

# We are IntechOpen, the world's leading publisher of Open Access books Built by scientists, for scientists

5,300

Open access books available

130,000

International authors and editors

155M

Downloads

Our authors are among the

154

Countries delivered to

TOP 1%

most cited scientists

12.2%

Contributors from top 500 universities



WEB OF SCIENCE™

Selection of our books indexed in the Book Citation Index  
in Web of Science™ Core Collection (BKCI)

Interested in publishing with us?  
Contact [book.department@intechopen.com](mailto:book.department@intechopen.com)

Numbers displayed above are based on latest data collected.

For more information visit [www.intechopen.com](http://www.intechopen.com)



# Plant Breeding and Microbiome

*Sergio Eduardo Contreras-Liza*

## Abstract

In this review, references to the use of microorganisms in the process of plant domestication, genetic improvement, and production of traditional and improved varieties have been identified. The domestication process may have had an adverse impact on the composition and functions of the associated microbiota and the microbiota associated with plants influences multiple regulatory processes of plants that together define their phenotype. According to scientific evidence, to increase agricultural production and the sustainability of production systems, future research should develop breeding methods that optimize the symbiosis between plants and microorganisms, to produce new plant phenotypes that result in the production of enough food to meet the needs of the human population.

**Keywords:** plant improvement, microorganisms, crop domestication, plant-microbe interaction

## 1. Introduction

Since plants colonized the land, they have developed mechanisms to respond to changing environmental conditions and to settle in extreme habitats. Recent studies indicate that several plant species require associations with microorganisms to tolerate stress and to survive [1]. The human contribution to plant breeding has not only been the development of new breeding methods, but also the acceleration of progress in the evolution of crops.

On the other hand, in recent years the interest in the use of rhizobacteria that promote plant growth has increased. The beneficial effects of these microorganisms involve the ability to act as phytohormones or biofertilizers, increasing the yield of many important crops. Ecological factors such as temperature and nutritional conditions of the soil affect the behavior of microorganisms; inoculation has a better stimulating effect on plant growth in nutrient-deficient soil conditions than in fertile soils [2].

Although most plants lack the adaptive capacity under stress conditions, this ability seems to be associated with certain microorganisms, which suggests asking the question Through what mechanisms can microorganisms and plants adapt to stress conditions? Can plant species improve their tolerance to environmental stresses when associated with certain microorganisms? The answer to these questions could change our concepts about plant breeding and could lead us to new routes towards sustainability.

If food production is to increase by 50% in the next 40 years in a scenario of scarce resources and climate change, it will require a considerable investment in capital, time, and effort. A major component of the solution will have to start from the improvement in agricultural technologies, to produce sufficient and safe food that meets the needs and preferences of the human population, without affecting the sustainability of the natural environment.

From a conceptual perspective, the effects of microorganisms on plants have long been grouped under the idea of “promoting and regulating plant growth.” However, the microbiota associated with plants influences multiple regulatory cascades of plants that together define their phenotype. In addition, the effect of the modified phenotype will depend on the context, as a function of the abiotic and biotic environmental parameters, giving rise to new phenotypes through the joint modification of genomic information and the microbiota associated with plants [3].

The plant microbiome not only helps plants survive in the ecosystem but also offers critical genetic variability, hitherto little used as a strategy by plant breeders, who have traditionally exploited only the genetic variability of the host plant to develop improved varieties of high yield or with tolerance to diseases, pests and abiotic stress [4]. In the words of Walters [5], resistance induced by microorganisms has the potential to revolutionize disease control in crops, but it remains an unconventional type of crop management. This is the subject of intense research at present.

## **2. Crop domestication and microbial diversity**

Domestication refers to the selection and artificial reproduction of wild species to obtain cultivated variants that thrive in man-made niches and that meet human or industrial requirements [6]. Several genotypic and phenotypic forms of domestication have been described in crops and animals, however, domestication is not exclusive to higher organisms.

Before domestication, the wild ancestors of cultivated plants evolved in association with a wide set of microorganisms and insects, with which they participated in pathogenic, predatory, commensal, and mutualistic interactions [7]; most of the species of insects and microorganisms associated with crops in their centers of origin remain to be described [8].

Domestication has transformed hundreds of wild plant species into productive crops for human use. However, cultivation practices and intense artificial selection for yield can come at a hidden cost: disrupting interactions between plants and beneficial microbiota. To improve agricultural production and sustainability, research must develop breeding methods to optimize symbiotic results in crop species [9]. Microbial diversity has also been shaped by the emergence of new, highly specific, man-made environments such as food and beverage fermentations [6]. The domestication of plants is now recognized as a major driver of microbial diversity associated with plants [10]. Among other traits, domestication has changed root architecture, exudation, or defense responses that could have modified plant microbiota, as explained by Martínez-Romero et al. [11]. The authors present the comparison of reported data on the microbiota from cereals and legumes and their ancestors, showing that different bacteria were found in domesticated and wild plant microbiomes.

To date, a few hundred genes and loci have been identified by classical genetic and association mapping as targets of domestication and post domestication divergence. However, only a few of these have been characterized, and for even fewer is the role of the wild-type allele in natural populations understood [12].

According to Pérez-Jaramillo et al. [13], there is an impact of the domestication of crops on soil management, phenotypes, physiology, and the diversity of rhizobacteria associated with crops; the domestication process may have had an adverse impact on the composition and functions of the associated microbiota. In this regard, Martín-Robles [14] states that colonization by mycorrhizae is lower and the infection rate by nematodes is higher in the roots of plants that grow in soils previously cultivated by domesticated plants. Furthermore, domesticated plants showed lower mycorrhizal colonization and higher nematode infection rates than their wild progenitors.

Berg and Raaijmakers [10] argue that seeds are the place of residence of various microbial communities whose composition is determined by the genotype of the plant, the environment, and management practices. To what extent and how domestication affects the microbiomes in plant seeds is still little studied and the microbiomes present in the seeds of wild relatives of modern cultivars should be used to conserve and restore beneficial microorganisms to induce tolerance to biotic and abiotic stress.

The results of Shi et al. [15] indicate that the rhizosphere fungal communities in rice are more influenced than the bacterial communities by the domestication of crops; a more intense relationship has also been verified for fungi and bacteria in cultivated species than in their wild relatives. According to the aforementioned study, wild rice and soybean varieties have a greater abundance of beneficial symbionts and a lower abundance of pathogens compared to cultivated varieties; the domestication process may have a more pronounced effect on fungal communities than on bacterial communities, affecting the microbial relationship in the rhizosphere of these crops.

Leff et al. [16] indicate that the communities of associated fungi in the sunflower (*Helianthus annuus*) are more strongly influenced by the genetic factors of the host plant than the bacterial communities, a finding that could influence the strategies to optimize the use of microbial communities to improve crop yield, suggesting that there would be a vertical transmission of fungi from seeds to adult plants.

Analyzing the evolution of *Phaseolus vulgaris*, Pérez-Jaramillo et al. [17] observed a gradual decrease in the relative abundance of Bacteroidetes, mainly Chitinophagaceae and Cytophagaceae, and an increase in the relative abundance of Actinobacteria and Proteobacteria, in particular Nocardiaceae and Rhizobiaceae, establishing a link between the domestication of the common bean, the specific morphological traits in the root and the community of rhizobacteria associated with this species.

Given the planting system as a monoculture, maize can be seen as a crop responsible for shaping the agricultural environment for the species that cohabit with it [18]. Brisson et al. [19] argue that the analysis of the co-occurrence network in the case of corn revealed that the microbial co-occurrence patterns in the rhizosphere of pure lines of corn were significantly more similar to those of teosinte (an ancestor of corn) than modern hybrids. These results suggest that advances in the development of maize hybrids have had a significant impact on the microbial communities of the rhizosphere and on the assembly of their interaction networks. Wagner et al. [20] found that interactions with soil microorganisms are important for the expression of heterosis in corn and Zambonin et al. [21], found no significant interaction between corn hybrids and inoculation with *Azospirillum* sp. for the variables studied including grain yield, and the specificity between maize hybrids and inoculation was not verified.

According to Walters et al. [22], some local varieties of corn grown under traditional agricultural practices with little or no fertilizer could have developed strategies to improve grain yield under conditions of low nitrogen content in the soil and in these varieties of corn, 29% - 82% of the assimilated nitrogen was derived from the atmospheric form N<sub>2</sub>. Rangel-Lucio et al. [23], found a degree of affinity or effect of the homologous strain of *Azospirillum* obtained from traditional H-28 and Chalqueño maize, and the re-inoculation in these same varieties and its subsequent recognition of the bacterial strain in modern varieties.

The composition of the metabolites in the rhizosphere of wheat is associated with differences between the genotypes of the domestication groups of this species, determined by a high heritability in some of these metabolites. In general,



domestication and reproduction have had important effects on the exudates in the wheat rhizosphere, suggesting the adaptive nature of these changes [24]. Furthermore, the prominent role of neutral processes in the assembly of the domesticated wheat microbiota has been revealed and it has been proposed that domestication has relaxed the selective processes in the wheat microbiota [25].

Cultivated tomatoes (*Solanum lycopersicum*) are more likely to have negative feedback between plants and soil than wild parents according to Carrillo et al. [26], which could partially explain its sensitivity to monoculture in agricultural soils.

### 3. The microbiome: a second genome for plants

The biome is characterized by multiple complex interactions between plants and the associated microbiota, that is, endophytes with different functions, including pathogenic microorganisms, and the environment. Hardoim [27] maintains that the phenotype of a plant is not only determined by its response to the environment, but also by the associated microbiota, the response of the microbiota to the environment, and the complex interactions between members of the ecosystem.

According to Corbin et al. [28], understanding what makes a plant a suitable host for its microbiota is essential to take advantage of the plant-microorganism complex in improving crops. Identifying the genes that allow plants to regulate the assembly of microbiota in their roots is essential for future breeding programs aimed at sustainably improving productivity and product quality.

Tosi et al. [29] have reviewed current strategies for the manipulation of the plant microbiome and classify them as (i) introduction and engineering of microbiomes, (ii) reproduction and engineering of the plant-host relationship, and (iii) selecting agricultural practices that improve soil and plant-associated microbial communities.

Wei and Jousset [3] propose an alternative framework to produce new phenotypes by modifying genomic information and the microbiota associated with plants, thanks to a novel technology that would allow the transmission of the endophytic microbiota to the next generation of plants. The authors indicate that more studies are still needed to implement reproduction at the holobiont level, possibly due to the limited vertical transmission of microorganisms. Even if the bacteria could be transmitted reliably in F1, they would disappear in subsequent generations during the selection process to achieve the desired phenotype.

Sessitsch and Mitter [30] consider that plants could be improved by breeding methods, in relation to greater efficiency in their interaction with microorganisms. While in recent decades, crops have been improved and selected for higher yield and resistance to pests and diseases, it is anticipated that efficient interaction with certain beneficial microorganisms will be an additional factor in plant reproduction. New agricultural practices may include microbiome reproduction, and engineering of specific microbiomes, for example, through strategic soil amendments in which the selective addition of plant exudates can maintain beneficial microorganisms, or through the direct application of microbial consortia. as probiotics [31, 32].

### 4. Sustainable agriculture and the plant microbiome

Sustainable agricultural practices are a response to the multifaceted problems that have originated from the prolonged and indiscriminate use of chemicals to improve crop production for many decades, for this reason, the search

for eco-friendly options to replace chemical fertilizers and pesticides has been accentuated [33].

According to Sessitsch and Mitter [30] in many parts of the world where low-income agriculture is a common situation and improved germplasm or agricultural practices are poorly available, make better use of the functions of plants microbiomes. It will especially support agricultural production under these conditions and will promote the bioeconomy in less developed countries that use microbial inoculants and that can establish strain collections for local environments.

The functioning of the ecosystem is largely governed by the microbial dynamics of the soil; many global ecosystems are in various states of vulnerability, evidenced by erosion, low productivity, and poor water quality caused by intensive agricultural activity and continued use of land resources. Microorganisms in agricultural soil are known to exert profound influences on soil fertility status, particularly with regard to nutrient availability, as well as suppression of plant diseases [34].

There is evidence that soil biodiversity confers stability to stress and disturbance [35], but the mechanism is not yet fully understood; seems to depend on the type of stress and disturbance or a combination of both. Alternatively, the structure of the soil biotic community can play a role in the resilience of the agro-ecosystem; however, possible explanations for this require further investigation.

Many bacterial strains with growth-promoting activity have been reported belonging to the genera *Azoarcus*, *Azospirillum*, *Azotobacter*, *Arthrobacter*, *Bacillus*, *Clostridium*, *Enterobacter*, *Gluconacetobacter*, *Pseudomonas*, and *Serratia*, among them, the species *Pseudomonas* sp. and *Bacillus* sp. are the most extensively studied [36]. The diversity of microorganisms associated with plant roots is enormous, in the order of tens of thousands of species. This complex microbial community associated with the rhizosphere is considered the second genome of the plant and is crucial for the health and nutrition of crops [37].

According to Finkel et al. [38], the study of plant microbiomes has drawn on both holistic ecological studies and mechanistic discoveries; both schools of thought are giving an increasingly close view of the ecological processes that govern the interactions between plants and microorganisms, as well as their molecular mechanisms.

Busby et al. [39] identified five priority themes for research in the study of the plant microbiome and its effect on agricultural sustainability: (1) development of microbiome-host model systems for cultivated and wild plants, with collections of associated microbial cultures and reference genomes, (2) definition of the main microbiomes and metagenomes in these model systems, (3) elucidate the rules of synthetic assembly in functional microbiomes, (4) determine the mechanisms of microorganisms in plant-microbiome interactions, and (5) characterize and refine the genotype-plant-environment-microbiome interaction. Achieving these goals could accelerate our ability to design and implement effective management of agricultural microbiomes and develop strategies that will in turn generate solutions for both consumers and producers for the global food supply.

It has been shown that there are bacterial strains capable of fixing N in non-legume species. Dent and Cocking [40] showed that strains of *Gluconacetobacter diazotrophicus*, a non-nitrogen-fixing, non-nodule bacterium, isolated from the intercellular juice of sugar cane, were inoculated under specific conditions to intracellularly colonize the roots and shoots of cereals (wheat, corn, and rice) as well as in crops as diverse as potatoes, tea, oilseeds, and tomato significantly improved yields, both in the presence or absence of synthetic nitrogen fertilizers, possibly due to a combination of symbiotic intracellular nitrogen fixation, increased photosynthesis rate and the activity of additional plant growth factors. Van Deynze et al. [41] proposed a model for the association of nitrogen-fixing microbes with corn maize

mucilage and identified the main functionalities for a productive diazotrophic association.

Pineda et al. [42] state that since insects can severely affect productivity in ecosystems, resistance to agricultural pests through the microbiome related to plants should be considered a key service to be included as a strategy in the management of a farm. Many of the ecosystem services of the soil microbiome are often not very effective in conventional production systems that use chemical pesticides and fertilizers and only become apparent when plants are exposed to abiotic stress conditions.

Berg et al. [43] suggest that combined strategies for genetic improvement and biocontrol should be developed to maintain the diversity and health of the ecosystem. The practices used in plant breeding, seed treatment, and agriculture, often caused by poor knowledge of the importance of endophytic fungi, are among the reasons for the loss of diversity of endophytic fungi in domesticated plants and also explain the efficacy reduced of some endophytic strains to confer benefits to plants.

According to Lugtenberg et al. [44], endophytic fungi play a key role in plant adaptation, resulting in higher yields and protection against biotic and abiotic stress, encoding a variety of secondary metabolites, including volatile organic compounds, especially in tolerant corn and rice. to a variety of stresses and for better postharvest control.

Horner et al. [45] indicate that modern agricultural practices have greatly increased crop production but have negatively affected soil health, suggesting that in the case of pea (*Pisum sativum*) the diversification of varieties can increase yield and promote interactions microbial, although the impacts on the associated microbial communities are unclear, despite the fundamental role in the functioning of the ecosystem.

## 5. Conclusions

To increase the level of sustainability, various agroecological management strategies of agricultural production systems have been reviewed, including the use of microorganisms in the process of plant domestication, genetic improvement, and the production of improved varieties. According to the references presented in the scientific literature, to increase agricultural production and the sustainability of production systems, future research should develop breeding methods that optimize symbiosis in crops [9], since the interactions with soil microorganisms could be important for the expression of heterosis in some species [20], proposing an alternative framework to produce new phenotypes by modifying genomic information and the microbiota associated with plants [3]; efficient interaction with certain beneficial microorganisms is expected to be an additional factor in plant production. These new agricultural practices can include the reproduction of the microbiome, the transplantation and engineering of specific microbiomes [30] and their transfer through seeds [3, 43] or *in vitro* culture [46]. This complex microbial community associated with the rhizosphere is considered the second genome of the plant and is crucial for the health and nutrition of crops [37].

IntechOpen

IntechOpen

### **Author details**

Sergio Eduardo Contreras-Liza  
Agronomy Department, Universidad Nacional José Faustino Sanchez Carrión. Av.  
Mercedes Indacochea 609, Huacho, Perú

\*Address all correspondence to: [scontreras@unjfsc.edu.pe](mailto:scontreras@unjfsc.edu.pe)

### **IntechOpen**

---

© 2020 The Author(s). Licensee IntechOpen. This chapter is distributed under the terms of the Creative Commons Attribution License (<http://creativecommons.org/licenses/by/3.0>), which permits unrestricted use, distribution, and reproduction in any medium, provided the original work is properly cited. 



## References

- [1] Velasco-Jiménez A, Castellanos-Hernández O, Acevedo-Hernández G, Aarland RC, Rodríguez-Sahagún A. Bacterias rizosféricas con beneficios potenciales en la agricultura Rhizospheric bacteria with potential benefits in agriculture. *Terra Latinoamericana*. 2020;38(2):333-345
- [2] Egamberdieva D. *The Management of Soil Quality and Plant Productivity in stressed environment with Rhizobacteria*. In: Maheshwari DK, editor. *Bacteria in Agrobiolgy: Stress Management*. Berlin Heidelberg: Springer-Verlag; 2012
- [3] Wei, Z., & Jousset, A. (2017). Plant breeding goes microbial. *Trends in Plant Science*, 22(7), 555-558 DOI: <https://doi.org/10.1016/j.tplants.2017.05.009>
- [4] Gopal M, Gupta A. Microbiome selection could spur next-generation plant breeding strategies. *Frontiers in microbiology*. 2016. DOI: 10.3389/fmicb.2016.01971
- [5] Walters DR. Induced resistance: Destined to remain on the sidelines of crop protection? *Phytoparasitica*. 2009;38(1):1-4. DOI: 10.1007/s12600-009-0067
- [6] Steensels J, Gallone B, Voordeckers K, Verstrepen KJ. Domestication of industrial microbes. *Current Biology*. 2019;29(10):381-393
- [7] Chen YH, Langellotto GA, Barrion AT, Cuong NL. Cultivation of domesticated rice alters arthropod biodiversity and community composition. *Annals of the Entomological Society of America*. 2013;106:100-110. DOI: 10.1603/AN12082
- [8] Chen YH, Gols R, Benrey B. Crop domestication and naturally selected species interactions. *Annual Review of Entomology*. 2015;60:35-58. DOI: 10.1146/annurev-ento-010814-020601
- [9] Porter SS, Sachs JL. Agriculture and the disruption of plant-microbial Symbiosis. *Trends in Ecology & Evolution*. 2020;35(5):426-439
- [10] Berg G, Raaijmakers JM. Saving seed microbiomes. *The ISME Journal*. 2018;12(5):1167-1170
- [11] Martínez-Romero E, Aguirre-Noyola JL, Taco-Taype N, Martínez-Romero J, Zuñiga-Dávila D. Plant microbiota modified by plant domestication. *Systematic and Applied Microbiology*. 2020;43(5):126106
- [12] Smýkal P, Nelson M, Berger J, Von Wettberg E. The impact of genetic changes during crop domestication. *Agronomy*. 2018. DOI: 10.3390/agronomy8070119
- [13] Pérez-Jaramillo JE, Carrión VJ, de Hollander M, Raaijmakers JM. The wild side of plant microbiomes. *Microbiome*. 2018;6(1):143
- [14] Martín-Robles N, García-Palacios P, Rodríguez M, Rico D, Vigo R, Sánchez-Moreno S, et al. Crops and their wild progenitors recruit beneficial and detrimental soil biota in opposing ways. *Plant and Soil*. 2020:1-15
- [15] Shi S, Chang J, Tian L, Nasir F, Ji L, Li X, et al. Comparative analysis of the rhizomicrobiome of the wild versus cultivated crop: Insights from rice and soybean. *Archives of Microbiology*. 2019;201(7):879-888
- [16] Leff JW, Lynch RC, Kane NC, Fierer N. Plant domestication and the assembly of bacterial and fungal communities associated with strains of the common sunflower, *Helianthus annuus*. *New Phytologist*. 2017;214(1):412-423
- [17] Pérez-Jaramillo JE, Carrión VJ, Bosse M, Ferrão LF, de Hollander M,

Garcia AA, et al. Linking rhizosphere microbiome composition of wild and domesticated *Phaseolus vulgaris* to genotypic and root phenotypic traits. The ISME Journal. 2017;11(10):2244-2257

[18] Peiffer, J. A., Spor, A., Koren, O., Jin, Z., Tringe, S. G., Dangl, J. L., Buckler, E. S. & Ley, R. E. (2013). Diversity and heritability of the maize rhizosphere microbiome under field conditions. Proceedings of the National Academy of Sciences, 110(16), 6548-6553

[19] Brisson VL, Schmidt JE, Northen TR, Vogel JP, Gaudin AC. Impacts of maize domestication and breeding on rhizosphere microbial community recruitment from a nutrient-depleted agricultural soil. Scientific Reports. 2019;9(1):1-14

[20] Wagner MR, Tang C, Salvato F, Clouse KM, Bartlett A, Sermons S, et al. Microbe-dependent heterosis in maize. *bioRxiv*. 2020:2020.05.05.078766

[21] Zambonin G, Pacentchuk F, Lima FN, Huzar-Novakowski J, Sandini IE. Response of maize crop hybrids, with different transgenic events, to inoculation with *Azospirillum brasilense*. Applied Research & Agrotechnology. 2019;12(1):33-40

[22] Walters WA, Jin Z, Youngblut N, Wallace JG, Sutter J, Zhang W, et al. Large-scale replicated field study of maize rhizosphere identifies heritable microbes. Proceedings of the National Academy of Sciences. 2018;115(28):7368-7373

[23] Rangel-Lucio JA, Rodríguez-Mendoza M, Ferrera-Cerrato R, Castellanos-Ramos J, Ramírez-Gama RM, Alvarado-Bárceñas E. Afinidad y efecto de *Azospirillum* sp. en maíz. Agronomía Mesoamericana. 2011;22(2):269-279

[24] Iannucci, A., Fragasso, M., Beleggia, R., Nigro, F., & Papa, R. (2017).

Evolution of the crop rhizosphere: Impact of domestication on root exudates in tetraploid wheat (*Triticum turgidum* L.). *Frontiers in plant science*, 8, 2124.

[25] Hassani, M. A., Özkurt, E., Franzenburg, S., & Stukenbrock, E. H. (2020). Ecological assembly processes of the bacterial and fungal microbiota of wild and domesticated wheat species. *Phytobiomes Journal*, PBIOMES-01.

[26] Carrillo J, Ingwell LL, Li X, Kaplan I. Domesticated tomatoes are more vulnerable to negative plant-soil feedbacks than their wild relatives. *Journal of Ecology*. 2019;107(4):1753-1766

[27] Hardoim PR, van Overbeek LS, Berg G, Pirttilä AM, Compant S, Campisano A, et al. The hidden world within plants: Ecological and evolutionary considerations for defining functioning of microbial endophytes. *Microbiology and Molecular Biology Reviews*. 2015;79(3):294-320. DOI: 10.1128/MMBR.00050-14

[28] Corbin KR, Bolt B, López CMR. Breeding for beneficial microbial communities using Epigenomics. *Frontiers in Microbiology*. 2020;11

[29] Tosi M, Mitter EK, Gaiero J, Dunfield K. It takes three to tango: The importance of microbes, host plant, and soil management to elucidate manipulation strategies for the plant microbiome. *Canadian Journal of Microbiology*. 2020;66(7):413-433

[30] Sessitsch A, Mitter B. 21st-century agriculture: Integration of plant microbiomes for improved crop production and food security. *Microbial Biotechnology*. 2015;8(1):32-33. DOI: 10.1111/1751-7915.12180

[31] Arif I, Batool M, Schenk PM. Plant microbiome engineering: Expected

- benefits for improved crop growth and resilience. *Trends in Biotechnology*. 2020;**S0167-7799**(20):30121-30129 <https://doi.org/10.1016/j.tibtech.2020.04.015>
- [32] Bakker MG, Manter DK, Sheflin AM, Weir TL, Vivanco JM. Harnessing the rhizosphere microbiome through plant breeding and agricultural management. *Plant and Soil*. 2012;**360**(1-2):1-13
- [33] Prashar P, Kapoor N, Sachdeva S. Rhizosphere: Its structure, bacterial diversity and significance. *Reviews in Environmental Science and Biotechnology*. 2014;**13**(1):63-77
- [34] Kennedy, A. C., & Smith, K. L. 1995. *Soil microbial diversity and the sustainability of agricultural soils*. In: *The significance and regulation of soil biodiversity* (pp. 75-86). Springer Netherlands.
- [35] Brussaard L, De Ruiter PC, Brown GG. Soil biodiversity for agricultural sustainability. *Agriculture, Ecosystems & Environment*. 2007;**121**(3):233-244
- [36] Maheshwari, D.K. (2011). *Bacteria in Agrobiolgy: Crop Ecosystems*. DOI 10.1007/978-3-642-18357-7\_2, Springer-Verlag Berlin, Heidelberg
- [37] Berendsen RL, Pieterse CM, Bakker PA. The rhizosphere microbiome and plant health. *Trends in Plant Science*. 2012;**17**(8):478-486
- [38] Finkel OM, Castrillo G, Paredes SH, González IS, Dangl JL. Understanding and exploiting plant beneficial microbes. *Current Opinion in Plant Biology*. 2017;**38**:155-163
- [39] Busby PE, Soman C, Wagner MR, Friesen ML, Kremer J, Bennett A, et al. Research priorities for harnessing plant microbiomes in sustainable agriculture. *PLoS Biology*. 2017;**15**(3):e2001793
- [40] Dent D, Cocking E. Establishing symbiotic nitrogen fixation in cereals and other non-legume crops: The greener nitrogen revolution. *Agriculture & Food Security*. 2017;**6**(1):7-9
- [41] Van Deynze A, Zamora P, Delaux P-M, Heitmann C, Jayaraman D, Rajasekar S, et al. Nitrogen fixation in a landrace of maize is supported by a mucilage-associated diazotrophic microbiota. *PLoS Biology*. 2018;**16**(8):e2006352
- [42] Pineda A, Kaplan I, Bezemer TM. Steering soil microbiomes to suppress aboveground insect pests. *Trends in Plant Science*. 2017;**22**(9):770-778
- [43] Berg G, Köberl M, Rybakova D, Müller H, Grosch R, Smalla K. Plant microbial diversity is suggested as the key to future biocontrol and health trends. *FEMS Microbiology Ecology*. 2017;**93**(5)
- [44] Lugtenberg BJ, Caradus JR, Johnson LJ. Fungal endophytes for sustainable crop production. *FEMS Microbiology Ecology*. 2016;**92**(12)
- [45] Horner A, Browett SS, Antwis RE. Mixed-cropping between field pea varieties alters root bacterial and fungal communities. *Scientific Reports*. 2019;**9**(1):1-10
- [46] Naqqash T, Hameed S, Imran A, Hanif MK, Majeed A, van Elsas JD. Differential response of potato toward inoculation with taxonomically diverse plant growth promoting Rhizobacteria. *Frontiers in Plant Science*. 2016;**7**:144. DOI: 10.3389/fpls.2016.00144