

Antibiotics are Current Approaches to Improve Productivity Using Soil Microbiome

Kanchi Ravi Padma^{1*}, K R Don², B Dinesh³, D Karthikeyan⁴

¹Biotechnology, Sri Padmavati Mahila Visvavidyalayam Women's University, Tirupati, India.

²Department of Oral Pathology and Microbiology, READER, Sree Balaji Dental College and Hospital, Bharath Institute of Higher Education and Research (BIHER) Bharath University, Chennai, Chennai, India.

³Department of Dental Surgery, Government Stanley Medical College and Hospital, Tirupati, India.

⁴Department of Dental Surgery, Government Stanley Medical College and Hospital, Chennai, India.

ABSTRACT

The tremendous minuscule complexity of species on Earth has long captivated environmentalists. Unquestionably, one of the most important areas of focus in bio-ecology is understanding the complex patterns of this variety and the prevailing influence to control them. However, a portion of ecology has always received attention and is only examined above and below ground. Furthermore, understanding the relationship between microflora and their bio-ecology is crucial to understanding the ecosystem. The main focus of this paper is the challenges related to the fate of antibiotics in soil degradation and their impact on the microbiota. Antibiotics especially alter the structural, functional, and genetic properties of the microbiome. Currently, the release of antibiotics into the soil triggers antibiotic-resistant genes (A.R.G.s). In addition, every researcher must understand several environmental factors such as temperature, rainfall, and humidity, along with those stresses that lead to enzymatic activity, and its potential for the metabolism of different carbon sources by diverse microbes has also been portrayed. Furthermore, microorganisms existing in soil significantly increase soil health, quality, and fecundity; all of these factors have been confirmed to increase the quality as increase the yield of agricultural products. The latest approach covers cropping; the use of this method has particularly favored the composition of the microbiome along with the plant-microbe interaction and significantly displayed enhanced crop yield.

Keywords: Microbiome, Antimicrobial agent, Plant-microbe Interaction, Bio-ecology, Cover cropping, Antibiotic resistance

Corresponding author: Kanchi Ravi Padma

e-mail ✉ thulasipadi@gmail.com

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INTRODUCTION

Soil microbes are crucial for enhancing soil fertility and agricultural crop productivity. Although several researchers have conducted substantial studies on the soil microbiome, a significant portion of the microbial life forms within the sully are yet unknown (Buckley & Schmidt, 2001). The diversity, functional organization, genetic makeup, and structural makeup of this soil microbiota are considered to be among the most significant indicators of soil fertility. However, Tilak *et al.* (2005) and Nair and Ngouajio (2012) stated that the microbiome found in agricultural soils has been proposed to play a major role in enhancing plant growth through processes like growth hormone synthesis, nitrogen fixation, and nutrient recycling from compost utilization. However, the use of collective farming techniques has been justified by the idea that it can control the microbial makeup of the soil, improving soil quality and promoting soil health. Enhancing crop maturity, growth, and yield through cover cropping is a promising strategy. Simply put, cover cropping is the practice of planting grass strips between crops to boost soil carbon stacking and

fertilizer (Olson *et al.*, 2010). This approach is regarded as traditional and aids in recycling nutrients back into the soil. It also has a major impact on insect control and the development of beneficial microbiota (Haramoto & Gallandt, 2004). Furthermore, adding cover crops has increased the microbial community's complexity and diversity compared to tilled soils. But unlike other sustainable methods that use low tillage and organic amendments, crop covering was found to have a positive impact on improving soil vitality (**Figure 1**).

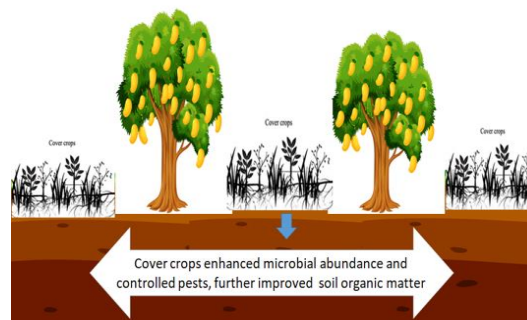


Figure 1. Cover crops are the latest techniques to improve agricultural production

Yet, a rich diversity of invertebrates participates in regional and global biogeochemical cycles alongside other microbial groups. In particular, the soil's microbiome is essential to the environment's ability to recycle nutrients, control temperature, break down organic matter, and cycle it (Zhou *et al.*, 2012). Because it interacts with microbial populations, this most recent crop-covering approach eventually improves soil quality.

However, little research has demonstrated how crop coverage might increase soil biodiversity. Several examples show how useful cover crops are in fruit orchards. Plant combinations that will encourage the development of saprophytic fungus and the bacterial community should be sown (Bloor *et al.*, 2009). The qualities of the soil were altered in 1956 by the use of green manure modification technology (Elfstrand *et al.*, 2007). Thus, the presence of microbiome in soil significantly improved fruit quality production. The area where soil interacts with plant roots to support primary productivity and plant growth is known as the rhizosphere (Berendsen *et al.*, 2012).

Plant health needs to recognize the plant-interacted microbial community as the second genome of the flora. Another example of a fruit crop that is important to tropical regions and has socioeconomic significance is the mango (*Mangifera indica* L.), which originated in Southeast Asia and is now grown all over the world due to its high nutritional value and delicious flavor (Tharanathan *et al.*, 2006; Vasugi *et al.*, 2012; Neguse *et al.*, 2019). Using chemical fertilizers results in a lack of vital nutrients from the soil and can even contaminate the water, even though mango trees grown on large tracts of land need protection from pest attacks (Massah & Azadegan, 2016). Progressively raising fruit yield output in contrast to previous strategies, the cover cropping approach was proven to be dependable. Soil characteristics, soil quality, and crop output were all enhanced by crop covering.

The earth system's most important component, soil, is essential to preserving human health. Considering that soil ecosystems support the growth of crops that supply staple foods. According to Beavington (2000) and Steffan *et al.* (2018), plants grown in the soil provide vital nutrients, minerals, and trace elements that humans ingest. The physical, chemical, and biological perspectives of soil microbiota have been shown to have direct effects on human health and well-being. While it is widely known that soil microflora naturally occurs, farmers supplement their crop development with specific antibiotics. However, some antibiotics can disrupt or alter the microbiome, which has an impact on the community as a whole. Antibiotics can change the phylogenetic makeup of microflora and disrupt its ecological processes. Numerous findings in the literature have illustrated how the addition of antibiotics to the soil ecology alters the microbial ecosystem.

Ding and He (2010) have disclosed the consequences that followed the introduction of antibiotics to an ecological system. The antibiotics' altered modes of action, such as nitrogen transformation, biomethanation, and sulfate reduction, were among these side effects. Several researchers have conducted their research using traditional methods like the isolation and screening of actinomycetes that produce antibiotics. Nonetheless, Baniya *et al.* (2018) claim that identifying novel antibiotics on soil microflora was made possible by these traditional methods of isolation and screening. However, several multidrug-resistant infections have emerged as a result of microbiota mutation, which is sneaky concerning the health

of the human population. As a result, it has been seen as a dangerous issue for infectious disease treatment. An in-depth investigation on this subject is necessary to identify the most recent innovative antibiotics that aid in the situation's management (Pathalam *et al.*, 2017).

Bio-ecology, or the symbiotic relationship between plants and microbes, has received a lot of attention from environmentalists (Mittelbach *et al.*, 2001). Nonetheless, a focus on the expression, behaviors, and study of microorganisms in their native environments is necessary for micro-ecological systems (Brock, 1993). However, the widespread use of antibiotics in all scientific domains, such as medicine, veterinary care, and pisciculture, has put the soil environment at risk (Aslam *et al.*, 2018; Beattie *et al.*, 2018). According to findings in the literature, millions of fatalities in 2015 have been linked to the increase in antibiotic-resistant bacteria (Zhang *et al.*, 2009; Tello 2012; Berglund, 2015; Brown-Jaque, 2015). Microbiome resistance was caused by pathogenic-resistant bacteria communicating with the environment, as other investigations have demonstrated. Consideration is given to the long-term consequences of antibiotics as well as the most recent applications for improving soil quality and agricultural productivity to address the issue. Therefore, we intend to evaluate the literature on antibiotics and soil microbiota in this review paper. It also looks at the abundance and variety of bacterial communities in soil ecosystems, as well as their behavioral and genetic resistance to antibiotics.

Antibiotics-resistant genes in microbiota

The continuous use of antibiotics is the primary factor limiting antibiotic resistance. It is expected that the soil microbiome will change genetically and develop antibiotic resistance when antibiotics are introduced into the environment. Antibiotics are used by farmers to prevent infections during plant growth, and pharmaceutical companies produce a lot of drugs and discharge their effluent into the environment. Because of this, both the bacterial and soil characteristics are altered by the widespread use of antibiotics and their improper disposal. India was the world's largest consumer of antibiotics for human health at around 10.7 units per person during the 20th century. Moreover, with an estimated 7.5 units consumed per person, China was the second-largest consumer, followed by the U.S. with 22.0 units. However, between 2000 and 2010, the BRICS countries (Brazil, Russia, India, China, and South Africa) accounted for 75% of the global increase in antibiotic consumption. As a result, of the BRICS countries, 23% of the increase in antibiotic retail sales in India and 57% of the increase in the medical sector in China (Laxminarayan & Chaudhury, 2016). Consequently, antibacterial/antimicrobial drugs focus on the survival and spread of resistant varieties in addition to being utilized for therapeutic or inhibitory purposes in veterinary, human, and agricultural contexts (Gebreyohannes *et al.*, 2013). Antibiotics are mostly used in agriculture, which makes up at least half of the U.S. population (Lipsitch *et al.*, 2002). The growth of resistant bacterial species in the soil ecosystem is primarily caused by the disposal of animal waste and the continued overuse of fertilizers. This most likely results from changes in their genetic composition during evolution, such as lateral gene transformation, which gives soil microbiomes persistent resistance to antibiotics. However, vital populations of the microbiome, which humans are exposed to

through animal-to-human contact through meat, meat products, eggs, milk, etc., are shielded from cattle, poultry, and pigs that are given antibiotics (Marshall & Levy 2011; Santajit & Indrawattana, 2016).

Antibiotics resistance profile in soil

A scientific review of databases from 2009 turned up at least fifteen reports on the presence of antibiotics in soil. Of those, about ten were tested in East Asian field locations where the soil was treated with animal manure, wastewater, or surface-contaminated water. Nevertheless, a total of 36 distinct antibiotic compounds belonging to six distinct classes of

antibiotics were measured. For both gram-positive and gram-negative bacilli, the minimum inhibitory concentrations reported for each antibiotic are displayed in **Table 1**. Compounds like Ampicillin (A.M.P.), Tetracycline (TET), Nitrofurantoin (NFT), Ciprofloxacin (C.I.P.), Penicillin, and Gentamycin are the most often studied ($\geq 50\%$ of studies). Even though sulfonamides have been the subject of relatively few studies, none of the recent research has noted the existence of the medically important β -lactams group.

The abundance of resistant gram-positive bacterial genera isolated from soils under different farming styles and their M.L.C values are presented in **Table 2**.

Table 1. Microbial diversity & antimicrobial resistance profile of Gram-Negative, Gram-positive microbiota from soils cultivated in conventional as well as organic farming methods

Gram Negative M.I.C. values							
Soil of Origin	Genus/species	Ampicillin	Aztreonam	Cefepime	Ciprofloxacin	Gentamicin	Nitrofurantoin
Organic wheat	<i>Pseudomonas</i> sp.	16	16	≤ 4	$\leq 0,5$	≤ 2	64
Organic wheat	<i>Serratia proteamacula</i>	16	≤ 8	≤ 4	$\leq 0,5$	≤ 2	64
Organic Wheat	<i>Flavobacterium</i> sp.	≤ 4	> 32	32	2	≤ 2	128
Organic Wheat	<i>Empedobacter</i> sp./ <i>Wautersiella falsenii</i>	≤ 4	> 32	≤ 4	4	8	128
Organic Wheat	<i>Pseudomonas putida</i>	> 32	32	≤ 4	$\leq 0,5$	≤ 2	> 128
Conventional Wheat	<i>Pseudomonas</i> sp.	> 32	> 32	≤ 4	$\leq 0,5$	≤ 2	> 128
Conventional Wheat	<i>Stenotrophomonas maltophilia/rhizophila</i>	16	16	≤ 4	1	≤ 2	128
Conventional Wheat	<i>Sphingobacterium</i> sp.	> 32	> 32	≤ 4	1	> 16	32
Conventional Wheat	<i>Chryseobacterium</i> sp.	> 32	> 32	≤ 4	$\leq 0,5$	4	64

Table 2. The abundance of resistant gram-positive bacterial genera isolated from soils under different farming styles and their M.L.C values

Gram Positive M.I.C. values							
Soil of origin	Genus/species	Ampicillin	Ceftriaxone	Ciprofloxacin	Clindamycin	Penicillin	Tetracycline
Organic wheat	<i>Bacillus</i> sp.	8	32	$\leq 0,5$	0.25	> 8	≤ 2
Organic wheat	<i>Bacillus</i> sp.	8	> 64	$\leq 0,5$	$\leq 0,12$	> 8	≤ 2
Organic wheat	<i>Bacillus</i> sp.	$\leq 0,12$	≤ 8	$\leq 0,5$	1	$\leq 0,06$	≤ 2
Conventional wheat	<i>Bacillus</i> sp.	4	32	$\leq 0,5$	0.25	4	≤ 2
Conventional wheat	<i>Bacillus</i> sp.	8	64	$\leq 0,5$	0.25	> 8	≤ 2
Organic rapeseed	<i>Bacillus weihenstephanensis</i>	1	16	$\leq 0,5$	0.25	2	≤ 2
Organic rapeseed	<i>Bacillus</i> sp.	4	64	$\leq 0,5$	0.5	8	≤ 2
Conventional rapeseed	Unknown	2	32	$\leq 0,5$	0.25	4	≤ 2
Conventional rapeseed	<i>Streptomyces</i> sp.	2	≤ 8	2	2	2	16
Conventional rapeseed	<i>Bacillus</i> sp.	8	32	$\leq 0,5$	0.25	> 8	≤ 2
Conventional rapeseed	<i>Bacillus pumilus/safensis</i>	$\leq 0,12$	16	$\leq 0,5$	0.5	$\leq 0,06$	≤ 2
Conventional rapeseed	<i>Paenibacillus xylanexedens</i>	≤ 4	16	$\leq 0,5$			

Conventional rapeseed	Unknown	8	> 64	≤ 0,5	0.25	> 8	≤ 2
Organic maize	Unknown	8	64	≤ 0,5	≤ 0,12	> 8	≤ 2
Organic maize	<i>Bacillus</i> sp.	2	32	≤ 0,5	≤ 0,12	2	≤ 2
Organic maize	<i>Paenibacillus</i> spp.	≤ 4	16	≤ 0,5			
Organic maize	<i>Arthrobacter</i> sp.	2	32	2	0.25	2	≤ 2
Conventional maize	<i>Bacillus</i> spp.	8	64	≤ 0,5	≤ 0,12	8	≤ 2
Conventional maize	<i>Bacillus</i> spp.	4	16	≤ 0,5	0.25	4	≤ 2
Conventional maize	<i>Bacillus</i> spp.	4	64	≤ 0,5	0.25	2	≤ 2
Conventional maize	<i>Paenibacillus</i> spp.	≤ 4	16	≤ 0,5			
Conventional maize	<i>Arthrobacter</i> sp.	2	32	2	0.25	2	≤ 2

Diverse soil microbes

The bacterial community is specifically dominated by Proteobacteria, Actinobacteria, Acidobacteria, Bacteroidetes, and several other genus/species, which are depicted in Figure 2. This bacterial community exists in both forests as well as agricultural soils. Consequently, particularly was found to be abundant in agricultural soil, whereas Verrucomicrobia & Planctomycetes in forest soil. A diverse group of bacterial

communities is present in the soil, and based on the cultivation of crops, the occurrence of microbes differs. As indicated, in the rhizosphere Proteobacteria, Actinomycetales, and Enterobacteriaceae were abundant in bulk soil, but in the soybean rhizosphere, all six genotypes were depleted with the mentioned microbes like Acidobacteria and Verrucomicrobia. Therefore, the growth of bacterial communities varies with soil type.

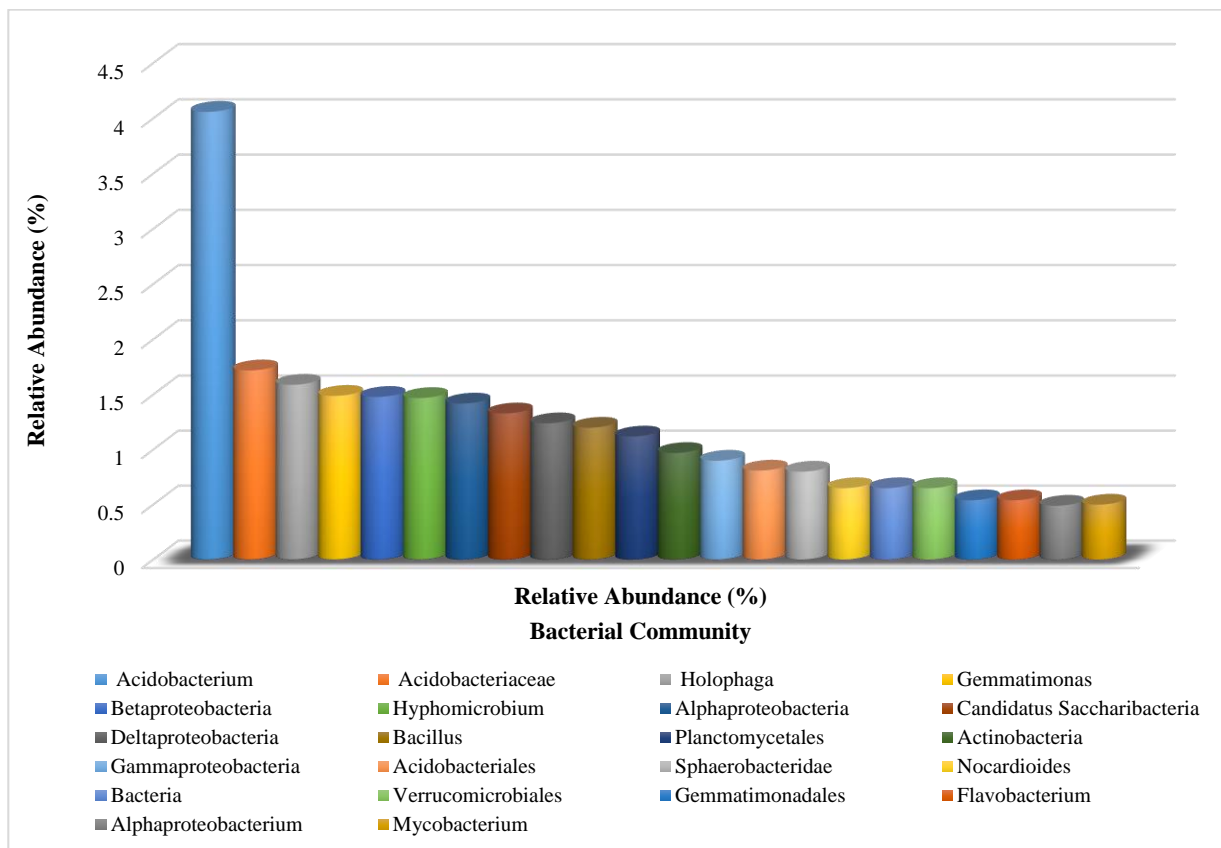


Figure 2. Diverse Bacterial Community occurrence in soil

Morphological characteristics of microbiome isolated from soil

The primary focus of Dezfully et al.'s (2015) study was on Kochi variety crops, and they identified bacteria that produce antibiotics from the rhizosphere zones of Kochi. Because microbial communities are more prevalent in sully than in other

ecosystems, soil that contains nitrogen-fixing bacteria has been selected for sampling. Rhizobial bacteria, on the other hand, exhibit more aggressive behavior. Many scientists have chosen to sully because it has novel antibiotics and can produce bacteria that are used to manufacture pharmaceuticals,

including actinomycetes (Oskay *et al.*, 2004; Wadetwar & Pati, 2013; Constancias *et al.*, 2015). A wider range of ecological habitats and a higher diversity of soil microbial variants are the results of the soil's demonstrated heterogeneity. These outcomes, however, were connected with the sample procedures we gathered and how they were put into practice for gathering samples in various settings. A conventional technique for gathering samples, the random sampling method was outlined by Williams and Vickers (1986); this process lends support to the current investigation. A conventional technique recommended by multiple scientists, Gram's staining was used to identify the morphological characteristics (Diddi *et al.*, 2013; Kaur *et al.*, 2014; Kumar *et al.*, 2016; Radwan *et al.*, 2022). Hence, to gain a deeper understanding of its morphological traits, soil bacterial isolates were appropriately stained using Gram's staining method, which showed that the majority of the isolates were Gram-positive. Even so, Wadetwar and Patil (2013) considered the results to be confirmatory, indicating that the majority of the soil microbiome was gram-positive upon testing.

The threat to soil biota ecosystem

Human activity is endangering the soil ecosystem (Wardle *et al.*, 2004; Barrios, 2007; Sharma *et al.*, 2009; AlAssad *et al.*, 2021). According to Bahram *et al.* (2018), Sully is a rich source of biologically active substances that could be studied as biopharmaceuticals. In addition to acting as a reservoir for antibacterial resistance, the environment can also act as a source of resistance factors that can spread to infections affecting humans (Wright, 2010; Forsberg *et al.*, 2012; Çora & Çora, 2022). Antibacterial agent resistance, on the other hand, is seen as one of the biggest threats to food safety and general public health and has grown in popularity over time (Laxminarayan *et al.*, 2013). Nevertheless, antibacterial resistance diseases cause hundreds to thousands of deaths annually. Furthermore, according to recent scientific predictions, in 2050, these numbers may reach 10 million, which may even increase and result in the development of cancerous cells (O'Neill, 2014). The Antibacterial resistance has a major influence on human health because pharmaceutical treatment failures result in millions of deaths and a subsequent rise in illnesses. The health of the community is at risk due to several different ways that sully transmits antibacterial resistance to humans through direct contact with the food chain, the air, or the water ecosystem (Ochoa-Hueso, 2017; Larsson *et al.*, 2018; Li *et al.*, 2018a) (Figure 3).

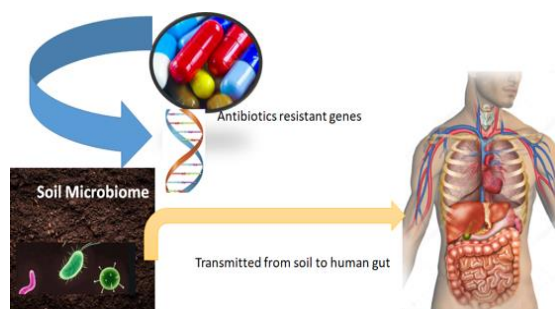


Figure 3. Transmission of antibiotics resistance genes from soil to human gut

Future perspectives

The main perspective of our current study is to examine the microbiome in agricultural soil. Since soil microbiome is inhabited with greater bacterial and fungal diversity. Application of the latest agricultural practices like crop covering helps to enhance soil health and increase yield, thereby reducing pathogenic diseases (Berglund, 2015). Every researcher must have a fundamental comprehension of soil microbiome and how the plant-microbe interaction resists the progression of pathogenic microbes. The next gene sequencing with 16S rRNA gene fragments helped to investigate the microbial community composition at higher taxonomic levels. The exploitation of humankind is enhanced release of these resistant genes and thereby dispersed in the global sector. The increased prevalence of antibiotic resistance genes in the polluted environment has shown clear and direct consequences for human health on land. Controlling sully biota, which involves both the smaller and larger microbiomes, is significant in protecting earthly health. However, the concept of "One Health" triggered scientists to explore effective ways to enhance the complicated interactions in ecologies.

CONCLUSION

Our article's primary focus is on the microbiota residing in the sully. There is always a demand to check the soil pollutants and pharmaceutical substances released into the environment. This change or alteration of microbiota is specifically due to added contents to soil ecosystems by manmade activity, and further screening and isolation of organisms from the soil ecosystem is essential. The examination of the expression of the functional metagenomics could be carried out using the next-generation sequence analysis. Finally, not only contaminants by antibiotics but also other pollutants result in an upsurge of antibiotic defiance genes, which, when transmitted through the food chain to humans, might result in the aggravation of other maladies. Plant-microbiome interaction studies were acknowledged from the 19th century. The occurrence of abundant microbiota, in turn, enhances the growth of plants, resilience to stress, and improved soil health. Various techniques were employed to increase field success, such as designing smart microbial consortia pest control practices, but the current new generation of crop covering approach enhanced the soil quality, which in turn augmented microbiota, which helped to increase the yield. Therefore, the theme "One Health" viewpoint automatically associates/links with the complete ecosystem.

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