Editorial

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Beneficial microorganisms for healthy soils, healthy plants and healthy humans

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The omnipresent creature of biosphere, microbiome is a popular topic in the scientific community as well as general public because of their benefits and applications in the several fields. In agriculture, microbes are used as biofertilizer and biopesticides for improvement of plant growth, development and yield without any harmful effect to soil, plant and human. The microbes could be also used for the maintaining the soil fertility and it health, which could further contributes to the healthy human health. Earlier, the research on microbiome has emerged from the environmental microbiome which provides an interdisciplinary platform for several fields like agriculture, biotechnology, industries, food science and especially human welfare. Now microbiome associated with plants have also been researched worldwide. In the editorial the microbiome associated with the plants and humans are detailed along with potential implication in the agriculture, environment and industry.

Healthy soil is one of the major factors to meet the food demands of rapidly growing population worldwide. It provides humans with ~90% of all the foods. The significance of healthy soil is growing at an alarming rate due to the rapid growth of the world's population. There will be less healthy soil to meet the supply of future food demands as there will be proportional increase in pressure on extraction of natural resources and urban expansion [1]. Soil is rather not a single environment but it includes an array of environments and represents a dynamic ecosystem. The major challenge to fulfill the demands of the future generations is management of the soils in a sustainable way. Globally, the environmental conditions that persist in soil are highly variable and decades of research has revealed that soil pH, concentration of organic carbon, texture, salinity and available nitrogen concentration exhibit an enormous range. These variations have been concluded to be the product of major factors including the climate, the micro as well as microorganisms, type of parent material and time [2].

The biological activity in different type soil is largely concentrated in the topsoil which consists of microbial communities occupying a tiny fraction. The soil microbial communities play major roles in supporting plant growth; maintaining health as well as fertility of soil and cycling of essential nutrients. Nevertheless, the preponderance of these microbial communities have not yet been isolated and their functions still remain unknown. The major known function of the soil microbiomes is that they carry out chief ecosystem services that are vital for existence of life on our planet, which includes carbon cycling and important essential nutrients and sustaining plant growth [3]. The rate of residue decomposition and nutrient cycling is greatly influenced by the microbial community composition. Fungi and bacteria are major decomposers in the soil ecosystem and thus are crucial for the mineralization of the nutrients and making their availability to plants and other organisms [4]. Mycorrhizal fungi, essential players in the soil microbial community play a major role in the translocation of the nutrients. The cycling of the nutrients is important for continuation of life on earth. Thus, protection of soil and maintaining its health is of high priority.

Plants are known to be colonized by the huge number and various groups of microbes such as bacteria, fungi and archaea which are one of the chief determining and control factors of its

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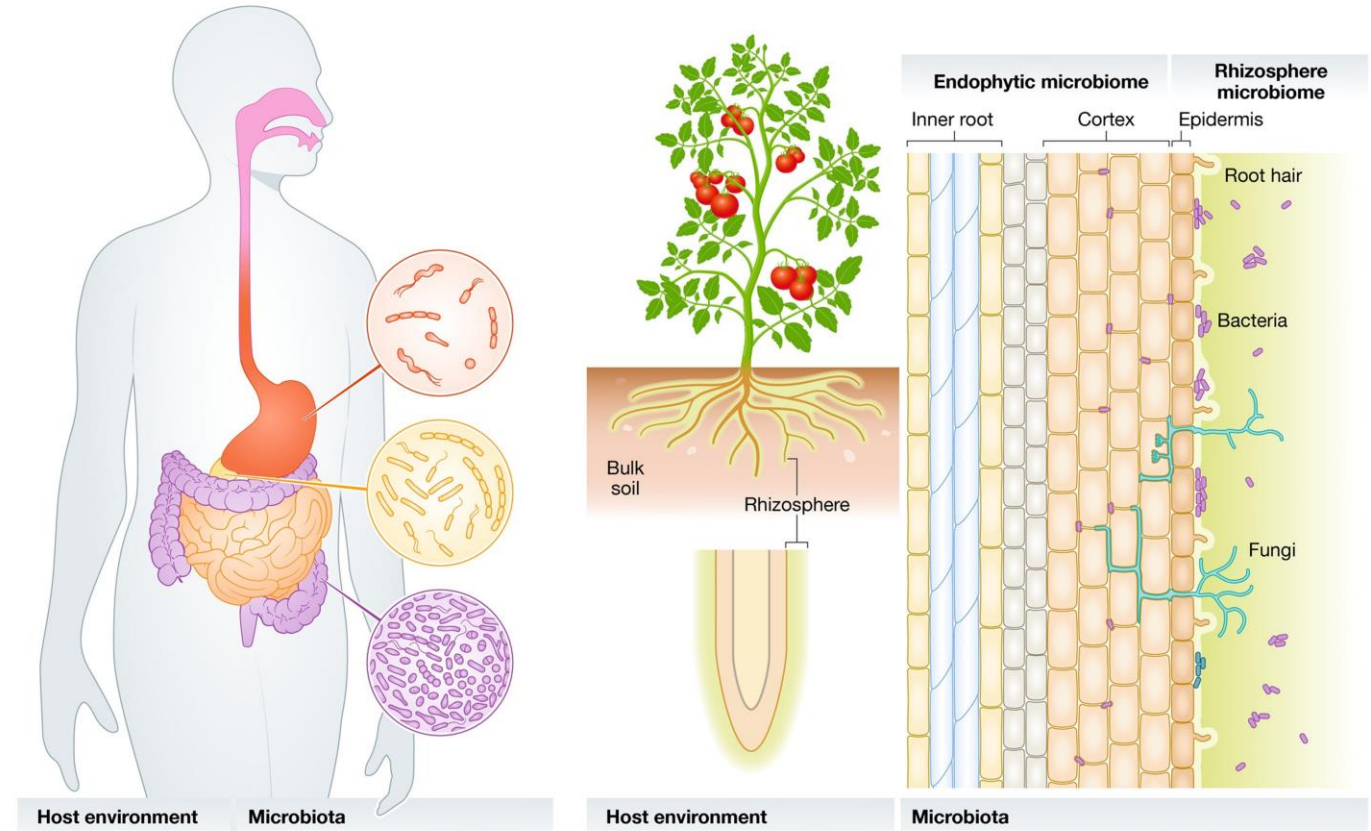

Host environment	Microbiota
Stomach	
• Acidic pH • Oxygenated	• Sparse bacterial load (10^1/g) • Low–moderate diversity • Predominating microbes – Firmicutes – Actinobacteria
Duodenum	
• Neutral pH • Low O_2 • Bile • Mucus • Mono- and disaccharides	• Increased bacterial load (10^3/g) • Low diversity • Predominating microbes – Firmicutes – Proteobacteria
Colon	
• Neutral pH • Low O_2 • Mucus • Host-indigestable polysaccharides	• High bacterial load (10^{12}/g) • High diversity • Predominating microbes – Firmicutes – Bacteroidetes

Host environment	Microbiota
Soil	
• Variable pH 3.5–10 • Oxygenated • Low nutrients	• High diversity (4×10^3–5×10^4 different bacterial species) • High numbers (10^6–10^{10} bacteria/g soil) • High competition with other microbiota and organisms (arthropods, nematodes, earth worms, …)
Rhizosphere	
• Neutral pH • Oxygenated • Mucilage and root exudates (sugars, amino acids, organic acids, …)	• Medium diversity • High numbers (10^6–10^{10} bacteria/g rhizosphere soil) • Low competition with other soil microbiota and organisms
Endosphere	
• Acidic pH • Low O_2 • High nutrient access	• Low diversity • Low numbers (10^4–10^8 bacteria/g plant) • No competition with soil microbiota and other soil organisms

Figure 1: The gut microbiota in humans and the soil and rhizome microbiota in plants exist under similar environmental conditions. Adapted from Hirt [7]

growth, productivity and health. Plant microbiome are harbors on surface (epiphytic), interior (endophytic) as well as root area (rhizospheric) of the plant that helps plant to combat abiotic and abiotic factors. Microbes residing in the different region of plant provide manifold attributes [5]. Phyllosphere is the complex ecosystem where plant host and microbes interacts extensively to create dynamic communities and it plays several beneficial roles for the health of the plant (figure 1). As the microbiome of skin phyllospheric microbiome is considered as first line defense which invades plant pathogens and defend the host plant and also protect the plant harsh environmental conditions such as heat. Phyllospheric microbes somewhere

also helps in the acquisition of the nutrients such as nitrogen. These types of microbes have different mechanism through which plant growth, crop yield and soil health enhanced such as production of plant growth promoting regulators (PGPRs) such as auxin, gibberellins and cytokinins, antimicrobial compounds, siderophores and fixation of nitrogen. There are several reports that have reported diverse phyllospheric microbiome for enhancing the health of the plant [6].

In a report, microbes were isolated from the epiphytic region of the tomato and it was identified as *Methylobacterium*. This bacterium was reported for the fixing the nitrogen, and producing phytohormones, siderophores and ACC (1-aminocyclopropane-1-carboxylate) deaminase enzyme which helps in improving the health of the plant [8]. In another report, phyllospheric bacterium of poplar, *Pseudomonas graminis* was reported for the fixing nitrogen as well showed mercury resistant which helps the host plant the heavy metal stress [9]. Wiraswati *et al*. [10], have isolated rice phyllosphere which were identified as *Bacillus* sp., *Brachybacterium* and *Enterobacter*. These all microbes were exhibiting antimicrobial against fungal pathogens *Pyricularia oryzae*. In another study, bacterial strain of the mango, *Bacillus velezensis* was reported for having biocontrol activity against anthracnose (Kent mangoes) [11]. Similarly, phyllospheric bacteria of plant *Avena fatua*, *Bacillus*, and *Pseudomonas* were reported for producing antimicrobial drug and also were effecting in remediating heavy metal contamination [12].

On the other hand, microbial community residing interior of the plant are also the one of the main drivers of the plant health. They dwell inside the plant tissues such as stem, roots, and leaves without harming the host. Endophytes play an important role in the plant health by acquisition and assimilation of nutrients, secretion and modulation of extracellular biomolecules such as phytohormones, signaling molecules, secondary metabolites and antimicrobial compounds [13]. In a report, desert cactus endophytic bacteria namely, *Bacillus amyloliquefaciens* was reported for conferring the drought stress in plant tomato and promotes its growth [14]. Kumar *et al*. [15], have reported, bacterial endophyte *Bacillus subtilis* for showing antimicrobial activity against *Xanthomonas oryzae* pv. *oryzae, hizoctonia solani*, *Fusarium verticelloides* and *Sclerotium rolfsii*. This bacterium was reported for producing indole-3-acetic acid and siderophores. In another report, endophytic fungus *Trichoderma phayaoense* was reported for the having ability to biocontrol gummy stem blight and wilt disease pathogen of muskmelon i.e. *Stagonosporopsis cucurbitacearum* and *Fusarium equiseti*, respectively [16].

Similarly like endophytes and phyllospheric microbiome, microbes harboring root area of the plant also plays a significant role in the health of their host. Rhizospheric microbiome also helps nutrient acquisition and assimilation by fixing and solubilization of nitrogen, phosphorus, potassium, and zinc, production of hydrogen cyanide, siderophores, ammonia, ACC deaminase enzymes and phytohormones that helps in direct as well as indirect plant growth promotion [17]. In an investigation by Sharma *et al*. [18], chickpea associated rhizospheric bacterium *Bacillus pumilus* was reported as halotolerant bacilli that combat the biotic as well as abiotic stress and boost the growth of the plant. In another report, rhizospheric bacterium *Pseudomonas libanensis* was reported for solubilizing phosphorus and alleviating drought stress that helps direct plant growth promotion [19]. In a similar report, *Pseudomonas* sp., and rhizospheric bacterium was reported solubilizing phosphorus and alleviating low temperature stress [20].

Over millions of years of co-evolution, microbes have adapted and formed ecological communities on earth. These microbial communities otherwise referred to as the microbiomes have the capability to survive in wide range of the hosts including inside or outside the living hosts as well as in air, soil and water. The interactions of these microbiomes either with their host or among themselves directly impact their residing ecosystem, physiology of the hosts as well as the microbial community composition [21]. Humans also co-evolved with a multi kingdom gut microbial ecosystem [22]. Soil and the human gut contain roughly the same number of active microbes, though the microbiome diversity of human gut is only 10% that the biodiversity of the soil. Since the pre-historic times, humans have been consuming soils as a supplement [23]. They have even used soil as detoxifying agents and for treatments for gastrointestinal ailments [24]. From early childhood, humans have been in contact with the soil; it has been tasted, inhaled and even taken the water which has been passed though soil. Humans have ingested the plants grown on soils along with microbial communities of soil. The human intestine is an ecosystem for trillion microbial cells with an aggregate 9.9 million microbial genes across the fecal microbiome [25]. The highest number of the cells within the human gut is found in the colon. Colon is the home for huge diversity and dense population of the microbe majorly dominated by the anaerobic ones which utilize carbohydrates [26].The development and advancements in the omics approaches together with the metabolic network modeling has shown how the host and the environmental factors affect the microbial ecology of the gut over the human life span [27, 28]. Culture independent techniques have demonstrated a large biodiversity of the microbes which is highly variable over time and across human

populations. Bacteroidetes and Firmicutes have been identified to be dominant in adults and Verrucomicrobia, Proteobacteria, and Actinobacteria are known to be frequent but generally as minor constituents [29, 30].

In conclusion, beneficial microbiomes associated with the plants and humans are the one of the key reason of the healthy plant and humans. These microbiomes play several significant role like acquisition of nutrients and protection from the plant pathogens in plants and digestion in humans. These microbiomes also have commercial application which is sustainable and these microbes could be more explored and used in the future for healthy environment, plants and humans.

CONFLICTS OF INTEREST

Author declares that there are no conflicts of interest.

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