

Harnessing Microbial Diversity for Agroecology-Based Crop Health Management

ISSN: 2770-6745

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Abstract

Microorganisms are ubiquitous and form imminent components of living systems on earth. Over four centuries scientific pursuit using novel biomolecular tools has helped in thorough understanding from individual microorganisms to complex microbiomes associated with living and non-living systems. Such understanding has enabled to exploit the microbial diversity for crop, human and animal welfare and microbes best fit the 'One Health' concept. Microbial systems also play vital role in soil, water and air quality maintenance. Today, the microbiome research is helping to develop technologies to manipulate the microbiomes for ensured food and nutritional security. The microbiomes exhibit structural and functional diversity which is an interactive outcome of the microbes and the living and non-living systems they are associated with. Both structural and functional diversity of microbiomes influence extensively the crop growth and development. In this paper, the microbiomes & their constitution across agroecologies, structural and functional diversity among microbiomes and the impact of the combined diversity on crop growth and development are discussed.

Introduction


Ecosystems form an essential component of life on earth as they provide natural resources and it is estimated that 'ecosystem services' benefits could be about USD 125 trillion/year [1] which is several folds higher than the total gross domestic product of the world. Microorganisms constitute about 60% of the total biomass of the earth (more than 5×10^{30}) and sequester ~350-550, 85-130 and 9-14Pg of carbon, nitrogen, and phosphorous, respectively [2]. Though the common feeling is that microorganisms are harmful, comprehensive research has proven beyond doubt that only a fraction of them are pathogenic while vast majority are beneficial and essential for ecosystem functioning. They are excellent indicators of a given ecosystem and its patterns and can help to unravel the strategies and limits of life. They form an important resource for new genes and model organisms for biotechnological applications and predict environmental changes. Microbial communities are extensively used as models for understanding intra- and inter-species interactions and evolution patterns. The continuous quest to unravel the microbial traits has generated voluminous knowledge and the modern molecular tools have provided the genetic and molecular basis of these traits.

Microbiomes

In simple terms, a microbiome may be defined as an ecological community comprising a community of microorganisms and their genomic elements in a given environment. The plant microbiomes comprise fungi, bacteria, archaea, protists and viruses. Structural and functional diversity of a microbiome is an outcome of the multi-faceted interactions among the microbial community members of an environment with their hosts in presence of the natural

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Submission:  June 12, 2025

Published:  September 26, 2025

Volume 5 - Issue 4

How to cite this article: Suseelendra D*, Harnessing Microbial Diversity for Agroecology-Based Crop Health Management. Biodiversity Online J. 5(4). BOJ. 000619. 2025.
DOI: [10.31031/BOJ.2025.05.000619](https://doi.org/10.31031/BOJ.2025.05.000619)

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resources around them. This new area of research which started in late 90s has grown substantially and contributed to the better understanding of the plant-microbe interactions and also novel concepts like meta-organism concept [3] or holobiont theory [4]. Diverse crop production systems across different agro-ecologies are known to recruit specific microbiomes. This recruitment is an outcome of topological and chemical strategies and is governed by host genetics and metabolic pathways [5,6]. This specific recruitment process leads to structural and functional diversity in microbiomes and spans throughout the life span of the plants. The plant microbiomes inhabit mainly rhizosphere, phyllosphere and endosphere. Endosphere inhabitants are commonly known as endophytes. Each of these communities, independently as well contribute to the growth and development of the crop plants.

Structural diversity

Broadly, structural diversity of a given microbiome indicates the different kinds of microorganisms that co-exist in a given niche. This diversity indicates the habitat, limits of life and conditions conducive for the survival and evolution of other microorganisms along with other living and non-living systems. The temporal and special distribution of different types of microorganisms could influence the composition of a given ecosystem. Morphological, physiological and biochemical methods can be initially employed to characterize the microbial richness. DGGE, structural metagenomics are employed to analyses the diversity and relative richness of microorganisms. Alpha diversity is a measure of the soil microbial (bacteria, fungi and mycorrhiza) richness and community composition. Based on Internet-based GIS applications coupled with microbiological, geochemical, and geographic data and maps, Stoner [7] developed a prototype to understand structural diversity of Yellowstone National Park. Depending on their co-evolution patterns, the microorganisms occupy different parts of the plants such as below ground plant parts (rhizosphere), above ground plant parts (phyllosphere) and inside the plants (endosphere).

Rhizosphere: The rhizospheric soil hosts a rich diversity of microorganisms and is the 'hot spot' for beneficial plant microbial colonization and activities [8]. Plants form rhizo-assemblages independent of their host phylogeny to meet their growth, nutrition and defence-induction requirements. Plant rhizosphere micro-ecosystem mainly comprises rhizosphere microorganisms that serve as indicators of soil health in terms of quality and fertility, pathogen suppression and plant stress tolerance [9]. Rhizosphere, with huge energy flux, constitutes the largest ecosystem on earth [10] and can be broadly classified as Endo-rhizosphere, Rhizoplane and Ecto-rhizosphere. Bacteria constitute the most predominant microbial diversity of the rhizosphere and occupy up to 15% of the total root surface area [11] with gram negative, non-sporulating, rod shaped proteobacteria and actinobacteria [12,13] and gram-positive *Bacillus*, *Arthrobacter* and *Frankia* [10]. Kloepper [14] recognized the role of plant growth promoting rhizobacteria and pioneering research has led to their characterization across agro-ecologies. Another important vertical of the rhizosphere inhabiting microbes include obligate intercellular Arbuscular Mycorrhizal Fungi (AMF) belonging to the orders of *Glomerales*, *Diversisporales*

Archaeosporales, and *Paraglomerales* [15]. With special structures known as vesicles and arbuscules, they significantly improve plant nutrient uptake and induce resistance against several abiotic stresses [16]. They form symbiotic associations with the roots of many plant species and help in increased nutrient uptake [17,18]. Furthermore, AMF have been shown to improve plant tolerance to various abiotic stresses such as drought, salinity, and heavy metal toxicity [19,20]. With the advent of metagenomics, characterization of the soil virus abundance has progressed and they are estimated to range from 107 to 109g⁻¹ of soil [13,21]. Soil viruses helped in managing bacterial plant pathogens [22]. However, the location and migration behavior of soil viruses are influenced by the plant root exudates and soil physiochemical properties [23].

Phyllosphere: The term phyllosphere includes the microorganisms occupying the aerial parts of the plant, especially leaf surfaces. The highly complex microbial communities in the phyllosphere consist of diverse groups of culturable and non-culturable microorganisms [24]. The major phyla of phyllosphere bacteria are Proteobacteria, Firmicutes, Bacteroides, and Actinobacteria [25,26]. Study of microbial diversity of phyllosphere poses a great challenge as heterogeneous groups of microbial communities compete for the limited surface area which makes it extremely difficult to understand the community structure, physiology and networking. Unlike rhizospheric microbiota, the phyllospheric microbes are exposed to harsh conditions such as very high/low temperatures, UV radiation, extreme weather events, biogeography, environmental pollution, and limited availability of water and nutrient [27]. In phyllosphere too, bacterial communities dominate ranging from 102 to 1012g⁻¹ of the leaf [28]. Thompson classified 1236 isolates from sugar beet phyllosphere into 78 known and 37 unknown bacterial species clusters and populations varied with plant age. Legard [29] identified 88 bacterial species on spring wheat belonging to 37 genera and pink and white yeasts, filamentous fungi and bacteria always dominated across sampling times and sites. However, Rasche [30] opined that the culture-dependent profiling of phyllosphere communities could miscalculate diversity. However, the culture-independent approaches like genomic characterization of the microbial diversity could give the complete and complex community structure of the environment. While alpha-, beta- and gamma-proteobacteria, actinobacteria, bacteriodes and firmicutes dominated the phyllosphere [31]. Kadivar & Stapleton [32] reported occurrence of acidobacteria, actinobacteria, and cyanobacteria also. Studies by Yang [33] and Lambais [34] projected that a vast majority of the bacterial sequences of the phyllosphere of the crops were novel and unidentified. Among the identified genera, the cultivable yeasts genera included *Cryptococcus*, *Sporobolomyces* and *Rhodotorula* [35] while filamentous fungi included *Cladosporium*, *Alternaria*, *Penicillium*, *Acremonium*, *Mucor*, and *Aspergillus* that ranged from 10² to 10⁸ cfug⁻¹ [28,36]. Other reports highlighted the occurrence of *Pseudomonas* spp. As the most abundant inhabitants' [37] methylotrophic bacteria [38] and actinobacteria, bacteroidetes, firmicutes, and proteobacteria associated with seed coat have been reported in phyllosphere [39]. From wheat plant, Ripa isolated species of *Aspergillus*, *Fusarium*, *Penicillium*, *Alternaria*,

Cladosporium, *Trichoderma* and other genera from wheat plants. Interestingly, in the tropical and temperate ecosystems a high diversity of actinomycetes in phyllosphere was observed [40,41].

Endosphere: The microorganisms that inhabit endosphere are called endophytes. The prerequisite for an endophyte is that it should colonize the aerial plant tissues internally at least once during the life cycle without any apparent damage to the plants. Endophytes include pathogenic and beneficial microorganisms and are either vertically or horizontally transmitted. They are broadly grouped as endosyms (endosymbionts), endopaths (pathogens) and endosympaths (both symbionts and pathogens). Among the so far known endophytes, about 80% of them belong to Ascomycotina, about 18% belong to Basidiomycotina and a very small fraction represent *Mucoromycotina*. Unlike phyllosphere inhabitants, endophytes are protected from hostile environment as they internally colonize tissues. The plants provide protection, nutrition and shelter to the microorganisms and get in return improved growth & development and induced resistance various stresses. Several genera of endophytes have been reported from maize, paddy, wheat, cotton, soybean, and sugarcane etc. while in sunflower, a few endophytes have been reported. Such diversity in the endophytic microbes across crop species further strengthens their co-evolution over time. Interestingly genera like *Chaetomium*, *Trichoderma*, *Paenibacillus*, *Bacillus*, *Flavobacterium*, *Pseudomonas*, and *Rhizobium* which have already been commercially exploited for their beneficial traits have been reported as endophytes of these crops.

Functional diversity

Each of the constituent microorganisms of the microbiomes perform a wide array of functions. These functions influence not only the microorganisms per se but also their immediate environment including the host plants. Microorganisms significantly influence plant growth and development via production of phytohormones, volatile and non-volatile secondary metabolites, iron-chelating siderophores, solubilization of nutrients and triggering host plant resistance [42,43]. The mechanisms include growth promotion, nutrient supplementation, pest suppression, defense induction against biotic and abiotic stresses, and stimulation of other vital metabolic processes. The functional diversity could be characterized using both culture-dependent (conventional tools such as plate count, BIOLOG, FAME, DNA-DNA reassociation and G+C fractionation and molecular such as genetic fingerprinting, DNA microarrays, FISH, and Q-PCR) and culture-independent (whole genome sequencing, functional metagenomics, meta-proteomics, proteo-genomics, and meta-transcriptomics) methods [44]. The functional diversity could be broadly grouped as biotic and abiotic stress management, plant growth promotion and overall crop health management. Most of the microbes are multi-tasking, though, variable qualitatively and quantitatively. However, based on the objective of the study, specific traits are characterized and commercially exploited. For instance, *Trichoderma* is primarily exploited as biocontrol agent that too against soil-borne pathogens, though it is known to solubilize phosphorus and also impart drought tolerance [45]. Similarly, Endophytes exhibit a variety of modes of

action against their target organisms such as antibiosis, production of volatile organic compounds, parasitism, production of a battery of hydrolases, competition for substrate and nutrients, resistance induction, and siderophores. These methods suppress the growth and fitness of the pathogen and at the same time through their growth promoting ability, improve growth and development of the plant. The functional diversity under major heads is presented below.

Plant disease management: Microbes that perform disease management function are generally termed as biocontrol agents. Such approach is considered as eco-friendly as it is nothing but exploitation of the natural co-evolution system. Several fungal and bacterial agents belonging to genera *Trichoderma*, *Beauveria*, *Metarhizium*, *Cheatomium*, *atoxigenic Aspergillus*, *Bacillus*, *Pseudomonas*, and *Paenibacillus* etc have been successfully commercialized for management of plant diseases. *Trichoderma* is a very well-known bioagent used to manage many soil-borne plant-pathogens [46]. *T. viride* and *T. harzianum* exhibit antagonism against several species of plant pathogenic fungi such as *Rhizoctonia solani*, *Pythium ultimum*, *Fusarium oxysporum*, *Sclerotinia sclerotiorum*, *Botrytis cinerea*, *Pseudocercospora* spp. and *Colletotrichum* spp. [47-49] Commercial formulations of *Trichoderma* spp. are available for the management of major soil-borne diseases such as wilts, root rots, seed rots, and seedling blights [50,51]. Similarly, among bacterial biocontrol agents, popular strains of *Pseudomonas* spp. Include CHA0 and pf-5 which have been commercialized to suppress phytopathogens and promotion of plant growth [52-54]. Strains of *Pseudomonas* spp. such as CHA0 and Pf-5 significantly inhibited various root pathogens of plants [52,55] and also induced systemic resistance against foliar diseases [56]. Biocontrol ability is displayed by microbes through several modes of action. Many BCAs directly attack the pathogens in a physical mode and kill them. Some of the best-known examples are successful demonstration of coiling of *Trichoderma* around the hyphae of *Phytophthora*, *Pythium*, *Macrophomina* and *Fusarium* and then subsequently penetrate into the hyphae and thus kill the pathogen. Foliar application with mixtures of microorganisms from leaves of cacao tree reduced the symptoms of *Phytophthora* sp. demonstrating competition as one mechanism of disease suppression in a plant. Another approach is production of a variety of hydrolases such as chitinases, cellulases, glucanases, and lipases etc. which act on the cell walls of the pathogens and disintegrate them. The third mode could be competing for space and nutrients with the pathogens and thus restricting the growth and development of the pathogens to below critical threshold levels to cause disease. Phenazine-1-carboxylic acid, 2, 4-diacetylphloroglucinol, pyrrolnitrin, and pyoleutirin are secondary metabolites produced by *Pseudomonas* spp. Which significantly inhibit the growth of plant pathogens. Similarly, *Bacillus* spp. produced a variety of antimicrobial peptides, bacteriocins, toxins, and enzymes that inhibited diverse phytopathogens [57], by inhibiting cell wall synthesis, altering membrane structures, and suppressing the formation of initiation complexes on the small subunit of the ribosomes of the plant pathogens [58]. Bacteriocins (polymyxin, circulin, and colistin) are peptides with antimicrobial activity, which can destroy related/

metabolically similar bacterial species [59]. Many of the antifungal compounds induce membrane leakage and thus loss of cell contents including nutrients this leads to loss of vigour and infectivity. For instance, a variety of lipopeptides have been reported to induce hyphal membrane leakage in plant pathogens. Beneficial PGPR including mycorrhizae could Induce Systemic Resistance (ISR) in plants [60,61]. ISR has been successfully demonstrated in many plant species for management of a broad spectrum of plant pathogens, including bacteria, fungi, viruses, and even herbivorous insects [62]. ISR mechanisms prime the plants to express rapid defense-responses upon pathogen attack [63] via upregulation of host defense factors responsible to produce phytoalexins and other molecules which prevent progress of the pathogens even after entering the plant system. *Fusarium solani* harboring tomato roots induced resistance against *Septoria lycopersici* by activating PR7 and PR5 genes.

Insect-pest management: Insect-pest management using biocontrol agents has been adopted across the global agricultural systems. *Bacillus thuringiensis* could be cited as the classical example of entomopathogenic microbe against lepidopteran pests. Not only Bt toxin has been commercially exploited but Bt gene has been exploited to produce genetically modified varieties of cotton, maize, and brinjal etc. Entomopathogens such as viruses, bacteria, fungi, and nematodes invade and multiply inside the insects and then spread to other insects [64,65]. Entomopathogens could be host-specific or generic in nature and are categorized as a. opportunistic pathogens; b. potential pathogens & c. secondary invaders; c. facultative pathogens and d. obligate pathogens [66]. Some of the common genera of entomopathogens include *Paecilomyces*, *Lecanicillium*, *Metarhizium*, *Isaria* (*Cordyceps*-teleomorph), *Beauveria*, *Paranosema*, *Paenibacillus*, *Bacillus*, *Lysinibacillus*, nuclear polyhedron viruses, granuloviruses, baculoviruses and alphabaculoviruses. While most of the entomopathogens enter insects through mouth, nematodes enter through integument or directly enter into hemocoel using their stylet. Beneficial bacteria modulated defense responses in plants and altered volatile compound emissions in response to insect infestations [67,68]. Interestingly, plant microbiomes were altered for enhanced resistance against insect-herbivory in the following generation [67]. Plant pathogenic bacteria can be vectored by insects [69]. Certain plant-beneficial rhizosphere bacteria could successfully colonize insect hosts and use them as a means of dispersal to the rhizosphere of new host plants.

Plant nutrient management: Microorganisms have been shown to help the plants through nutrient supplementation and influenced the efficiency with which nutrients were taken up by the plants [70]. Extensive research has demonstrated that the PGPRs play a vital role in facilitating the nutrient supply to various plant species [71]. Praveen Kumar [72] observed that combined inoculation of *Pseudomonas* sp. and *Rhizobium* strains enhanced nutrient uptake in green gram. Bhat [73] reported nutrient-demand dependent regulatory mechanisms in the plants that could alter the behavior of the ion transporters in the roots. Thus, a demand-based regular intake of nutrients required exhaustive

coordination between root growth regulators and ion transporter activities [74]. Salwan [75] found that the bacterial communities in the microhabitats of the rhizoplane and root endosphere of the root microbiome played a crucial role in facilitating plant growth. Plant growth promoting rhizobacteria could either activate ion transport systems inside roots or directly enhance nutrient availability in the rhizosphere [76]. The potential of several strains of *Rhizobium*, *Azospirillum*, *Azotobacter*, and *Methylobacterium* to fix nitrogen has been demonstrated beyond doubt. The biological nitrogen fixation process is of utmost importance and the symbiotic association between leguminous plants and rhizobia manifests in meeting partial nitrogen requirement of the former by creating a suitable anaerobic environment for the optimal functioning of nitrogenase [77]. In associative free-living diazotrophs, a highly sophisticated oxygen-labile nitrogenase is responsible converting atmospheric nitrogen into ammonia [78]. However, the role of some microbes in N₂ fixation is questioned recently for want of proof of concept [79]. Phosphorus occurs naturally in both inorganic and organic forms [80] and species of *Bacillus*, *Pseudomonas*, *Azospirillum*, *Azotobacter*, and *Methylobacterium* could solubilize insoluble forms of phosphate, zinc, iron and silica. The release of low molecular weight organic acids [81] and hydrolysis of phosphoric acid esters by phosphatases [82] have been shown to be responsible for such solubilization. Mycorrhizae establish a symbiotic relationship with roots in order to get vital nutrients from the host plant and then give back mineral nutrients including N, P, K, Ca, Zn, and S. As a result, AMF give the plants nutritional assistance even in unsuitable root cell environments [83]. Plants and associated microorganisms have co-evolved and thus established synergistic interactions [84]. This co-evolution has provided insights into developing promising eco-friendly technologies for crop health management as alternatives to the synthetic chemicals. The rhizobacteria can stimulate growth of the colonized host plant through direct and indirect mechanisms. The direct mechanisms include supplementing plants with nutrients, production of phytohormones and their regulators. The indirect mechanisms include nutritional competition; siderophore production; pathogen suppression, pathogen toxin inhibition; and induced resistance [84-86]. Iron is an essential micronutrient required for growth and development of microorganisms as regulates several key metabolic processes. The siderophores produced by the microorganisms chelate specific ferric iron molecules, especially under iron-limited conditions, thus depriving the phytopathogens of iron and thereby protecting plant health [87]. Siderophore-producing endophytic *Pseudomonas* GRP3 reduced iron deficiency symptoms in *Vigna radiata* with increased chlorophyll content whereas *Streptomyces acidiscabies* E13 produced siderophores which enhanced the growth of *Vigna unguiculata* under nickel stress conditions. Other plant growth promotion traits include production of extracellular polysaccharides, biofilm production and HCN production etc. through which plants are protected during their growth and development.

Biostimulants: Biostimulant is a substance or a microorganism or a combination of both with an ability to stimulate physiological

processes in plants resulting in enhanced nutrient uptake, growth, yield, nutrient use efficiency, crop quality and tolerance to biotic and abiotic stresses, regardless of its nutrient content. However, when microorganisms are present, they should per se not be directly influencing the above effects. Biostimulants include a wide array of products such as botanical extracts, seaweed extracts, biochemicals, protein hydrolysates, amino acids, vitamins, cell-free microbial products, antioxidants, anti-transpirants, and humic acid, fulvic acid and their derivatives. However, they do not include pesticides or plant growth regulators. Biostimulants have been brought under regulation recently to ensure quality products for the consumers. Biostimulants can complement the chemical inputs and temper the beneficial rhizosphere microbiomes such as fungi and bacteria [88,89]. The major effects manifested by biostimulants on crops include improved seed germination, root development, and crop performance; improved appearance of the plant produce; stimulation of innate immunity by producing various biomolecules; bioremediation; reduced leaching; promoting nutrient uptake; and nutrient use efficiency [90]. A meta-analysis study by Li [91], revealed that the biostimulant application resulted in 17.9% add-on yield benefit with vegetables in arid climates and nutrient and organic matter deficient saline, sandy soils benefitting the most.

Factors influencing the structural and functional diversity

The structural diversity of a habitat is a net result of interaction among plants, edaphic factors, and interactions among various microorganisms. For instance, the forest structural diversity was reported to be linked to the soil microbial diversity [92], as the forest canopy complexity could fuel the production of decomposition substrates and thus harbour diverse bacterial and fungal communities. Rhizosphere microbial diversity and soil community composition is an outcome of the interactions between physico-chemical properties of the soil (sand: clay content, bulk density, water holding capacity, pH, C:N ratio, soil porosity, mineral composition etc.) and the soil-living-systems. The structural diversity of a given ecosystem is the outcome of the interaction among the root exudates, the microbial diversity and secondary metabolites produced by the microorganisms. The root respiration hinders the presence of Rhizosphere bacterial community structure is an outcome of the interactions between root exudates vis-à-vis various biotic and abiotic factors. For instance, Mac Donald [93] concluded that crop cultivars, root characteristics, age and plant phenophase played critical role in determining the rhizosphere bacterial community structure. During early growth phase of the plants, the fast-growing strategy organisms requiring simple substrates dominated the rhizospheres [94] while at later phenophases, the reduced oxygen levels resulted in relatively slow-growing bacterial communities capable of degrading more complex substrates [95]. Using knock-out mutants, Kudjordine [96] showed that benzoxazinoids released by the maize roots significantly influenced the composition of root-associated microbiota, especially Actinobacteria and Proteobacteria. Similarly, *Avena barbata* bacterial rhizosphere community assembly was a result of the dynamic root exudation chemistry and bacterial

substrate preferences [97]. On the contrary, the plant and environmental parameters influence the phyllosphere microbial diversity. According to Kecskeméti [98], species of *Enterobacter*, *Methylobacterium*, *Erwinia*, *Pseudomonas*, *Citrobacter*, *Frigoribacterium*, *Pantoea*, *Curtobacterium*, *Bacillus*, *Sphingomonas*, *Acinetobacter*, and dominated grapevine phyllosphere whereas species of *Mesorhizobium*, *Staphylococcus*, *Propionibacterium*, *Burkholderia*, *Pseudomonas*, *Ralstonia*, *Dyella* and *Bacillus* were predominant endophytes [99]. Fungi inhabiting the leaf displayed metabolic functions such as leaf litter decomposition leading to recycling of the carbon and nitrogen [100,101]. Endophytes significantly influenced plant growth promotion and induction of resistance against biotic and abiotic stresses [40,102]. The physiology of the plant and the environment were the determinant factors of actinobacterial association in plants and their establishment as endophytes [103]. Nwachukwu [104] observed that sunflower rhizospheric soils in South Africa were dominated by proteobacteria and Planctomycetes whereas in bulk soils Firmicutes and Actinobacteria were predominant. They also observed significant differences in bacterial structure at phyla and family levels as influenced by physicochemical parameters of the soils. Pan [105] explored the structural diversity of the secondary metabolites of microbes using One Strain Many Compounds Strategy (OSMAC) by modifying various parameters such as cultivation conditions, co-cultivation etc. The microbial diversity could be measured using 16s/18S/ITS or 16s rRNA sequencing; shotgun sequencing and metagenomic approaches.

Agroecology-based crop health management

Every agro-ecology has a niche biodiversity. The current concept of biological crop health management systems often is focused on formulations that contain one or a few microbial strains to address specific stresses or tasks. For instance, a *Trichoderma* formulation is deployed to manage primarily soil-borne plant pathogens or nematodes. Similarly, a formulation of 2 or 3 microbes is used to address crop nutrition. Today, a few thousands of microbial products are on the shelf and all with proven bio-efficacy. Interestingly, as elaborated above, crops have been shown to recruit their specific microbiomes. The ecology of the plant microbiomes is complex and thus plant health is an outcome of intra- and inter-microbiome interactions. Very few studies attempted to understand the interactions within and among microbiomes [106]. Since, the microorganisms are endowed with multiple beneficial traits, optimization of the formulations to harness maximum benefits from a given microorganism could result in enhanced crop productivity and farm profitability. Care must be exercised while choosing candidate strain to exploit its optimum potential rather than maximum potential so that strains possessing maximum benefits could be used in formulation rather than strains possessing one best trait. For instance, if the crop needs certain amount of N, P, and Zn, depending on the crop requirement, a strain possessing all these traits to a reasonable level could be a better candidate instead of one strain that has maximum that best supplements one nutrient. The current agricultural systems are overexploiting the natural resources. Tampering with the

structural and functional microbial diversity of the ecosystems could lead to disastrous situations such as natural resource base degradation, huge losses in ecosystem services and imbalance in diversity and thereby destabilizing the life systems on the planet. Decreases in biodiversity are occurring in nearly all regions on Earth, with critical consequences for how ecosystems function [107]. Such erosion has been reported in microbial diversity due to misuse and abuse of synthetic agro-chemicals. On the contrary, long term organic farming has resulted in improved soil microbial populations and resulting in improved crop yields, quality and soil health [108]. The diverse crop production systems of an agro-ecology promote specific microbial communities spatially and temporally. Hitherto, focus on such spatial and temporal microbial diversity of a given crop production system is limited [109-114]. Wide fluctuations of the population dynamics of both pathogens and biocontrol agents have been observed in presence and absence of crop plants. In absence of properly designed microbial ecology studies in conjunction with cropping patterns, such dynamics cannot be mapped to perfect the microbial technologies to near-real situations. Similarly, different cropping systems also influence structural and functional diversity of the microbiome. Hence, care must be taken to select candidate strains or their combinations which are compatible among themselves as well as with the agro-ecosystem to harness the desired enhanced productivity in a sustainable way.

Conclusion

The extensive damage caused by the synthetic chemical agro-inputs to our immediate environment has been demonstrated explicitly. Several health-related problems have propped up in recent years due to pollution of soil, water and air due to misuse and abuse of these chemical agro-inputs. As a panacea, microbe-mediated crop health management has gained importance. Microorganisms have been proven beyond doubt to be integral components of the life systems on earth. Their structural and functional diversity is an outcome of the diverse ecologies in which they are operative. So far, we have used formulations comprising one or a few microorganisms for crop health management which has often resulted in inconsistent field performance. Thus, there is a need for holistic understanding of the crop production systems vis-à-vis structural and functional microbial diversity so as to harness the beneficial traits of the microbiomes for optimized benefit.

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