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## The Critical Role and Application of Microbes towards Sustainable Development and Human Wellbeing

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Global South.*

Microorganisms (also called microbes) make up a large portion (1 trillion (10<sup>12</sup>) species or 60%) of the Earth's living as they are abundant and diversified in nature. Though they are vital for ecosystems and human welfare, their roles are often ignored or underrated. While most studies are underway in the global north to figure out how to utilise microbes in agriculture, industries, medical, space mission, and many other sectors, this kind of research is limited in the global south, particularly in Sub-Saharan Africa. Also, there has been scarce knowledge regarding the importance of microorganisms. The present paper aims to highlight and discuss current knowledge on the roles and/ or applications of microorganisms and their contribution toward sustainable development and human welfare in the global south. It also aims to help the scientists and/ or researchers in sub-Saharan Africa comprehends the use of microbial communities. We reviewed 84 published original research and review articles to explore microbial roles and their applications. We establish that many microbes play critical roles, which include but are not limited to ecological, pharmaceuticals, food source, biofuel or energy production, drugs or medicine development, nitrogen and carbon fixation, biocontrol agents, bioremediation, decomposition of organic matters, and soil formation. Since microbes potentially ensure the functioning of the Earth's ecosystem and support human welfare, research on this subject should be prioritised in the global south to improve human development and well-being.

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**INTRODUCTION**

Microorganisms such as bacteria, fungus, protozoa, viruses, algae, cyanobacteria, or blue-green algae make up the microbial community (Reed & Martiny, 2007; Schulz *et al.*, 2013; Yang *et al.*, 2017). They make up a large portion (60%) of the Earth's living stuff (Pajares *et al.*, 2016) as they are abundant (ca.  $5 \times 10^{30}$ ) and diversified in nature worldwide, possibly more so than any other organism (Fuhrman, 2009; Liu *et al.*, 2018; Doug, 2015). They are useful to life on our planet as they support the Earth's ecosystem processes and functions (Afzal *et al.*, 2019; Bardgett *et al.*, 2008; Falkenmark, 2013; Juretschko *et al.*, 2002; Kumar & Verma, 2018; Vurukonda *et al.*, 2016). Microbial communities control many critical environmental processes (Gouda *et al.*, 2018; Shade *et al.*, 2012; Soldan *et al.*, 2019; Tyc *et al.*, 2017). Their wide range of benefits in the ecosystem are facilitated by their metabolic activity (Afzal *et al.*, 2019; Bargaz *et al.*, 2021), interactions with plants and animals (Ahemad & Khan, 2012; Mastan *et al.*, 2019; Santoyo *et al.*, 2016), and utilisation in food production and biotechnological processes (Kumar & Verma, 2018; Loreau, 2000; Rashid *et al.*, 2016; Sahu, 2019). Most of these processes rely on microbes breaking down substrates into smaller chemicals that they use for growth and metabolism (Loreau, 2000; Shade *et al.*, 2012, 2012).

Some of them are important in mitigating climate change (Philippot *et al.*, 2013), developing green production technologies, and increasing crop growth, health, and productivity (Akinsemolu, 2018; Ali *et al.*, 2018; Schulz *et al.*, 2013). They aid in the mineralisation of nutrients, decomposition, and the elimination of natural and manmade pollutants (Albert *et al.*, 2014; Allison,

2005; Juretschko *et al.*, 2002; Pajares *et al.*, 2016). Furthermore, some microbes support the production of oxygen and decomposition of organic matter (Allison, 2005) and human health through the development of drugs (Hussain *et al.*, 2017) and supplying nutrients to plants (Bardgett *et al.*, 2008; Loreau, 2000). Soil bacteria, for instance, are entailed in biological transformations and enhancement of carbon, nitrogen, and other nutrient pools, which aid plant community establishment (Rashid *et al.*, 2016; Schulz *et al.*, 2013). Microbes that lessen chemical fertiliser application rate by improving soil fertility and, thus, plant nutrition are known as plant growth-promoting rhizobacteria (PGPR) (Adesemoye *et al.*, 2009; Sturz & Nowak, 2000). The PGPR or combinations of PGPR and arbuscular mycorrhiza fungus (AMF) are claimed to improve the efficient use of nutrient fertilisers (Adesemoye *et al.*, 2009).

Furthermore, some microbes are food for small organisms; for instance, ants and beetles consume fungi in tropical forests (Albert *et al.*, 2014; Cunha *et al.*, 2017; Strickland *et al.*, 2009). Furthermore, several microbes in animals' guts break down indigestible food sources making food available for the animal's absorption (Albert *et al.*, 2014; Strickland *et al.*, 2009). This is because certain bacteria can digest sugar polymers into simple glucose, making it available to animals that otherwise could have been unavailable for most herbivores (Cunha *et al.*, 2017; Strickland *et al.*, 2009). Furthermore, bacteria and fungi can improve soil structure by promoting the formation of soil aggregates and pores (Rashid *et al.*, 2016). Because of this, microbes are referred to as critical for the survival

of plants and animals (Akinsemolu, 2018; Pajares *et al.*, 2016) and can be referred to as a chief life controller on the planet. Besides, microorganisms can help achieve sustainable agriculture, environmental conservation, and the creation of bioenergy crops (Philippot *et al.*, 2013). Modern agriculture has effectively utilised the capability of microbes in transferring the gene of interest (nutrients) from one species to plants or crops of human value (such as the production of crops with increased nutrients or increased defensive mechanisms) through the use of Ti plasmids from bacteria, the important microbes used in modern agriculture include *Agrobacterium tumefaciens* and *Bacillus thuringensis* which has been involved in the production of crop plants with increased nutrients (golded rice, sunflower and canola) and increased defensive mechanism (Bt corn, Bt cotton), respectively. Table 1 summarises some of the roles and/ or applications of microorganisms. However, some of these roles and their contribution to the sustainable development and human wellbeing are discussed in the succeeding sections.

1 **Table 1: The roles and applications of microorganisms towards sustainable development and human wellbeing**

S/N	Role/application of microbe	Reference
1	Environmental clean-up, treatment of wastewater, bioremediation, phytoremediation	Afzal <i>et al.</i> (2019), Mendoza-Hernández <i>et al.</i> (2019), Sahu (2019), Santoyo <i>et al.</i> (2016), Wagner <i>et al.</i> (2002)
2	Enhance plant growth, health, and yield	Afzal <i>et al.</i> (2019), Park <i>et al.</i> (2015), Soldan <i>et al.</i> (2019), Sturz & Nowak (2000)
3	Restore the fertility of degraded land and soils, e.g., bacterial and fungal inocula increase the nutrient bioavailability	Adesemoye <i>et al.</i> (2009), Lobo <i>et al.</i> (2019), Rashid <i>et al.</i> (2016)
4	Enhance drought and salinity stress tolerance in crops, e.g., using microbial communities to develop drought-tolerant varieties, shifting the crop calendars and resource management practices and allowing utilisation of marginal lands	Ahmad <i>et al.</i> (2011), Bharti <i>et al.</i> (2014), Chatterjee <i>et al.</i> (2017), Kumar & Verma (2018), Liu <i>et al.</i> (2018), Marasco <i>et al.</i> (2013), Masmoudi <i>et al.</i> (2019), Miliute <i>et al.</i> (2015), Vurukonda <i>et al.</i> (2016)
5	Soil humus formation, biomineralisation	Logue <i>et al.</i> (2015), Loreau (2000)
6	Enhance plant growth by preventing or alleviating biotic (diseases/pathogens) and abiotic stresses (sanity or drought), e.g., plant growth-promoting microbes and mycorrhizal fungi	Berg (2009), Bharti <i>et al.</i> (2014), Chatterjee <i>et al.</i> (2017), de Andrade <i>et al.</i> (2019), Kumar & Verma (2018), Masmoudi <i>et al.</i> (2019), Vurukonda <i>et al.</i> (2016)
7	Regulate plant hormones, improve nutrition acquisition and siderophore production, enhance the antioxidant system, enhance the supply of nutrients and water during stress	Kumar & Verma (2018), Loreau (2000), Rashid <i>et al.</i> (2016), Sahu (2019)
8	Mineralisation of nutrients, decomposition, and the elimination of natural and manmade pollutants	Albert <i>et al.</i> (2014), Allison (2005), Juretschko <i>et al.</i> (2002), Pajares <i>et al.</i> (2016)
9	Nutrient fixation, nitrogen fixation, phosphate solubilisation, and potassium solubilisation towards increased land productivity	Adesemoye <i>et al.</i> (2009), Gouda <i>et al.</i> (2018), Liu <i>et al.</i> (2018)
10	Improve soil structure, fertility, and stability and promote soil aggregate formation	Adesemoye <i>et al.</i> (2009), Rashid <i>et al.</i> (2016)
11	Drug development/formulation towards the improvement of animal and human wellbeing	Hussain <i>et al.</i> (2017), Kumar <i>et al.</i> (2019)
12	Potential for antimicrobial, antifungal potential (e.g., plant disease management), drugs and vaccines development	Dalmasso <i>et al.</i> (2014), Hussain <i>et al.</i> (2017), Lee <i>et al.</i> (2015), Marijani (2022), Masmoudi <i>et al.</i> (2019), Xu <i>et al.</i> (2019)
13	Regulate climate by absorbing CO <sub>2</sub> and releasing O <sub>2</sub> , e.g., cyanobacteria ( <i>Synechococcus</i> ) and algae	Barantal <i>et al.</i> (2012), Logue <i>et al.</i> (2015)
14	Aid in nature conservation and the mitigation of climate change	Philippot <i>et al.</i> (2013)
15	Biological control agents, i.e., bacteria targeting pests and pathogens with antibiotics, hydrolytic enzymes, nutrient limitation, and priming plant defences, control invasive species, etc.	Agrillo <i>et al.</i> (2019), Chithrashree <i>et al.</i> (2011), El-Borollosy & Oraby (2012), Ghazalibiglar <i>et al.</i> (2016), Harada <i>et al.</i> (2018),

S/N	Role/application of microbe	Reference
		Lee <i>et al.</i> (2015), Masmoudi <i>et al.</i> (2019), Méndez-Bravo <i>et al.</i> (2018)
16	Digestive and fermentation in animals enable the utilisation of dry plant feedstuffs for herbivores	Burgos <i>et al.</i> (2018), Cunha <i>et al.</i> (2017), Curtis <i>et al.</i> (2006), Dalmasso <i>et al.</i> (2014), Konopka (2009)
17	Enhance crop acquisition of phosphorus, e.g., phosphate solubilising bacteria, thus increasing P-fertilizer use efficiency	Bargaz <i>et al.</i> (2021), Lobo <i>et al.</i> (2019)
18	Biogas or biofuel production, development of bioenergy crops	Heeg <i>et al.</i> (2014), Javed <i>et al.</i> (2019), Philippot <i>et al.</i> (2013)

2

## Role of Microbial Communities towards Sustainable Development and Human Wellbeing

### Carbon and Nitrogen Fixation

The most important role of the microbes on Earth is their ability to recycle the major elements (i.e., carbon (C), oxygen (O), and nitrogen (N)) that make up the living systems (Fuhrman, 2009). The pathway by which these elements, chemical compounds, and other forms of matter or nutrients flow through the living and non-living components of an ecosystem is called the biogeochemical cycle (Pajares *et al.*, 2016). They routinely pass from one organism to another and from one part of the biosphere to another through biogeochemical cycles (Juretschko *et al.*, 2002). Neither chemical elements nor organic matter is lost when they move through components of an ecosystem; instead, they are recycled or accumulated in reservoirs (Schulz *et al.*, 2013). In addition, microbes regulate biogeochemical cycles, i.e., the nitrogen, phosphorus, and sulphur cycle (Barantal *et al.*, 2012; Konopka, 2009), which depend on their metabolic processes through physical involvement or production of chemical enzymes involved in respective processes (Falkowski *et al.*, 2008). Even though microbes are involved in many biogeochemical cycles of many important elements in the Earth, in this review, only the nitrogen and carbon cycles have been discussed in detail due to their vital role

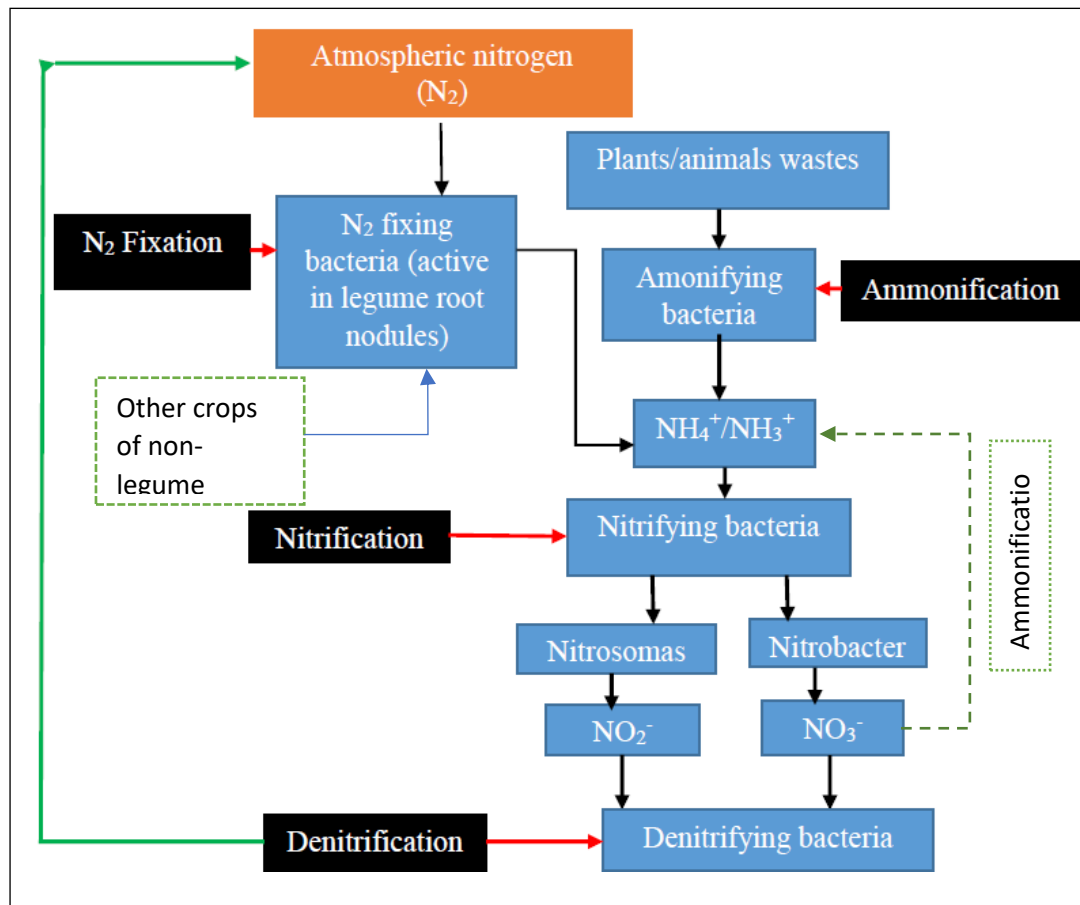
and importance in the ecosystem and global sustainability.

### *The Nitrogen Fixation*

Nitrogen is an essential element for all life forms on Earth (Tang *et al.*, 2019). However, in the Earth's atmosphere, nitrogen gas (N<sub>2</sub>) is usually available in an unusable form for biological organisms. Therefore, N<sub>2</sub> is transformed by microorganisms into either nitrates (NO<sub>3</sub>) or nitrites (NO<sub>2</sub>) which are the most important nitrogen compounds utilised by plants (Rashid *et al.*, 2016; Schulz *et al.*, 2013), as also shown in figure one. The chemical process of converting N<sub>2</sub> into a usable form for living organisms is called nitrogen fixation (Figure 1) (Rashid *et al.*, 2016). The microorganism, i.e., *Rhizobium* bacteria, capable of converting N<sub>2</sub> from the air into fixed nitrogen, a form that plants can use are called nitrogen-fixing bacteria (Méndez-Bravo *et al.*, 2018). The process has been intensively utilised in modern agriculture as a strategy to reduce the utilisation of mineral fertiliser to create safe and more profitable farming while conserving ecosystem quality. Recently studies and efforts have been made towards the utilisation of microbes with the capability of fixing nitrogen as biofertiliser as a step towards replacement of chemical mineral fertiliser used in farming areas which have been observed to have negative environmental impacts despite its importance in conventional agriculture.



**Figure 1: The Schematic representation of the nitrogen cycle shows four roles of bacteria as indicated by red arrows in the cycle**

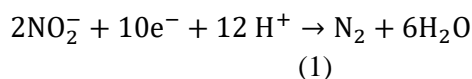


Nitrogen-fixing microbes use nitrogenase enzymes and mechanisms to fix nitrogen (Gouda *et al.*, 2018). These bacteria convert tons of nitrogen to ammonium (NH<sub>4</sub><sup>+</sup>), nitrite (NO<sub>2</sub><sup>-</sup>), and nitrates (NO<sub>3</sub><sup>2-</sup>) and add it to the soil, allowing plants to survive even in nutrient-poor soils (Schulz *et al.*, 2013). This means that the soil would be deprived of nitrogen if there were no nitrogen-fixing bacteria. These bacteria are divided into two groups: free-living bacteria (non-symbiotic) and symbiotic (mutualistic) bacteria. The free-living bacteria include *Cyanobacteria* (blue-green algae), *Azotobacter*, *Azolla*, *Azospirillum*, *Agrobacterium*, *Clostridium*, *Gluconobacter*, *Flavobacterium*, and *Herbaspirillum* (Rashid *et al.*, 2016). They are habitually associated with non-legumes (Berg, 2009; Gouda *et al.*, 2018). *Azospirillum* species and *Frankia* are associated with cereal grasses and certain dicotyledonous species (actinorhizal plants), respectively. *Rhizobium* and

*Bradyrhizobium* are associated with leguminous plants (Fabaceae) or members of the pea family (Gouda *et al.*, 2018). The symbiotic nitrogen-fixing bacteria live in the root hairs of the host plants (Rashid *et al.*, 2016). Apart from nitrogen-fixing bacteria, there are also ammonifying, nitrifying, and denitrifying bacteria (Figure 1). Ammonifying bacteria release ammonia from organic compounds, i.e., dead plants and animals (Gouda *et al.*, 2018). This process is known as ammonification (Rashid *et al.*, 2016, Figure 1), and this is important to ensure the release of NH<sub>4</sub>-N from organic materials to be available for other nitrogen cycle chemical reactions or plant uptakes; however, very few plant species have the ability to utilise direct NH<sub>4</sub>-N for its biological processes.

The bacteria involved in the ammonification process are called saprobic bacteria or ammonia-oxidising bacteria and include the

genera *Bacillus*, *Clostridium*, *Proteus*, *Pseudomonas*, and *Streptomyces* (Liu *et al.*, 2018). Nitrifying bacteria oxidise ammonia or ammonium into nitrites (NO<sub>2</sub><sup>-</sup>) or nitrates (NO<sub>3</sub><sup>2-</sup>) (Rashid *et al.*, 2016, Figure 1), the N forms which are highly utilised by plants in their biochemical processes. This process is called nitrification (Liu *et al.*, 2018; Rashid *et al.*, 2016). The bacteria which convert ammonia into nitrite and nitrate are *Nitrosomonas* and *Nitrobacter*, respectively. They are collectively known as denitrifiers. Other denitrifying bacteria include *Achromobacter*, *Micrococcus denitrificans*, *Thiobacillus denitrificans*, and most species of *Pseudomonas* and *Serratia* (Rashid *et al.*, 2016). Denitrification is a process in which nitrogen dioxide is converted back to atmospheric nitrogen (Equation 1).



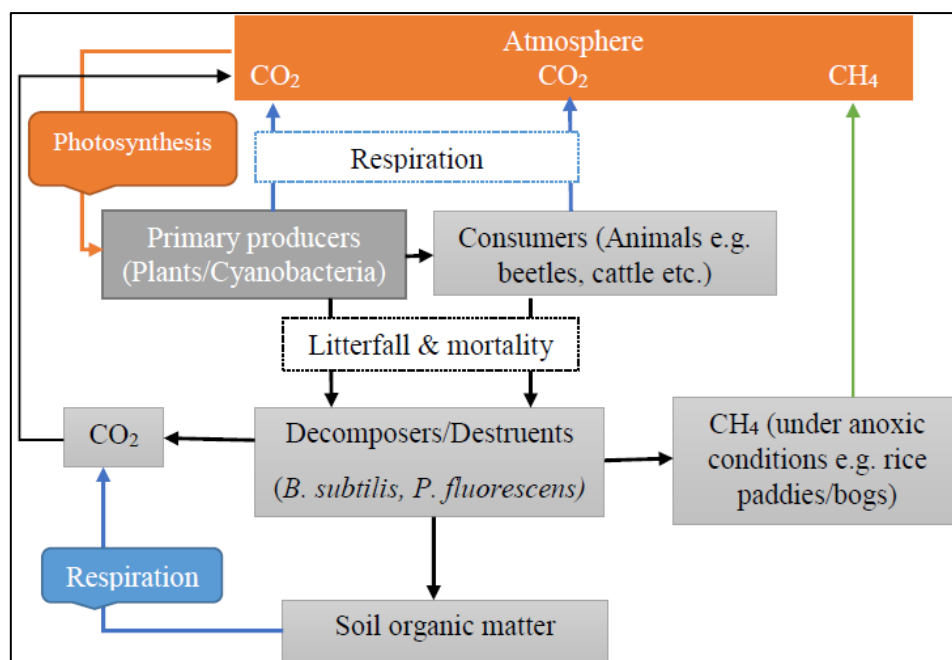
### The Carbon Fixation

Carbon is used by plants and animals to synthesise organic substances, i.e., carbohydrates, lipids, and

proteins, which are then used to build internal structures or as a source of energy. The carbon is discharged into the environment as these organisms die (Figure 2). It occurs during putrefaction or the breakdown of organic matter of living organisms (Barantal *et al.*, 2012). Microorganisms keep the carbon cycle going from the atmosphere to the soil and back again (Allison, 2005). The biological carbon cycle is simply the natural recycling of nutrients stored in organic matter into an inorganic form (Figure 2.). The source of carbon is atmospheric carbon dioxide (CO<sub>2</sub>), which prior to its incorporation into living organisms, is transformed into a usable organic form (Barantal *et al.*, 2012; Fierer *et al.*, 2003, Figure 2). The process of transforming CO<sub>2</sub> into a usable organic substance is known as carbon fixation (Cleveland *et al.*, 2006, Figure 2). A familiar example of this process is photosynthesis (Equation 2), which is carried out by autotrophs, i.e., green plants and cyanobacteria (Figure 2).



**Figure 2: The schematic carbon cycle showing the production and utilisation of carbon in the form of carbon dioxides (CO<sub>2</sub>)**

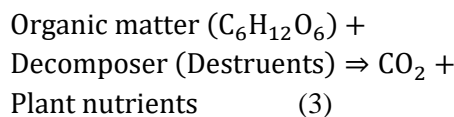


Some microorganisms (e.g., bacteria: *B. subtilis* and *P. fluorescens*) are responsible for the biodegradation or decomposition of organic

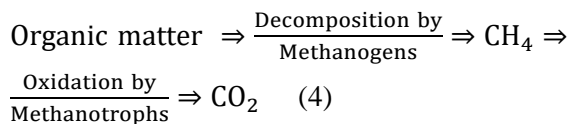
matter (Bardgett *et al.*, 2008). This results in the breakdown of organic matter into carbon forms, which are utilised by other organisms. It also



releases other mineral nutrients (nitrogen, phosphorus, potassium) bound up in dead organic matter into the soil (Rashid *et al.*, 2016). Researchers argue that if destruents stopped recycling inorganic nutrients, primary productivity on Earth would cease (Fierer *et al.*, 2003; Juretschko *et al.*, 2002). For instance, organic matter on the tropical forest floor and in the soil would never decay without microbes (Reed & Martiny, 2007). Therefore, they are the decomposers that make mineral nutrients available to primary producers (Equation 3) and are soil microbes that enable the recycling of plant nutrients from dead animals and plant materials. However, it should be noted that organic matter degradation and the development of biological cycles are the results of the interaction of microbial communities rather than a single organism.



During decomposition, methane (CH<sub>4</sub>) is also released into the atmosphere (Heeg *et al.*, 2014, Figure 2). This is facilitated by the microorganisms called chemoorganotrophs and methanogens that decompose the organic matter of dead organisms. Since methanogens are unable to break down complex organic matter directly, they use waste products of the organotrophs, CO<sub>2</sub>, and acetate to produce CH<sub>4</sub>. The CH<sub>4</sub> is then oxidised by microorganisms called methanotrophs into CO<sub>2</sub> (Equation 4).



Moreover, in tropical forest ecosystems, fungi are the primary decomposers of litter (Barantal *et al.*, 2012; Rashid *et al.*, 2016). They are unable to make their own carbohydrates because they lack chlorophyll. Due to this, they are classified as saprophytes as they live and depend on the dead materials of animals and plants while decomposing these materials to obtain energy. The fungi are able to decompose litter, which has

a great amount of cellulose and lignin. This is because they have more lignin-digesting enzymes compared to other microorganisms, e.g., wood-decaying fungi (Koranda *et al.*, 2014). The decomposition by fungi proceeds faster in the presence of oxygen than in anoxic environments. Unlike bacteria, fungi use their hyphae to penetrate larger pieces of organic matter because they have enzymes to decompose lignin (Barantal *et al.*, 2012; Fuhrman, 2009). Because of this, fungi are considered the main decomposers in many tropical forests. Therefore, decomposer microbes are so critical not only to sustainable agriculture through nutrient supply for crops and ensuring high productivity, but also in making the environment clean for humans to live in.

### Soil Formation, Nutrient Availability, and Aggregation

The interactions of soil microbial communities, e.g., bacteria and fungi, play a key role as actors in mineral weathering and biomineralisation (Loreau, 2000). Their role in soil humus formation is due to their ability to decompose organic matter (Barantal *et al.*, 2012; Koranda *et al.*, 2014). When the leaves or plants and animals die, they are decomposed by microorganisms, allowing the humus to mix with the soil (Logue *et al.*, 2015). Mineral weathering via chemicals and forces exerted by fungi and other microbial communities contributes to soil formation. Because of this, such microorganisms are considered as architects of soils (Schulz *et al.*, 2013). The exudates from bacteria, fungi, and decomposed cells in soils are also responsible for enhancing the soil organic matter, which in turn improves the soil structure, function, and quality (Rashid *et al.*, 2016; Schulz *et al.*, 2013). Previous works claim that fungal inocula, together with organic fertiliser, could be a very valuable tool for improving soil fertility and aggregation (Gouda *et al.*, 2018; Kumar & Verma, 2018; Rashid *et al.*, 2016). However, it is important to note the soil structure is not solely influenced by the mineral constituents of the soil but also by the microbes present in pores.

Furthermore, microbes such as fungi give tropical plant roots access to nutrients in the soil by

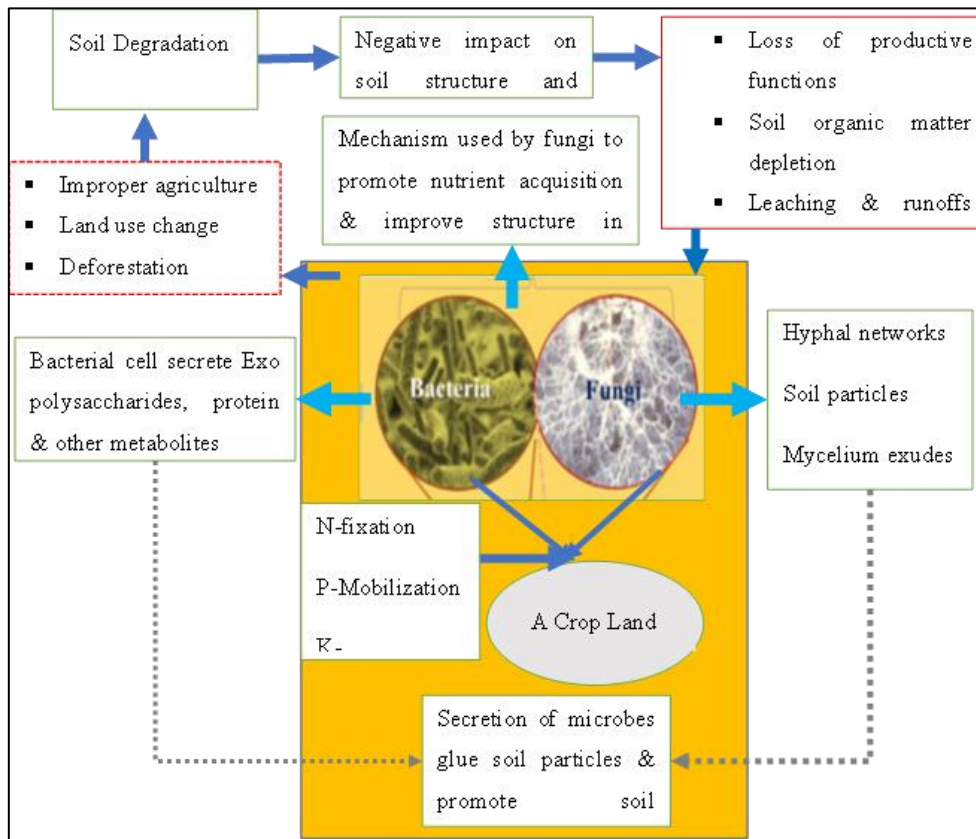
forming close associations with tree roots. For example, most vascular tropical plants' roots and small root hairs form an association with mycorrhizal fungi whose hyphae provide an efficient absorptive structure (Strickland *et al.*, 2009). It is estimated that nearly 90% of all tree roots are in these associations (Schulz *et al.*, 2013). These symbiotic associations are called mycorrhizae. Mycorrhizal fungi include those that live either on the plant surface (ectotrophic or sheathing) or in the host (endotrophic or vesicular–arbuscular). Mycorrhizal associations are involved in nutrients, e.g. nitrogen and phosphorus uptake, and transfer from the soil to the roots (Lobo *et al.*, 2019). In addition to the role of nutrient uptake, the hyphae also secrete enzymes capable of breaking down organic molecules and making inorganic nutrients available to plants (Konopka, 2009). In addition, mycorrhizal associations support nutrient cycling, growth, and primary productivity in tropical rainforests and the plant community structure. It facilitates water uptake by the roots and enhances the roots' resistance to pathogens. It also enables tropical trees to exchange carbon between themselves through a fungal mat. Overall, this association is valuable to both parties; the plants gain nutrients, whereas the fungi obtain carbohydrates from the plant.

Furthermore, the microbes have the potential to restore the fertility of degraded habitats and improve soil organic matter, remediate soil structure and stability, nutrient availability, and aggregation through various processes (Kumar & Verma, 2018; Rashid *et al.*, 2016; Tang *et al.*, 2019). The fungal cells can release mucilaginous exudates, which are composed of extracellular surface polysaccharides. These exudates are responsible for the formation of aggregates, which

are useful for improving soil aeration and porosity (Rashid *et al.*, 2016). Bacteria, on the other hand, release exopolysaccharides that form organo–mineral complexes, which help to bind soil particles into aggregates (Rashid *et al.*, 2016). Bacterial and fungal inocula can increase the nutrient bioavailability through nitrogen fixation and mobilisation of phosphorus (Lobo *et al.*, 2019), potassium, and iron in the crop plants (Gouda *et al.*, 2018; Rashid *et al.*, 2016). This inoculation is vital for the restoration of degraded soils (Rashid *et al.*, 2016). Compared to single inoculum, co-inoculation of bacteria and fungi are advantageous for restoring fertility and the organic matter content of the soil (Rashid *et al.*, 2016).

For instance, arbuscular mycorrhizal fungi and biological N-fixing bacteria contribute 5–20% to the total N demand of grassland and savannah annually (Rashid *et al.*, 2016). It has been shown that the contribution of arbuscular mycorrhizal fungi to temperate and boreal forests is 80%, while the total P acquired by plants through bacteria and fungi is 75% (Rashid *et al.*, 2016). Furthermore, *Phomopsis liquidambari*, an endophytic fungus, was also reported to play a crucial role in rice (*Oryza sativa*) habitat adaptation by enhancing N and P acquisition and utilisation (Tang *et al.*, 2019). In general, the basic mechanisms through which bacteria and fungi promote soil aggregation and nutrient bioavailability include N fixation, P, K and Fe mobilisation through the production of organic acids and siderophores (Figure 3). In addition to this, these microbes produce organo–polysaccharides and proteins (golmalin, mucilages and hydrophobins) to promote soil aggregate stability (Figure 3).

**Figure 3: The schematic portrays showing basic mechanisms used by bacteria and fungi to improve soil organic matter, nutrient availability, and aggregation**



**Source:** (Adapted with modification from Rashid *et al.* (2016))

### Promote Plant Growth and Health

Some plants develop associations with members of their ecosystem in order to survive (Kumar & Verma, 2018; Marasco *et al.*, 2013; Miliute *et al.*, 2015). Plant-associated microbes play a crucial role in the growth and health of plants (Berg, 2009). *Bacillus*, *Pseudomonas*, *Serratia*, *Stenotrophomonas*, and *Streptomyces*, as well as the fungal genera *Ampelomyces*, *Coniothyrium*, and *Trichoderma*, are examples of organisms that influence plant health, while members of the bacterial genera *Azospirillum* and *Rhizobium* are model microbes for plant growth promotion (Berg, 2009). During growth and development, plants form a symbiotic interaction with soil microbes, i.e., bacteria and fungus (Gouda *et al.*, 2018; Santoyo *et al.*, 2016). One of the most beneficial relations between plants and microorganisms is that of endophytic bacteria (Afzal *et al.*, 2019; Miliute *et al.*, 2015). Non-

pathogenic bacteria and fungi that live in the living tissue of healthy plants without harming them are known as endophytes (Mastan *et al.*, 2019; Xu *et al.*, 2019). These bacteria can offer numerous benefits to the host plant, i.e., promoting the growth and protection of plants from pathogens (Gouda *et al.*, 2018; Santoyo *et al.*, 2016).

They are able to communicate and interact with the host plant more efficiently compared to rhizospheric bacteria (Santoyo *et al.*, 2016). Endophytic bacteria, a subclass of rhizospheric bacteria (Philippot *et al.*, 2013), is commonly known as plant growth-promoting rhizobacteria (PGPR) (Afzal *et al.*, 2019; Gouda *et al.*, 2018). In these associations, bacteria provide several benefits to their host plants (Santoyo *et al.*, 2016), i.e., helping them to withstand biotic and abiotic stresses that can challenge their growth and health (Afzal *et al.*, 2019; Hallmann *et al.*, 1997; Miliute

*et al.*, 2015). In addition, endophytic bacteria that thrive inside plants help to improve plant nutrient uptake (Adesemoye *et al.*, 2009) and growth under challenging environment conditions (Hallmann *et al.*, 1997; Rosenblueth & Martínez-Romero, 2006; Sturz & Nowak, 2000). Some microbes, e.g., PGPR *Bacillus amyloliquefaciens*, *Bacillus pumilus*, *Pseudomonas fluorescens*, and the arbuscular mycorrhiza fungus (AMF), *Glomus intraradices* promote plant growth via novel volatile organic compounds (Adesemoye *et al.*, 2009; Park *et al.*, 2015). While PGPR or combinations of PGPR and AMF has the potential to improve the efficient use of nutrient fertilisers (Adesemoye *et al.*, 2009), phosphate solubilising bacteria can enhance crop performance by improving crop phosphorus acquisition via root system (Bargaz *et al.*, 2021; Lobo *et al.*, 2019).

The mechanisms of endophytic bacteria to promote plant growth occurs either direct or indirect (Santoyo *et al.*, 2016; Sturz & Nowak, 2000). Host plants benefit directly by improving their nutrient uptake and growth and stress (Afzal *et al.*, 2019; Mei & Flinn, 2010; Santoyo *et al.*, 2016). Indirectly, endophytic bacteria improve plant health by targeting pests and pathogens with antibiotics, hydrolytic enzymes, nutrient

limitation, and by priming plant defences (Afzal *et al.*, 2019; Sturz & Nowak, 2000). Direct promotion of plant growth occurs when endophytic bacteria facilitate the acquisition of essential nutrients (i.e., nitrogen, phosphorus and iron) or modulate hormones (i.e., phytohormones auxin, cytokinin and gibberellin) levels in a plant (Santoyo *et al.*, 2016). When endophytic bacteria decreases, limits, or prevents plant damage that might be caused by phytopathogen (i.e., soil bacteria, fungi and nematodes), this is known as indirect promotion of plant growth (Santoyo *et al.*, 2016). Previous studies, e.g., Gouda *et al.* (2018), Hallmann *et al.* (1997), Mei & Flinn (2010), Miliute *et al.* (2015), Rosenblueth and Martínez-Romero (2006), and Sturz and Nowak (2000) reported several plants including wheat, potato, tomato, rice, and canola that endophytic bacteria can promote their growth (Table 2). The PGPR's activity as a plant growth promoter is described in detail by Gouda *et al.* (2018) and Santoyo *et al.* (2016). Table 2 shows some of the plants from which common endophytic bacterial genera were isolated as reported in various literature (Gouda *et al.*, 2018; Hallmann *et al.*, 1997; Mastan *et al.*, 2019; Mei & Flinn, 2010; Miliute *et al.*, 2015; Rosenblueth & Martínez-Romero, 2006; Sturz & Nowak, 2000).

**Table 2: Examples of plants from which common endophytic bacterial genera were isolated**

Plant	Endophytic bacterial genera
Rice (wild and cultivated)	<i>Agrobacterium</i> , <i>Azoarcus</i> , <i>Azorhizobium</i> , <i>Azospirillum</i> , <i>Bacillus</i> , <i>Bradyrhizobium</i> , <i>Burkholderia</i> , <i>Chromobacterium</i> , <i>Enterobacter</i> , <i>Herbaspirillum</i> , <i>Ideonella</i> , <i>Klebsiella</i> , <i>Micrococcus</i> , <i>Pantoea</i> , <i>Pseudomonas</i> , <i>Rhizobium</i> , <i>Serratia</i> , <i>Stenotrophomonas</i>
Alfalfa	<i>Bacillus</i> , <i>Erwinia</i> , <i>Microbacterium</i> , <i>Pseudomonas</i> , <i>Salmonella</i>
Soybean	<i>Erwinia</i> , <i>Agrobacterium</i> , <i>Pseudomonas</i> , <i>Klebsiella</i> , <i>Enterobacter</i> , <i>Pantoea</i> , <i>Bacillus</i>
Banana	<i>Azospirillum</i> , <i>Burkholderia</i> , <i>Citrobacter</i> , <i>Herbaspirillum</i> , <i>Klebsiella</i>
Sugar cane	<i>Acetobacter</i> , <i>Gluconacetobacter</i> , <i>Herbaspirillum</i> , <i>Klebsiella</i>
Black pepper	<i>Arthrobacter</i> , <i>Bacillus</i> , <i>Curtobacterium</i> , <i>Micrococcus</i> , <i>Pseudomonas</i> , <i>Serratia</i>
Tomato	<i>Brevibacillus</i> , <i>Escherichia</i> , <i>Pseudomonas</i> , <i>Salmonella</i>
Canola	<i>Acidovorax</i> , <i>Agrobacterium</i> , <i>Aureobacterium</i> , <i>Bacillus</i> , <i>Chryseobacterium</i> , <i>Cytophaga</i> , <i>Flavobacterium</i> , <i>Micrococcus</i> , <i>Pseudomonas</i> , <i>Rathayibacter</i> ,



Plant	Endophytic bacterial genera
Wheat	<i>Bacillus</i> , <i>Burkholderia</i> , <i>Flavobacterium</i> , <i>Klebsiella</i> , <i>Microbispora</i> , <i>Micrococcus</i> , <i>Micromonospora</i> , <i>Mycobacterium</i> , <i>Nacardiodes</i> , <i>Rathayibacter</i> , <i>Streptomyces</i>
Carrot	<i>Agrobacterium</i> , <i>Bacillus</i> , <i>Klebsiella</i> , <i>Pseudomonas</i> , <i>Rhizobium</i> , <i>Salmonella</i> , <i>Staphylococcus</i>
Red clover	<i>Acidovorax</i> , <i>Agrobacterium</i> , <i>Arthrobacter</i> , <i>Bacillus</i> , <i>Bordetella</i> , <i>Cellulomonas</i> , <i>Comamonas</i> , <i>Curtobacterium</i> , <i>Escherichia</i> , <i>Klebsiella</i> , <i>Methylobacterium</i> , <i>Micrococcus</i> , <i>Pantoea</i> , <i>Pasteurella</i> , <i>Phyllobacterium</i> , <i>Pseudomonas</i> , <i>Psychrobacter</i> , <i>Rhizobium</i> , <i>Serratia</i> , <i>Sphingomonas</i> , <i>Variovorax</i> , <i>Xanthomonas</i>
Clover	<i>Agrobacterium</i> , <i>Bacillus</i> , <i>Methylobacterium</i> , <i>Pseudomonas</i> , <i>Rhizobium</i>
Radish	<i>Proteobacteria</i> , <i>Salmonella</i>
Cotton	<i>Bacillus</i> , <i>Burkholderia</i> , <i>Clavibacter</i> , <i>Erwinia</i> , <i>Phyllobacterium</i> , <i>Pseudomonas</i>
Potato	<i>Acidovorax</i> , <i>Acinetobacter</i> , <i>Actinomyces</i> , <i>Agrobacterium</i> , <i>Alcaligenes</i> , <i>Arthrobacter</i> , <i>Bacillus</i> , <i>Capnocytophaga</i> , <i>Chryseobacterium</i> , <i>Comamonas</i> , <i>Corynebacterium</i> , <i>Curtobacterium</i> , <i>Enterobacter</i> , <i>Erwinia</i> , <i>Klebsiella</i> , <i>Leuconostoc</i> , <i>Methylobacterium</i> , <i>Micrococcus</i> , <i>Paenibacillus</i> , <i>Pantoea</i> , <i>Pseudomonas</i> , <i>Psychrobacter</i> , <i>Serratia</i> , <i>Shewanella</i> , <i>Sphingomonas</i> , <i>Stenotrophomonas</i> , <i>Streptomyces</i> , <i>Vibrio</i> , <i>Xanthomonas</i>
Pineapple	<i>Azospirillum</i> , <i>Burkholderia</i>
Maise	<i>Achromobacter</i> , <i>Agrobacterium</i> , <i>Arthrobacter</i> , <i>Bacillus</i> , <i>Burkholderia</i> , <i>Corynebacterium</i> , <i>Curtobacterium</i> , <i>Enterobacter</i> , <i>Erwinia</i> , <i>Herbaspirillum</i> , <i>Microbacterium</i> , <i>Micrococcus</i> , <i>Paenibacillus</i> , <i>Phyllobacterium</i> , <i>Pseudomonas</i> , <i>Rhizobium</i> , <i>Serratia</i>
Grapevine	<i>Comamonas</i> , <i>Enterobacter</i> , <i>Klebsiella</i> , <i>Moraxella</i> , <i>Pantoea</i> , <i>Pseudomonas</i> , <i>Rahnella</i> , <i>Rhodococcus</i> , <i>Staphylococcus</i> , <i>Xanthomonas</i>
Cucumber	<i>Agrobacterium</i> , <i>Bacillus</i> , <i>Burkholderia</i> , <i>Chryseobacterium</i> , <i>Clavibacter</i> , <i>Curtobacterium</i> , <i>Enterobacter</i> , <i>Micrococcus</i> , <i>Paenibacillus</i> , <i>Phyllobacterium</i> , <i>Pseudomonas</i> , <i>Serratia</i> , <i>Stenotrophomonas</i>

In addition, since plants are constantly challenged by various phytopathogens (i.e., *Pseudomonas syringae*, *Agrobacterium tumefaciens*, and other bacteria, fungi, oomycetes, and viruses), their survival and fitness are compromised (Ali *et al.*, 2018). To respond to this, pathogenesis-related proteins against phytopathogens have been used to develop bacterial-resistant plants (Ali *et al.*, 2018; de Andrade *et al.*, 2019). For instance, some endophytic bacteria isolated from mulberry demonstrated potential to manage plant diseases based because of their antimicrobial activities (Xu

*et al.*, 2019). Overall, plant growth and health can be improved by PGPR as a biofertiliser as it increases the accessibility (Adesemoye *et al.*, 2009) or uptake of nutrients from a restricted soil nutrient pool and reduces plant biotic and abiotic stress (Hussain *et al.*, 2017; Santoyo *et al.*, 2016; Xu *et al.*, 2019). Thus, plant-microbe interaction is vital for sustainable agriculture (Mei & Flinn, 2010), particularly in sub-Saharan Africa, where the agricultural sector faces many challenges such as limited access to chemical mineral agro-inputs such as fertiliser and, whenever available are at

very high prices which can be afforded by smallholder farmers.

Furthermore, some microbes promote plant growth by preventing or alleviating drought and salinity stress in plants (Afzal *et al.*, 2019; Kumar & Verma, 2018; Mapelli *et al.*, 2013; Vurukonda *et al.*, 2016). Drought is one of the main limitations on agricultural productivity worldwide as it affects the physiological and morphological traits of plants (Kumar & Verma, 2018; Mapelli *et al.*, 2013). Previous research has demonstrated various strategies, e.g. using bacteria to cope with drought stress through the development of drought-tolerant varieties (Kumar & Verma, 2018; Marasco *et al.*, 2013; Masmoudi *et al.*, 2019; Vurukonda *et al.*, 2016). They showed that microorganisms have the potential to help plants cope with drought (Kumar & Verma, 2018; Vurukonda *et al.*, 2016) and saline and heavy metals stress (Masmoudi *et al.*, 2019). Plant growth-promoting rhizobacteria showed the ability to impart drought tolerance in plants by producing exopolysaccharides, phytohormones, 1-aminocyclopropane-1-carboxylate deaminase, volatile compounds, inducing accumulation of osmolytes, antioxidants, upregulation or down-regulation of stress-responsive genes and alteration in root morphology in the acquisition of drought tolerance (Vurukonda *et al.*, 2016). Pepper plants inoculated with bacterial isolates from desert plant species unveiled improved plant water uptake ability, enhanced drought tolerance and root system (Marasco *et al.*, 2013).

Also, some bacteria exhibited the potential to promote plant growth under salinity conditions (Ahmad *et al.*, 2011; Bharti *et al.*, 2014; Mapelli *et al.*, 2013). A study revealed that *Salicornia* plants grown under hypersaline ecosystems revealed resistance to a wide set of abiotic stresses due presence of the halophilic/halotolerant bacteria (*Halomonas*) (Mapelli *et al.*, 2013). The *Halomonas* usually inhabit salty and arid ecosystems (Mapelli *et al.*, 2013; Vurukonda *et al.*, 2016). Salinity-induced detrimental effects on growth, oil content, and physiological state in *Mentha arvensis* were also mitigated by plant growth-promoting rhizobacteria (Bharti *et al.*, 2014). *Pseudomonas frederiksbergensis*, a soil bacterium also confirmed to improve salt tolerance and boost red pepper plant growth (Chatterjee *et al.*, 2017). Examples of plant growth-promoting bacteria that enhance drought tolerance in some plants are shown in Table 3. For a detailed effect or mechanism of phytohormonal activity in imparting drought tolerance in plants, the reader is referred to Gouda *et al.* (2018), Kumar & Verma (2018), and Vurukonda *et al.*, 2016). Hence, using soil microbe-plant coevolution is critical because it can assist plants in responding to harsh abiotic settings, resulting in better economic viability, soil fertility, and environmental sustainability.

Table 3 shows Plant growth promoting bacteria and plants benefiting from drought tolerance. Source: (de Andrade *et al.*, 2019; Gouda *et al.*, 2018; Kumar & Verma, 2018; Masmoudi *et al.*, 2019; Vurukonda *et al.*, 2016)

**Table 3: Plant growth promoting bacteria and plants benefiting from drought tolerance**

Bacteria	Plant
<i>Sinorhizobium medicae</i>	<i>Medicago truncatula</i>
<i>Azospirillum Brasilense</i>	Tomato
<i>Azospirillum lipoferum</i> and <i>Bacillus</i> Spp.	Maize ( <i>Zea mays</i> )
<i>Pseudomonas libanensis</i> TR1 and <i>Pseudomonas reactans</i> Ph3R3	<i>Brassica oxyrrhina</i>
<i>Azospirillum brasilense</i> NO40, <i>Bacillus amyloliquefaciens</i> 5113, <i>Azospirillum brasilense</i> NO40, <i>Rhizobium leguminosarum</i> (LR-30), <i>Mesorhizobium ciceri</i> (CR-30 and CR-39), and <i>Rhizobium phaseoli</i> (MR-2)	Wheat ( <i>Triticum aestivum</i> )
<i>Phyllobacterium brassicearum</i> strain STM196, <i>Azospirillum Brasilense</i> Sp 245	<i>Arabidopsis</i>



<i>Bacillus subtilis</i>	Platycladus orientalis
<i>Pseudomonas putida</i> H-2-3	Soybean
<i>Bacillus thuringiensis</i>	Lavandula dentate
<i>Pseudomonas putida</i> MTCC5279 (RA)	Cicer arietinum L.
<i>Rhizobium leguminosarum</i> (LR-30), <i>Mesorhizobium ciceri</i> (CR-30 and CR-39), and <i>Rhizobium phaseoli</i> (MR-2)	Wheat
<i>Trichoderma harzianum</i>	Rice ( <i>Oryza sativa</i> L.)
<i>Azospirillum</i> sp.	Lettuce

### Biological Control Agent and Suppressors of Diseases or Pathogens

Pathogenic microbes harm the majority of plants and animals, affecting food production and ecosystem stability (Agrillo *et al.*, 2019; Ghazalibiglar *et al.*, 2016). However, microorganisms from different environments can be used for biocontrol purposes through the identification of their bioactive molecules (Agrillo *et al.*, 2019; Masmoudi *et al.*, 2019). Microbes with potential impacts against phytopathogenic fungi and/or insects, such as *Pseudomonas* sp., *Cellulosimicrobium* sp., and *Bacillus* sp., have been studied extensively (Agrillo *et al.*, 2019; Ghazalibiglar *et al.*, 2016). Compounds isolated from diverse microorganisms have shown to be effective against a variety of phytopathogenic fungi (Agrillo *et al.*, 2019; Lee *et al.*, 2015).

For example, a novel antifungal compound derived from *Pseudomonas protegens* was found to have fungicidal activity against *Alternaria* sp. and greatly reduced fungal infection on tomato fruits in a prior investigation (Agrillo *et al.*, 2019). Further, an experiment carried out by Masmoudi *et al.* (2019) showed that *Bacillus velezensis* and *B. subtilis* subsp. *spizizenii* are effective biological agents in protecting tomato fruits from fungal pathogens attacks. Endophytic bacteria, i.e. *Bacillus* sp, *Curtobacterium* sp, *Pantoea* sp, and *Pseudomonas* sp are also considered biological control agents for plant disease management based on the study by Xu *et al.* (2019). Through their volatiles emissions, some rhizobacteria isolates belonging to the genera *Bacillus* spp, *Pseudomonas* spp, and *Arthrobacter* spp are advised as biological control of soil-borne oomycetes as they inhibited *Phytophthora*

*cinnamomi* growth (Méndez-Bravo *et al.*, 2018). These examples from various studies indicate that some microbes constitute vital antimicrobial activities against phytopathogens as they possess bioactive molecules. Thus, they could be utilised as a biological control agent (Lee *et al.*, 2015).

Additionally, some of the microbes suppress disease-causing microorganisms or their competitors (Chithrashree *et al.*, 2011; Ghazalibiglar *et al.*, 2016; Harada *et al.*, 2018, Table 4). They achieve this by releasing antibiotic substances or chemicals (Xu *et al.*, 2019). Microbes such as *Bacillus megaterium*, *Bacillus subtilis*, and *P. fluorescens* are a few examples of bacteria that play this role (El-Borollosy & Oraby, 2012; Lee *et al.*, 2015, Table 4). While *B. subtilis* has been used to subdue or suppress seedling blight of sunflowers, which is caused by *Alternaria helianthi*, *P. fluorescens* bacteria suppressed a disease-causing fungus known as *Rhizoctonia solani* in crops (Masmoudi *et al.*, 2019).

Due to their ability to suppress disease-causing microorganisms, some of these microbes are commercialised for disease suppression. The bioactivity of *Paenibacillus* isolates as biological control agents have been used against a range of plant pathogenic fungi, bacteria and nematodes (Ghazalibiglar *et al.*, 2016). Also, *Paenibacillus polymyxa* induced systemic resistance in plants, i.e., tomatoes, against pathogens (Ghazalibiglar *et al.*, 2016). Using bacterial liquid crude cultures of *B. subtilis*, *P. fluorescens*, and *Azotobacter chroococcum* species showed the ability to induce systemic resistance within cucumber plants (*Cucumis sativus*) against *Cucumber mosaic cucumovirus* (El-Borollosy & Oraby, 2012).

**Table 4: Some of the microbes which have been utilised as biological agents against disease-causing pathogens in plants/crops**

Plants/crops	Diseases /Pathogens	Biological control microbes	References
Cabbage ( <i>Brassica oleracea</i> )	Black rot ( <i>Xanthomonas campestris</i> )	<i>Paenibacillus</i> sp	Ghazalibiglar <i>et al.</i> (2016)
Cucumber	<i>Cucumber mosaic cucumovirus</i>	<i>Pseudomonas Fluorescens</i> , <i>Pseudomonas aeruginosa</i> , <i>Azotobacter chroococcum</i> , <i>Bacillus subtilis</i>	El-Borollosy & Oraby, (2012)
Greengram ( <i>Vignaradiate</i> L.)	Fungicide-induced phytotoxicity		Ahmad <i>et al.</i> (2011)
Mustard ( <i>Brassica compestris</i> )		<i>Pseudomonas putida</i>	Ahmad <i>et al.</i> (2011)
<i>Panax ginseng</i>	Root diseases ( <i>Phytophthora cactorum</i> )	<i>Bacillus amyloliquefaciens</i>	Lee <i>et al.</i> (2015)
Pepper	Gray leaf spot disease ( <i>Stemphylium lycopersici</i> )	<i>Brevibacterium</i>	<i>iodinum</i> Son <i>et al.</i> (2014)
Rice ( <i>Oryza sativa</i> L.)	Bacterial leaf blight ( <i>Xanthomonas oryzae</i> )	<i>Bacillus</i> sp.	Chithrashree <i>et al.</i> (2011)

Furthermore, some microbes, e.g., bacteriophages, are important in improving human health. They have been studied for drugs or vaccines to help in disease (i.e., cancer and chronic neurodegenerative) treatment and prevention. The bacteriophages can attack and kill a target bacterium within minutes of infection (Dalmasso *et al.*, 2014). The human gut contains ca.  $10^{15}$  bacteriophages (Dalmasso *et al.*, 2014). Bacteriophages are used to treat bacterial diseases in humans and have recently been licensed for use in the food chain to reduce pathogens (Dalmasso *et al.*, 2014). Further, microorganisms have also

been used to control invasive species, especially plants (Table 4). The fungus *Puccinia abrupta*, *Puccinia xanthii*, *Entyloma compositarum*, and *Plasmopara halstedii* (Fauzi, 2009; Kumar, 2009) were previously used to control the invasive weed *Parthenium hysterophorus* (Ojija *et al.*, 2021a, 2021b; Ojija & Ngimba, 2021). Table 5 shows Some of the fungus species used as a biological control against invasive plants in different parts of the world. Source: Capinera, (2009), Kelaniyangoda & Ekanayake, (2010), Kowalski *et al.* (2015), Kumar, (2009), Seastedt, (2015), Shahrtash & Brown, (2021).

**Table 5: Fungus species used as a biological control against invasive plants in different parts of the world**

Invasive plant or weed	Fungus
Parthenium ( <i>Parthenium hysterophorus</i> )	<i>Puccinia abrupta</i> , <i>Puccinia xanthii</i> , <i>Entyloma compositarum</i> , and <i>Plasmopara halstedii</i>
Soda apple ( <i>Solanum viarum</i> )	Tobacco mild green mosaic virus
Dodder species	<i>Alternaria destruens</i>
Deciduous tree species, Blackberry weed ( <i>Prunus serotina</i> )	<i>Chondrostereum purpureum</i>
<i>Hakea gummosis</i> and <i>H. sericea</i>	<i>Colletotrichum acutatum</i>
Turf grass ( <i>Poa annua</i> )	<i>Cylindrobasidium leave</i>
Yellow nutsedge ( <i>Cyperus esculentus</i> )	<i>Puccinia canaliculata</i>
Persimmon ( <i>Diospyros virginiana</i> )	<i>Acremonium diospyri</i>
Milkweed vine ( <i>Morrenia odorata</i> )	<i>Phytophthora palmivora</i> ( <i>P. citrophthora</i> )
Dodder ( <i>Cuscuta chinensis</i> and <i>C. australis</i> )	<i>Colletotrichum gloeosporioides</i>
Water hyacinth ( <i>Eichhornia crassipes</i> )	<i>Cercospora rodmanii</i>
Sickle-pod and coffee senna ( <i>Cassia</i> spp.)	<i>Alternaria cassia</i>
Velvet leaf ( <i>Abutilon theophrastus</i> )	<i>Colletotrichum coccodes</i>
Round-leaved mallow ( <i>Malva pussila</i> )	<i>Colletotrichum gloeosporioides</i>
Dandelion ( <i>Taraxacum officinale</i> )	<i>Sclerotinia minor</i>
Dyers woad ( <i>Isatis tinctoria</i> )	<i>Puccinia thlaspeos</i>

### Primary Producer, Biogas Production, and Bioremediation

Most microorganisms (e.g. cyanobacteria, cyanophyta, and algae) act as primary producers (Fierer *et al.*, 2003). These are photosynthetic microbes that utilise CO<sub>2</sub> from the atmosphere and convert it to organic material (Fierer *et al.*, 2003). They produce foods (i.e., carbohydrates) that are used by other organisms. The process of taking up as well as fixing CO<sub>2</sub> is called carbon fixation (Fierer *et al.*, 2003; Juretschko *et al.*, 2002). These

microbes perform photosynthesis in the same way that plants do, accounting for nearly half of all primary production on the planet. The photosynthetic activity ensures that there is oxygen in the atmosphere. Among the most significant photosynthetic cyanobacteria in marine ecosystems is *Synechococcus*, which accounts for 25% of the primary production that occurs in marine environments (Fierer *et al.*, 2003). It is also a primary component of freshwater plankton and microbial mats. Cyanobacteria and algae live in water, damp soil,

and rocks, and they are the carbon source for marine life. They produce oxygen that supports life on Earth (Barantal *et al.*, 2012) and thus, help in regulating climate by absorbing CO<sub>2</sub> from the atmosphere (Barantal *et al.*, 2012; Logue *et al.*, 2015). Earlier studies claim that O<sub>2</sub> released into the atmosphere by photosynthetic microbes is approximately 50% of the O<sub>2</sub> on the planet (Loreau, 2000).

Furthermore, due to shortage, and increased demand for energy worldwide, extensive studies have been carried out to find an alternative source of energy (Heeg *et al.*, 2014; Lobo *et al.*, 2019). The use of microorganisms to produce biofuel or biogas is presently the focus of much research (Lobo *et al.*, 2019). The anaerobic biomass digestion, which is initiated by bacteria, and biogas production technology has received substantial attention (Heeg *et al.*, 2014; Lobo *et al.*, 2019). Biogas production whose main component is methane is advocated to be the best approach (Heeg *et al.*, 2014). Methane can be used as a multipurpose and renewable energy carrier (Heeg *et al.*, 2014).

Apart from biogas production for energy, some microbes can be used to remove pollutants from the environment (Mendoza-Hernández *et al.*, 2019). This technique is referred to as phytoremediation, which uses plant growth-promoting bacteria (Mendoza-Hernández *et al.*, 2019). Bacteria from the genera *Serratia*, *Enterobacter*, *Serratia*, *Serratia*, and *Enterobacter* have shown potential for phytoremediation (Mendoza-Hernández *et al.*, 2019). These bacteria are eco-friendly as they cause no harm to the environment (Mendoza-Hernández *et al.*, 2019; Sahu, 2019). Wastewater treatment systems are the best examples of the technological processes that utilise microbes (Pajares *et al.*, 2016). They are used to remove pharmaceuticals during wastewater treatment and break down complex materials, i.e., herbicides, pesticides, and other soil pollutants (Sahu, 2019; Wagner *et al.*, 2002). Similarly, certain moulds and yeast oxidise petroleum products aerobically as they use oil as electron donors or energy sources to change the oil into CO<sub>2</sub> (Wagner *et al.*,

2002). These properties make some microorganisms to be used in bioremediation for cleaning up oil spills and other contaminants and neutralising agricultural chemicals (Sahu, 2019; Wagner *et al.*, 2002). Therefore, microbes can be used to restore ecosystem health when the environment is contaminated by oil, heavy metals, and other forms of pollutants. This enables human to live in healthy environment which support their sustainable development and wellbeing.

### **Digestive Role in Animals, Source of Food and Drugs**

Many organisms are inhabited by a variety of microorganisms, i.e., archaea, bacteria, and fungi in their rumen (Burgos *et al.*, 2018; Cunha *et al.*, 2017), oral cavity, intestinal, respiratory, and urogenital tract, and skin (Curtis *et al.*, 2006; Konopka, 2009). Being in the human body and other animals, microbes perform a variety of activities that maintain each individual's health (Cunha *et al.*, 2017). They coordinate the breakdown or digestion and fermentation of different food components ingested by the host. Host-indigestible fibre can be digested by bacteria and fungi, and bacteria ferment the products to form volatile fatty acids, which are important nutrients (Cunha *et al.*, 2017). While some animals, e.g., leaf and wood-eating insects, depend on symbiotic gut microorganisms to digest cellulose in their food supply, other insects (e.g. ants and beetles) consume fungi directly as a food source (Albert *et al.*, 2014). In humans, the metabolic reactions of intestinal microbes produce vitamin B12 and vitamin K, and microbial flora in the gut enhances essential steroid absorption (Albert *et al.*, 2014). Microbes in ruminant animals (i.e., cows, deer, giraffes, and wildebeest) are important for secondary fermentation (Cunha *et al.*, 2017). Generally, ingested food after regurgitation passes into the rumen, where complex carbohydrates undergo continuous fermentation into CO<sub>2</sub>, fatty acids, and CH<sub>4</sub> (Cunha *et al.*, 2017).

Secondary fermentation in the rumen by bacteria, protozoans, and fungi removes energy from the plant food ingested by the animal (Cunha *et al.*,

2017; Strickland *et al.*, 2009). Some of the energy is also removed when plant tissues pass from the rumen to the caecum and large intestine. Termites, for instance, host these bacteria and protozoans in their guts that perform similar activities (Strickland *et al.*, 2009). In the gut, the protozoans digest cellulose while bacteria generate CH<sub>4</sub> from the organic compound produced from the cellulose degradation (Strickland *et al.*, 2009).

Moreover, most of the termites' guts also have bacteria that fix atmospheric nitrogen, making it usable for the termites. Thus, it can be concluded that microorganisms play a basic role in human and other animals' digestion by degrading sugar polymers into simple glucose. Because microbes assist in digesting and fermenting food we eat and produce chemicals that shape our metabolic rates, they are considered to play an essential role in our body shape. Overall, the rumen microbiota is vital for producing the nutrients that the host requires for reproduction, growth, and the generation of milk and meat (Cunha *et al.*, 2017).

Microorganisms are further considered important assets for isolating useful drug molecule discovery paradigms (Hussain *et al.*, 2017). Some have been identified or used as a source of drugs to overcome the emergence of drug resistance pathogens (Hussain *et al.*, 2017; Kumar *et al.*, 2019). Previous studies report that actinomycetes possess bioactive molecules for drug development. Some of the potential bioactive compounds found in actinomycetes have broad-spectrum biological activities, i.e., antibacterial, antifungal, antitumor, antihypertensive etc. (Kumar *et al.*, 2019). Thus, microbes with bioactive compounds can be exploited in pharmaceutical industries for drug development and formulation.

## CONCLUSION

From this review, the role of microbes observed to range from different fields which can have a direct influence in improving human livelihood by replacing some technologies in use today which have environmental and health concerns ranging from medical, agriculture, and food processing and climate change. The utilisation of microbes in

most developing countries is still low despite the high biodiversity available because of limited technological advances. The sustainable development of people all over the world can be ensured by using microorganisms in an environmentally friendly way that does not jeopardise the environment and existing biodiversity on which we rely. Because our paper is limited to the importance of microbial biodiversity, we recommend that other research must be done to discuss their negative impacts and how they can be avoided since knowing the positive and negative sides of microbes is the step forwards toward better utilisation of the one trillion available microbe species where less than 1% is known and utilised, and 99.99% of them have yet to be discovered and utilised for sustainable development and human wellbeing.

## Conflict of Interest

The author declares that the review was conducted in the absence of any commercial or financial relationships that could be construed as a potential conflict of interest

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## REFERENCES

- Adesemoye, A. O., Torbert, H. A., & Kloepper, J. W. (2009). Plant Growth-Promoting Rhizobacteria Allow Reduced Application Rates of Chemical Fertilizers. *Microbial Ecology*, 58, 921–929.
- Afzal, I., Shinwari, Z. K., Sikandar, S., & Shahzad, S. (2019). Plant beneficial endophytic bacteria: Mechanisms, diversity, host range and genetic determinants.



- Microbiological Research*, 221, 36–49. <https://doi.org/10.1016/j.micres.2019.02.001>
- Agrillo, B., Mirino, S., Tatè, R., Gratino, L., Gogliettino, M., Cocca, E., Tabli, N., Nabti, E., & Palmieri, G. (2019). An alternative biocontrol agent of soil-borne phytopathogens: A new antifungal compound produced by a plant growth promoting bacterium isolated from North Algeria. *Microbiological Research*, 221, 60–69. <https://doi.org/10.1016/j.micres.2019.02.004>
- Ahemad, M., & Khan, M.S. (2012). Effect of fungicides on plant growth promoting activities of phosphate solubilising *Pseudomonas putida* isolated from mustard (*Brassica campestris*) rhizosphere. *Chemosphere*, 86, 945–950. <https://doi.org/10.1016/j.chemosphere.2011.11.013>
- Ahmad, M., Zahir, Z. A., Asghar, H. N., & Asghar, M. (2011). Inducing salt tolerance in mung bean through coinoculation with rhizobia and plant-growth-promoting rhizobacteria containing 1-aminocyclopropane-1-carboxylate deaminase. *Can. J. Microbiol.*, 57, 578–589. <https://doi.org/10.1139/w11-044>
- Akinsemolu, A. A. (2018). The role of microorganisms in achieving the sustainable development goals. *Journal of Cleaner Production*, 182, 139–155. <https://doi.org/10.1016/j.jclepro.2018.02.081>
- Albert, B., Casamayor, E., & Fierer, N. (2014). The microbial contribution to macroecology. *Frontiers in Microbiology*, 5, 1–8. <https://doi.org/doi:10.3389/fmicb.2014.00203>
- Ali, S., Ganai, B. A., Kamili, A. N., Bhat, A. A., Mir, Z. A., Bhat, J. A., Tyagi, A., Islam, S. T., Mushtaq, M., Yadav, P., Rawat, S., Grover, A. (2018). Pathogenesis-related proteins and peptides as promising tools for engineering plants with multiple stress tolerance. *Microbiological Research*, 212–213, 29–37. <https://doi.org/10.1016/j.micres.2018.04.008>
- Allison, S. D. (2005). Cheaters, diffusion and nutrients constrain decomposition by microbial enzymes in spatially structured environments: Constraints on enzymatic decomposition. *Ecology Letters*, 8, 626–635. <https://doi.org/10.1111/j.1461-0248.2005.00756.x>
- Barantal, S., Schimann, H., Fromin, N., & Hättenschwiler, S. (2012). Nutrient and Carbon Limitation on Decomposition in an Amazonian Moist Forest. *Ecosystems*, 15, 1039–1052. <https://doi.org/10.1007/s10021-012-9564-9>
- Bardgett, R. D., Freeman, C., & Ostle, N. J., 2008. Microbial contributions to climate change through carbon cycle feedbacks. *ISME Journal* 2, 805–814. <https://doi.org/10.1038/ismej.2008.58>
- Bargaz, A., Elhaisoufi, W., Khourchi, S., Benmrid, B., Borden, K. A., & Rchiad, Z. (2021). Benefits of phosphate solubilising bacteria on belowground crop performance for improved crop acquisition of phosphorus. *Microbiological Research*, 252, 126842. <https://doi.org/10.1016/j.micres.2021.126842>
- Berg, G. (2009). Plant–microbe interactions promoting plant growth and health: perspectives for controlled use of microorganisms in agriculture. *Applied Microbiology and Biotechnology*, 84, 11–18. <https://doi.org/10.1007/s00253-009-2092-7>
- Bharti, N., Barnawal, D., Awasthi, A., Yadav, A., & Kalra, A. (2014). Plant growth promoting rhizobacteria alleviate salinity induced negative effects on growth, oil content and physiological status in *Mentha arvensis*. *Acta Physiologiae Plantarum*, 36, 45–60. <https://doi.org/10.1007/s11738-013-1385-8>
- Burgos, F. A., Ray, C.L., & Arias, C. R. (2018). Bacterial diversity and community structure of the intestinal microbiome of Channel Catfish (*Ictalurus punctatus*) during ontogenesis. *Systematic and Applied Microbiology*, 41,



- 494–505.  
<https://doi.org/10.1016/j.syapm.2018.04.006>
- Capinera, J. L. (2009). Use of Microbes for Control and Eradication of Invasive Arthropods Hajek, E. A. , Glare, T. R. , and O'Callaghan, M. O. (Eds.) 2008. Use of Microbes for Control and Eradication of Invasive Arthropods (Progress in Biological Control vol. 6). *Florida Entomologist*, 92, 524–525.  
<https://doi.org/10.1653/024.092.0322>
- Chatterjee, P., Samaddar, S., Anandham, R., Kang, Y., Kim, K., Selvakumar, G., & Sa, T. (2017). Beneficial Soil Bacterium *Pseudomonas frederiksbergensis* OS261 Augments Salt Tolerance and Promotes Red Pepper Plant Growth. *Frontiers in Plant Science*, 8, 705.  
<https://doi.org/10.3389/fpls.2017.00705>
- Chithrashree, U. A. C., Chandra Nayaka, S., Reddy, M. S., & Srinivas, C. (2011). Plant growth-promoting rhizobacteria mediate induced systemic resistance in rice against bacterial leaf blight caused by *Xanthomonas oryzae* pv. *oryzae*. *Biological Control*, 59, 114–122.  
<https://doi.org/10.1016/j.biocontrol.2011.06.010>
- Cleveland, C. C., Reed, S. C., & Townsend, A. R., 2006. Nutrient regulation of organic matter decomposition in a Tropical rain forest. *Ecology*, 87, 492–503.  
<https://doi.org/10.1890/05-0525>
- Cunha, C. S., Veloso, C. M., Marcondes, M. I., Mantovani, H. C., Tomich, T. R., Pereira, L. G. R., Ferreira, M. F. L., Dill-McFarland, K. A., & Suen, G. (2017). Assessing the impact of rumen microbial communities on methane emissions and production traits in Holstein cows in a tropical climate. *Systematic and Applied Microbiology*, 40, 492–499.  
<https://doi.org/10.1016/j.syapm.2017.07.008>
- Curtis, T. P., Head, I. M., Lunn, M., Woodcock, S., Schloss, P. D., & Sloan, W. T. (2006). What is the extent of prokaryotic diversity? *Philosophical Transactions of the Royal Society B*, 361, 2023–2037.  
<https://doi.org/10.1098/rstb.2006.1921>
- Dalmasso, M., Hill, C., & Ross, R. P. (2014). Exploiting gut bacteriophages for human health. *Trends in Microbiology*, 22, 399–405.  
<https://doi.org/10.1016/j.tim.2014.02.010>
- de Andrade, F. M., de Assis Pereira, T., Souza, T. P., Guimarães, P. H. S., Martins, A. D., Schwan, R. F., Pasqual, M., & Dória, J. (2019). Beneficial effects of inoculation of growth-promoting bacteria in strawberry. *Microbiological Research*, 223–225, 120–128.  
<https://doi.org/10.1016/j.micres.2019.04.005>
- El-Borollosy, A. M., & Oraby, M. M. (2012). Induced systemic resistance against Cucumber mosaic cucumovirus and promotion of cucumber growth by some plant growth-promoting rhizobacteria. *Annals of Agricultural Sciences*, 57, 91–97.  
<https://doi.org/10.1016/j.aosas.2012.08.001>
- Falkenmark, M. (2013). Growing water scarcity in agriculture: future challenge to global water security. *Philosophical Transactions of the Royal Society A*. 371, 20120410.  
<https://doi.org/10.1098/rsta.2012.0410>
- Falkowski, P. G., Fenchel, T., & Delong, E. F. (2008). The microbial engines that drive Earth's biogeochemical cycles. *Science*, 320, 1034–1039.  
<https://doi.org/10.1126/science.1153213>
- Fauzi, M. T. (2009). Biocontrol Ability of *Puccinia abrupta* var. *partheniicola* on Different Growth Stages of Parthenium Weed (*Parthenium hysterophorus* L.). *HAYATI Journal of Biosciences* 16, 83–87.  
<https://doi.org/10.4308/hjb.16.3.83>
- Fierer, N., Allen, A. S., Schimel, J. P., & Holden, P. A. (2003). Controls on microbial CO<sub>2</sub> production: a comparison of surface and subsurface soil horizons: Controls on microbial respiration. *Global Change Biology*,

- 9, 1322–1332. <https://doi.org/10.1046/j.1365-2486.2003.00663.x>
- Fuhrman, J. A. (2009). Microbial community structure and its functional implications. *Nature*, 459, 193–199. <https://doi.org/10.1038/nature08058>
- Ghazalibiglar, H., Hampton, J. G., van Zijll de Jong, E., & Holyoake, A. (2016). Is induced systemic resistance the mechanism for control of black rot in Brassica oleracea by a Paenibacillus sp.? *Biological Control*, 92, 195–201. <https://doi.org/10.1016/j.biocontrol.2015.10.014>
- Gouda, S., Kerry, R. G., Das, G., Paramithiotis, S., Shin, H. S., & Patra, J. K. (2018). Revitalisation of plant growth promoting rhizobacteria for sustainable development in agriculture. *Microbiological Research*, 206, 131–140. <https://doi.org/10.1016/j.micres.2017.08.016>
- Hallmann, J., Quadt-Hallmann, A., Mahaffee, W. F., & Kloepper, J. W. (1997). Bacterial endophytes in agricultural crops. *Canadian Journal of Microbiology*, 43, 895–914. <https://doi.org/10.1139/m97-131>
- Harada, L. K., Silva, E. C., Campos, W. F., Del Fiol, F. S., Vila, M., Dąbrowska, K., Krylov, V. N., & Balcão, V. M., 2018. Biotechnological applications of bacteriophages: State of the art. *Microbiological Research*, 212–213, 38–58. <https://doi.org/10.1016/j.micres.2018.04.007>
- Heeg, K., Pohl, M., Sontag, M., Mumme, J., Klocke, M., & Nettmann, E. (2014). Microbial communities involved in biogas production from wheat straw as the sole substrate within a two-phase solid-state anaerobic digestion. *Systematic and Applied Microbiology*, 37, 590–600. <https://doi.org/10.1016/j.syapm.2014.10.002>
- Hussain, A., Rather, M. A., Dar, M. S., Dangroo, N. A., Aga, M. A., Qayum, A., Shah, A. M., Ahmad, Z., Dar, M. J., & Hassan, Q. P. (2017). Streptomyces puniceus strain AS13. Production, characterisation and evaluation of bioactive metabolites: A new face of dinactin as an antitumor antibiotic. *Microbiological Research*, 207, 196–202. <https://doi.org/10.1016/j.micres.2017.12.004>
- Javed, M. R., Noman, M., Shahid, M., Ahmed, T., Khurshid, M., Rashid, M. H., Ismail, M., Sadaf, M., & Khan, F. (2019). Current situation of biofuel production and its enhancement by CRISPR/Cas9-mediated genome engineering of microbial cells. *Microbiological Research*, 219, 1–11. <https://doi.org/10.1016/j.micres.2018.10.010>
- Juretschko, S., Loy, A., Lehner, A., & Wagner, M. (2002). The Microbial Community Composition of a Nitrifying-Denitrifying Activated Sludge from an Industrial Sewage Treatment Plant Analysed by the Full-Cycle rRNA Approach. *Systematic & Applied Microbiology*, 25, 84–99. <https://doi.org/10.1078/0723-2020-00093>
- Kelaniyangoda, D., & Ekanayake, H. (2010). *Puccinia melampodii* Diet. and Holow. as a Biological Control Agent of Parthenium hysterophorus. *Journal of Food & Agriculture* 1, 13–19. <https://doi.org/10.4038/jfa.v1i1.1835>
- Konopka, A. (2009). What is microbial community ecology? *ISME Journal*, 3, 1223–1230. <https://doi.org/10.1038/ismej.2009.88>
- Koranda, M., Kaiser, C., Fuchslueger, L., Kitzler, B., Sessitsch, A., Zechmeister-Boltenstern, S., & Richter, A. (2014). Fungal and bacterial utilisation of organic substrates depends on substrate complexity and N availability. *FEMS Microbiology Ecology*, 87, 142–152. <https://doi.org/10.1111/1574-6941.12214>
- Kowalski, K. P., Bacon, C., Bickford, W., Braun, H., Clay, K., Leduc-Lapierre, M., Lillard, E., McCormick, M. K., Nelson, E., Torres, M., White, J., & Wilcox, D. A. (2015). Advancing the science of microbial symbiosis to support invasive species management: a case study on

- Phragmites in the Great Lakes. *Frontiers in Microbiology*, 6. <https://doi.org/10.3389/fmicb.2015.00095>
- Kumar, A., & Verma, J. P. (2018). Does plant—Microbe interaction confer stress tolerance in plants: A review? *Microbiological Research*, 207, 41–52. <https://doi.org/10.1016/j.micres.2017.11.004>
- Kumar, P., Kundu, A., Kumar, M., Solanki, R., & Kapur, M. K. (2019). Exploitation of potential bioactive compounds from two soil derived actinomycetes, *Streptomyces* sp. strain 196 and RL24. *Microbiological Research*, 229, 126312. <https://doi.org/10.1016/j.micres.2019.126312>
- Kumar, S. (2009). Biological control of *Parthenium* in India: status and prospects. *Indian Journal of Weed Science* 41, 1–18.
- Lee, B. D., Dutta, S., Ryu, H., Yoo, S. J., Suh, D. S., & Park, K. (2015). Induction of systemic resistance in *Panax ginseng* against *Phytophthora cactorum* by native *Bacillus amyloliquefaciens* HK34. *Journal of Ginseng Research* 39, 213–220. <https://doi.org/10.1016/j.jgr.2014.12.002>
- Liu, Y., Liu, J., Yao, P., Ge, T., Qiao, Y., Zhao, M., & Zhang, X. H. (2018). Distribution patterns of ammonia-oxidising archaea and bacteria in sediments of the eastern China marginal seas. *Systematic and Applied Microbiology*, 41, 658–668. <https://doi.org/10.1016/j.syapm.2018.08.008>
- Lobo, C. B., Juárez Tomás, M. S., Viruel, E., Ferrero, M. A., & Lucca, M. E. (2019). Development of low-cost formulations of plant growth-promoting bacteria to be used as inoculants in beneficial agricultural technologies. *Microbiological Research*, 219, 12–25. <https://doi.org/10.1016/j.micres.2018.10.012>
- Logue, J. B., Findlay, S. E. G., & Comte, J. (2015). Editorial: Microbial Responses to Environmental Changes. *Frontiers in Microbiology*, 6. <https://doi.org/10.3389/fmicb.2015.01364>
- Loreau, M. (2000). Biodiversity and ecosystem functioning: recent theoretical advances. *Oikos*, 91, 3–17. <https://doi.org/10.1034/j.1600-0706.2000.910101.x>
- Mapelli, F., Marasco, R., Rolli, E., Barbato, M., Cherif, H., Guesmi, A., Ouzari, I., Daffonchio, D., & Borin, S. (2013). Potential for Plant Growth Promotion of Rhizobacteria Associated with *Salicornia* Growing in Tunisian Hypersaline Soils. *BioMed Research International*, 1–13. <https://doi.org/10.1155/2013/248078>
- Marasco, R., Rolli, E., Vigani, G., Borin, S., Sorlini, C., Ouzari, H., Zocchi, G., & Daffonchio, D. (2013). Are drought-resistance promoting bacteria cross-compatible with different plant models? *Plant Signaling and Behavior*, 8, e26741. <https://doi.org/10.4161/psb.26741>
- Marijani, E. (2022). Prevalence and Antimicrobial Resistance of Bacteria Isolated from Marine and Freshwater Fish in Tanzania. *International Journal of Microbiology*, 1–8. <https://doi.org/10.1155/2022/4652326>
- Masmoudi, F., Abdelmalek, N., Tounsi, S., Dunlap, C. A., & Trigui, M. (2019). Abiotic stress resistance, plant growth promotion and antifungal potential of halotolerant bacteria from a Tunisian solar saltern. *Microbiological Research*, 229, <https://doi.org/10.1016/j.micres.2019.126331>
- Mastan, A., Rane, D., Dastager, S. G., & Vivek Babu, C. S. (2019). Development of low-cost plant probiotic formulations of functional endophytes for sustainable cultivation of *Coleus forskohlii*. *Microbiological Research*, 227, 126310. <https://doi.org/10.1016/j.micres.2019.126310>
- Mei, C., & Flinn, B. (2010). The use of beneficial microbial endophytes for plant biomass and stress tolerance improvement. *Recent Patents*

- on *Biotechnology*, 4, 81–95. <https://doi.org/10.2174/187220810790069523>
- Méndez-Bravo, A., Cortazar-Murillo, E. M., Guevara-Avendaño, E., Ceballos-Luna, O., Rodríguez-Haas, B., Kiel-Martínez, A. L., Hernández-Cristóbal, O., Guerrero-Analco, J. A., & Reverchon, F. (2018). Plant growth-promoting rhizobacteria associated with avocado display antagonistic activity against *Phytophthora cinnamomi* through volatile emissions. *PLoS ONE*, 13, e0194665. <https://doi.org/10.1371/journal.pone.0194665>
- Mendoza-Hernández, J. C., Vázquez-Delgado, O. R., Castillo-Morales, M., Varela-Caselis, J. L., Santamaría-Juárez, J. D., Olivares-Xometl, O., Arriola Morales, J., & Pérez-Osorio, G. (2019). Phytoremediation of mine tailings by *Brassica juncea* inoculated with plant growth-promoting bacteria. *Microbiological Research*, 228, 126308. <https://doi.org/10.1016/j.micres.2019.126308>
- Miliute, I., Buzaitė, O., Baniulis, D., & Stanys, V. (2015). Bacterial endophytes in agricultural crops and their role in stress tolerance: a review. *Zemdirbyste-Agriculture*, 102, 465–478. <https://doi.org/10.13080/z-a.2015.102.060>
- Ojija, F., Arnold, S. E. J., & Treydte, A. C. (2021a). Plant competition as an ecosystem-based management tool for suppressing *Parthenium hysterophorus* in rangelands. *Rangelands*, S0190052820301218. <https://doi.org/10.1016/j.rala.2020.12.004>
- Ojija, F., Manyanza, N. M., & Mataba, G. R. (2021b). Distribution, habitat and conservation status of critically endangered aloes in Tanzania. *South African Journal of Botany*, 1–7. <https://doi.org/10.1016/j.sajb.2021.08.024>
- Ojija, F., & Ngimba, C. (2021). Suppressive abilities of legume fodder plants against the invasive weed *Parthenium hysterophorus* (Asteraceae). *Environmental and Sustainability Indicators*, 1–22. <https://doi.org/10.1016/j.indic.2021.100111>
- Pajares, S., Bohannan, B. J. M., & Souza, V. (2016). Editorial: The role of microbial communities in tropical ecosystems. *Frontiers in Microbiology*, 7. <https://doi.org/10.3389/fmicb.2016.01805>
- Park, Y. S., Dutta, S., Ann, M., Raaijmakers, J. M., & Park, K. (2015). Promotion of plant growth by *Pseudomonas fluorescens* strain SS101 via novel volatile organic compounds. *Biochemical and Biophysical Research Communications*, 461, 361–365. <https://doi.org/10.1016/j.bbrc.2015.04.039>
- Philippot, L., Raaijmakers, J. M., Lemanceau, P., & van der Putten, W. H. (2013). Going back to the roots: the microbial ecology of the rhizosphere. *Nature Reviews Microbiology*, 11, 789–799. <https://doi.org/10.1038/nrmicro3109>
- Rashid, M. I., Mujawar, L. H., Shahzad, T., Almeelbi, T., Ismail, I. M. I., & Oves, M. (2016). Bacteria and fungi can contribute to nutrients bioavailability and aggregate formation in degraded soils. *Microbiological Research*, 183, 26–41. <https://doi.org/10.1016/j.micres.2015.11.007>
- Reed, H. E., & Martiny, J. B. H. (2007). Testing the functional significance of microbial composition in natural communities: Functional significance of microbial composition. *FEMS Microbiology Ecology*, 62, 161–170. <https://doi.org/10.1111/j.1574-6941.2007.00386.x>
- Rosenblueth, M., & Martínez-Romero, E. (2006). Bacterial Endophytes and Their Interactions with Hosts. *MPMI*, 19, 827–837. <https://doi.org/10.1094/MPMI-19-0827>
- Sahu, O. (2019). Sustainable and clean treatment of industrial wastewater with microbial fuel cell. *Results in Engineering*, 4, 100053. <https://doi.org/10.1016/j.rineng.2019.100053>
- Santoyo, G., Moreno-Hagelsieb, G., del Carmen Orozco-Mosqueda, Ma., & Glick, B. R. (2016). Plant growth-promoting bacterial endophytes. *Microbiological Research*, 183,



- 92–99. <https://doi.org/10.1016/j.micres.2015.11.008>
- Schulz, S., Brankatschk, R., Dümig, A., Kögel-Knabner, I., Schloter, M., & Zeyer, J. (2013). The role of microorganisms at different stages of ecosystem development for soil formation. *Biogeosciences*, 10, 3983–3996. <https://doi.org/10.5194/bg-10-3983-2013>
- Seastedt, T. R. (2015). Biological control of invasive plant species: a reassessment for the Anthropocene. *New Phytologist*, 205, 490–502. <https://doi.org/10.1111/nph.13065>
- Shade, A., Peter, H., Allison, S. D., Baho, D.L., Berga, M., Bürgmann, H., Huber, D. H., Langenheder, S., Lennon, J. T., Martiny, J. B. H., Matulich, K. L., Schmidt, T. M., & Handelsman, J. (2012). Fundamentals of Microbial Community Resistance and Resilience. *Frontiers in Microbiology*, 3. <https://doi.org/10.3389/fmicb.2012.00417>
- Shahrtash, M., & Brown, S. P. (2021). A path forward: promoting microbial-based methods in the control of invasive plant species. *Plants*, 10, 943. <https://doi.org/10.3390/plants10050943>
- Soldan, R., Mapelli, F., Crotti, E., Schnell, S., Daffonchio, D., Marasco, R., Fusi, M., Borin, S., & Cardinale, M. (2019). Bacterial endophytes of mangrove propagules elicit early establishment of the natural host and promote growth of cereal crops under salt stress. *Microbiological Research*, 223–225, 33–43. <https://doi.org/10.1016/j.micres.2019.03.008>
- Son, J. S., Sumayo, M., Hwang, Y. J., Kim, B. S., & Ghim, S. Y. (2014). Screening of plant growth-promoting rhizobacteria as elicitor of systemic resistance against gray leaf spot disease in pepper. *Applied Soil Ecology*, 73, 1–8. <https://doi.org/10.1016/j.apsoil.2013.07.016>
- Strickland, M. S., Lauber, C., Fierer, N., & Bradford, M. A. (2009). Testing the functional significance of microbial community composition. *Ecology*, 90, 441–451. <https://doi.org/10.1890/08-0296.1>
- Sturz, A. V., & Nowak, J. (2000). Endophytic communities of rhizobacteria and the strategies required to create yield enhancing associations with crops. *Applied Soil Ecology*, 15, 183–190. [https://doi.org/10.1016/S0929-1393\(00\)00094-9](https://doi.org/10.1016/S0929-1393(00)00094-9)
- Tang, M. J., Zhu, Q., Zhang, F. M., Zhang, W., Yuan, J., Sun, K., Xu, F. J., & Dai, C. C. (2019). Enhanced nitrogen and phosphorus activation with an optimised bacterial community by endophytic fungus *Phomopsis liquidambari* in paddy soil. *Microbiological Research*, 221, 50–59. <https://doi.org/10.1016/j.micres.2019.02.005>
- Tyc, O., Song, C., Dickschat, J. S., Vos, M., & Garbeva, P. (2017). The Ecological Role of Volatile and Soluble Secondary Metabolites Produced by Soil Bacteria. *Trends in Microbiology*, 25, 280–292. <https://doi.org/10.1016/j.tim.2016.12.002>
- Vurukonda, S. S. K. P., Vardharajula, S., Shrivastava, M., & SkZ, A. (2016). Enhancement of drought stress tolerance in crops by plant growth promoting rhizobacteria. *Microbiological Research*, 184, 13–24. <https://doi.org/10.1016/j.micres.2015.12.003>
- Wagner, M., Loy, A., Nogueira, R., Purkhold, U., & Lee, N. (2002). Microbial community composition and function in wastewater treatment plants. *Antonie van Leeuwenhoek*, 665–680.
- Xu, W., Wang, F., Zhang, M., Ou, T., Wang, R., Strobel, G., Xiang, Z., Zhou, Z., & Xie, J. (2019). Diversity of cultivable endophytic bacteria in mulberry and their potential for antimicrobial and plant growth-promoting activities. *Microbiological Research*, 229, 126328. <https://doi.org/10.1016/j.micres.2019.126328>
- Yang, L., Liu, Y., Cao, X., Zhou, Z., Wang, S., Xiao, J., Song, C., & Zhou, Y. (2017). Community composition specificity and

potential role of phosphorus solubilising bacteria attached on the different bloom-forming cyanobacteria. *Microbiological Research*, 205, 59–65.  
<https://doi.org/10.1016/j.micres.2017.08.013>