for widespread adoption. Effective technology transfer and economic incentives can enhance adoption among resource-constrained farmers.

Synthetic biology-based products and processes have emerged as a novel approach to plant-microbe interactions. Regulatory frameworks similar to those for transgenic technology may be required. Policies promoting big-data applications and precision agriculture in the areas of pest, weed, disease, and fertilizer management require attention. [248, 249, 250]

Appropriate regulatory policies, supporting infrastructure measures, financial viability, and end-user awareness will help microbial products and processes reach their development potential.

Chapter - 16

Future Perspectives and Emerging Technologies

Microbiomes harboring environmental and plant growth-promoting microorganisms play vital roles in sustaining health and productivity in natural and managed ecosystems. The development of agricultural inputs exploiting these multifunctional microbiomes may provide sustainable solutions to meet the increasing demands for food and raw materials while preserving ecosystem functions. Development and commercialization of microbial products, however, must be supported by regulatory frameworks and guidelines that also ensure the safe use of newly engineered microbes.

Future agricultural production must be environmentally sustainable and climate-smart, breaking the current carbon economy that relies on fossil fuel-based inputs. Recent advances in synthetic biology and microbial engineering techniques, together with the increasingly affordable sequencing of DNA and RNA, may open new avenues for exploiting natural plant-microbe interactions. These techniques can enable the precise assembly of custom-designed microbiomes that perform functions for which natural communities are poorly equipped or highly undesirable. Simultaneously, the application of artificial intelligence, big data analytics, and precision agriculture hold great potential for transforming agriculture practices into holistic systems that better integrate the on-farm environment with nutrient and disease management decisions to yield crops with improved health and quality.

Synthetic biology and microbial engineering

Emerging developments in synthetic biology harness genetic engineering, metabolic network design, and other techniques to create new biological systems. Edited or engineered microbial communities have great potential in supporting agriculture, promoting crop health, and enhancing production. Advances in artificial intelligence (AI), big data, and precision agriculture promise to revolutionize agriculture through efficient and eco-friendly farm management at every scale, from major to smallholder farmers.

Are offering exciting opportunities to edit, construct, or synthetically design genes, pathways, and microbial communities with customized functions. Crops have become healthier and more productive due to the introduction of synthetic biosynthetic genes, the enhanced activity of metabolic fluxes, and the application of synthetic chemical or bioengineering techniques.

Synthetic biology approaches allow construction of optimized metabolic pathways and circuits by manipulating transcriptional, translational, and post-translational regulators. These approaches improve sugarcane photosynthesis efficiency, increase carbon supply for Rubisco activity, boost sugar and alcohol composition of maize grains, and obtain transgenic rice and tomato plants that synthesize bealacetone. Recent advances in editing and synthetic biology tools can also enable precise engineering of desired crops.

Metagenomic studies of rice-anthracnose respond either positively or negatively; the first kind is associated with increased saprobic, fermentative, and pathogenic processes, whereas the last type harbors many saprobic taxa correlating with reduced disease. Mining and engineering plant-associated spatial-temporally co-occurring microorganisms for targeted functions may produce beneficial effects on plant health and yield.

AI has been beneficial in various aspects of agriculture, including disease diagnosis and forecasting in different crops. AI-based decision-making technologies permit assessment of the influence of specific environmental conditions on actual yield and the alteration of weather patterns and microclimates of regions to optimize precision agriculture.

Microbiome editing for crop health

Microbial communities regulate reactivity and functioning in all ecosystems; therefore, environmental shifts affecting their composition may have cascading consequences. Today, there is growing interest in environmental microbiome engineering with the aim of increasing either ecosystem resilience or the pace and stability of biogeochemical cycling through manipulation of the assemblage of microorganisms responsible for these processes.

In crops, the microbiome plays a pivotal role in modulating growth and health. Future advances in microbiome editing could facilitate the mitigation of abiotic and biotic stressors in crops based on the small-scale manipulation of the microbial community composition. Such editing should primarily include the reinforcement of positive interactions with epiphytic and invading pathogens with sufficient biodiversity, such as actinomycetes, that stimulate innate immunity responses in the host and increase disease resistance, e.g. through metabolic augmentation of phytoalexins with proven biocontrol function against pathogens.

Microbial communities regulate reactivity and functioning in all ecosystems; therefore, environmental shifts affecting their composition may have cascading consequences. Today, there is growing interest in environmental microbiome engineering with the aim of increasing either ecosystem resilience or the pace and stability of biogeochemical cycling through manipulation of the assemblage of microorganisms responsible for these processes.

AI and big data in microbial ecology

Large-scale microbial sequencing projects and advances in bioinformatics have dramatically advanced knowledge of microbial ecology. However, ecological knowledge has not yet been effectively integrated into practical applications for environmental management, restoration, and agricultural production. These gaps are being addressed with the application of synthetic biology, AI, machine learning, and big data analysis. Advances in precision agriculture utilizing these approaches will facilitate data-driven and precision management of environmental factors impacting plant-microbe interactions and disease in crops, contributing to sustainable plant production.

Big data include massive and complex datasets that cannot be analyzed using traditional methods. They originate from various sources, including laboratory-based information collections and sequencing of environmental samples across time and space. AI and machine learning combine massive information on different factors affecting disease incidence with deep models of disease development dynamics to identify disease development patterns, relationships, and causation. The predictive models built on such analyses can then be simplified for practical use by growers. Advances in AI and big data methods can improve the accuracy of achieve smart and sustainable agricultural production.

Precision agriculture and microbes

Precision agriculture is the use of technology, tools, machinery, and practices to respond to variability in field conditions through artificial intelligence (AI) and data science in order to produce higher-quality products with reduced environmental and ecological effects. Genomic, transcriptomic, proteomic, and metabolomic big-data technologies are expected to lead to significant breakthroughs in the understanding of plant-microbe interactions and support precision-based crop protection and production. Recent advances in these areas, together with new data-accessing techniques and the associated ability to fully understand the biologically active operations of the crop microbiome, suggest that a sustainable approach to precision agricultural production is within reach and also applicable to the management and maintenance of ecosystem health and biodiversity.

Research programs focusing on synthetic biology and microbial engineering in gene expression and functional pathways are now providing new information for the design and assembly of integrated and sophisticated plant—microbe systems for crop protection and improvement. Microbiome editing technologies that promote the composition or function of a specific microbiome using a synthetic microbial community in a plant also enable environmental stress management, disease suppression, and improvement of agricultural production systems. AI and big data techniques, together with multimodal agriculture involving various forms of sensor monitoring, allow for precise real-time determination of plant growth status and promote data-driven precision agriculture.

Vision for sustainable plant-microbe systems

Microbes constitute a substantial portion of the Earth's biodiversity; successful agriculture and healthy crops depend on the appropriate modulating action of specific microbial communities in field and horticultural crops. Research groups worldwide are engaged in discovering and refining diseases of major crops and establishing scientific models to understand the complex role of microorganisms in disease patterns of fusarium wilt, anthracnose, mosaic, and black rot. Nevertheless, data indicate considerable gaps and limitations in understanding influential interactions among crops and supporting populations of endophytic, phyllospheric, and rhizospheric microorganisms.

Recent advances in basic and applied research, coupled with genetic modifications and metagenomics, enable innovative management strategies for achieving crops with improved performance and reduced devastation from diseases. The exploration and application of beneficial microorganisms, including growth-promoting genera, nitrogen-fixing bacteria, mycorrhizae, antagonistic fungi and bacteria, and herbicide-degrading populations, have become major fields of investigation. Integration of these biotechnological applications into biological control strategies has broadened crop-protection options with the promise of greater environmental compatibility, but profitability remains an issue. To fulfill the integrated-disease-management (IDM) concept, the various microbial aspects must be linked with corresponding population patterns to reveal their connection and relevance within ecological frameworks.

Chapter - 17

Conclusion

Microorganisms facilitate and sustain ecosystem functioning across various habitats. Understanding their characteristics and preserving ecosystem health and functioning are essential for future societies. Such perspectives are especially relevant in agriculture, a predominant anthropogenic ecosystem that provides food and fiber for a growing population. For centuries, agricultural microbiology has explored the effects of harmful microorganisms in agriculture, with the ultimate goal of disease management and ensuring production stability. Recent developments have shifted attention from disease-causing microorganisms to those that contribute positively, transforming disease-management strategies in arable crops. However, disease outbreaks still represent a major threat to production systems, leading to investments in research and development of products to limit their impact. An integrated approach to soil-plant health management is necessary, and health as opposed to disease should become the focus of research.

Microorganisms influence production systems by participating in processes from nutrient cycling to disease suppression and through trade-offs among ecosystem functions. Research has examined these roles as discrete topics. Future studies should adopt an integrated approach that acknowledges both beneficial and harmful microorganisms and accommodates the complexity of their interactions with environmental factors, other organisms, and plants, integrating knowledge from different disciplines and involving stakeholders in formulations and implementations. Interventions that exploit natural systems to enhance health and minimize reliance on synthetic inputs represent the most feasible pathway for sustainable production systems. A combination of bioproducts, agronomy, and plant resistance has great potential, and smarter, reduced-chemical-input strategies are more likely to be accepted by farmers.

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