

## Review

# Influence of Agricultural Practices on Bacterial Community of Cultivated Soils

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**Abstract:** Bacterial communities play an important role in maintaining stable functioning of soil ecosystems, participating in decomposition of plant residues, accumulation of organic matter, formation of soil aggregates and in the cycle of nutrients. For agroecosystems, maintaining the diversity of microbiocenosis is especially critical because they are essentially less stable and are dependent on external control. The agricultural practices used today (plowing, application of synthetic fertilizers) can negatively affect the richness and diversity of the soil bacterial communities. The solution to this problem may be the application of alternative farming methods to preserve the structural and functional richness of soil (reduced tillage, conservation tillage, no tillage, organic farming). Data on composition and diversity of soil microbiocenosis are important for further forecasting the impact of agriculture and development of effective methods on preserving and increasing soil fertility. This review presents the results of recent studies on the impact of agriculture on the soil bacterial communities. Attention is mainly paid to the effects of applying inorganic and organic fertilizers on the structure and diversity of soil microbiocenosis; the influence of the farming system (different methods of soil cultivation, organic and traditional systems); the influence of cover crops and crop rotation on the microbial community of agricultural soils.

**Keywords:** agricultural practices; agricultural soils; bacterial communities; crop rotation; fertilizers; soil cultivation



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## 1. Introduction

Soil is an invaluable resource that ensures the sustainable functioning of ecosystems at various levels. For many years, soil has played a critical role in the production of food for humanity. In the course of the long-term agricultural use of soil, unique systems have been formed—agroecosystems. These are closed communities with reduced species diversity, less resistance and dependence on external nutrient supply. Existing agricultural practices that are currently widely used around the world threaten soil biodiversity in agroecosystems and, therefore, plant productivity [1]. While traditional farming methods can significantly increase yields in the short term, they cannot be viewed as a strategy to ensure sustainable and resource-efficient agriculture in the future [2].

Agricultural practice involves a diverse set of soil and plant management practices. Tillage is an integral part of traditional agriculture and is aimed at loosening soil, combating weeds and phytopathogens, while increasing soil fertility by incorporating plant residues. However, traditional tillage methods have been reported to aggressively disrupt soil surface and negatively impact the properties of agricultural soils, including extensive soil erosion and reduced biodiversity [3]. In addition, tillage leads to direct contact of plant residues with soil microorganisms, which is accompanied by an accelerated mineralization of organic matter [4]. The practices of reduced (conservation) tillage, as well as no till, are considered to be a more sustainable alternative. Their advantages are lower energy costs, soil and

water conservation by reducing soil disturbance and returning part of plant residues [3]. In addition to tillage, agricultural methods include fertilization and crop rotation/crop diversification. Despite the shown increase in fertility and improvement in soil physical structure when applying organic fertilizers, in real practice, chemical nitrogen fertilizers are often preferred. They are especially used in regions with a high intensity of agriculture, due to the rapid (although short-term) positive impact on crop yields. Thus, agricultural practices are able to alter soil properties and influence the soil microbiome [5].

Diversity of soil microbes is critical for sustainable functioning of soil ecosystems [6]. Soil microbes play an important role in the nutrient cycle in agricultural soils [3]. They are involved in humus accumulation, decomposition of soil organic matter, fixation of nitrogen and phosphorus, stimulation of plant growth and protection from pathogenic microorganisms [7]. Soil biodiversity has been shown to be very sensitive to agricultural practices [1]. Thus, structural and functional changes in the soil microbiome can serve as an indicator of different farming methods' impact on soil quality [8]. Research in recent years has focused on studying the diversity and function of soil microbes in agroecosystems using microbial DNA technologies [9]. Next-generation sequencing (NGS) or high-throughput sequencing (HTS) have a great potential for investigating the hidden diversity of microbial communities [10]. At present, a considerable amount of data has been accumulated on the composition of microbiomes of agricultural soils under various management methods, but the task of interpreting this information is still relevant [11–13]. The number of soil microorganisms' taxa is huge, but the "ideal" composition of the community is unknown [14]. Increases in bacterial diversity in response to management practices may not always be directly correlated with improved soil quality and increased crop yields. Machine-learning methods are even being developed to tackle this problem, and they have shown good results in predicting soil health parameters based on microbiome research [15]. This review summarizes the results of modern studies on the impact of such agricultural methods as the application of inorganic and organic fertilizers, plowing, crop rotation and cover crops on soil bacterial community. The main focus is on the works studying taxonomic composition and diversity of soil microbiomes using molecular methods (amplification of the 16S rRNA gene, sequencing).

## 2. The Effect of Fertilizers on the Bacteriocenosis of Agricultural Soils

### 2.1. Inorganic Fertilizers' Influence

Agroecosystems are systems that are highly dependent on external nutrient input to support crop yields. Therefore, mineral fertilizers are predominantly introduced into agricultural soils in forms accessible to plants [16]. Nitrogen and phosphorus fertilizers are most commonly used among the three types of inorganic fertilizers to increase yields in arable fields [17]. However, over-application can cause severe soil degradation, changes in soil pH and organic carbon content. Thus, although the use of inorganic fertilizers provides plants with nutrients, they can also alter soil productivity by affecting microbial communities [18]. However, to date, rather controversial results have been obtained regarding the effect of inorganic fertilizers on the bacterial community of soils (Table 1). A number of works show the negative impact of fertilization, especially in the long term. It has been shown that it can reduce the biodiversity and abundance of bacteria in chernozems [19]. The introduction of nitrogen N, phosphorus P and potassium K in the form of complex fertilizer (NPK) most significantly reduced the diversity and the total number of bacterial species, being a more important factor for prokaryotic communities in the rhizosphere than plant species.

**Table 1.** Effect of fertilizers on the bacterial community of agricultural soils.

| Location                                    | Soil Type                                       | Fertilizer   | Duration         | Microbial Community Response  | References |
|---|---|--|------------------|---|------------|
| Harbin city, Heilongjiang Province, China   | Black soils                                     | Inorganic fertilizer: N <sub>1</sub> (150 kg N ha <sup>−1</sup> y <sup>−1</sup> ), N <sub>2</sub> (300 kg N ha <sup>−1</sup> y <sup>−1</sup> ), N <sub>1</sub> P <sub>1</sub> (150 kg N plus 75 kg P <sub>2</sub> O <sub>5</sub> ha <sup>−1</sup> y <sup>−1</sup> ) and N <sub>2</sub> P <sub>2</sub> (300 kg N plus 150 kg P <sub>2</sub> O <sub>5</sub> ha <sup>−1</sup> y <sup>−1</sup> ) | 34 years         | Decreased diversity and abundance of the bacterial and archaeal community. Increase in relative abundance of Actinobacteria, Proteobacteria, TM7 and Verrucomicrobia phyla, decrease in Acidobacteria and Nitrospirae in all fertilization treatments compared to unfertilized controls.  | [19]       |
| Cuttack, India                              | Aeric Endoaquept with a sandy clay loam texture | N, NP, NK, NPK, FYM (farmyard manure), FYM + N, FYM + NP, FYM + NK and FYM + NPK   | 47 years         | Only N—stimulation of Firmicutes, Actinobacteria and Nitrospira phyla, suppression of Proteobacteria, Acidobacteria, Cyanobacteria, Fibrobacteres, Spirochaetes, TM7, GNO4, some diazotrophs taxa Burkholderiales, Enterobacteriaceae.<br>In general—the smallest species richness.<br>NPK—increase in the relative abundance of Proteobacteria, Bacteroidetes, Cyanobacteria and WS3 phyla.<br>The highest proportion of bacterial OTUs.<br>FYM—stimulation of Chlorobi, Chloroflexi, Acidobacteria and Elusimicrobia. | [20]       |
| Suwon, Republic of Korea                    | Silt loam soil                                  | NPK, PK, NK, NP N—as urea, 190 kg ha <sup>−1</sup> , P—as fused superphosphate, 101.6 kg ha <sup>−1</sup> , K—as potassium sulphate, 166.7 kg ha <sup>−1</sup>   | 18 years         | Different fertilization regimes affected the composition of the bacterial community at the phylum level but did not affect α-diversity. All fertilization regimes—suppression of Acidobacteria and Nitrospira. N only—decrease in Chloroflexi and Planctomycetes, increase in TM7. NPK and NK—increase in Firmicutes content.   | [21]       |
| Taihe County, Jiangxi Province, South China | Red soil (Ferralsol Cambisol)                   | N1P1K—low N (225 kg ha <sup>−1</sup> y <sup>−1</sup> ), low P (29 kg ha <sup>−1</sup> y <sup>−1</sup> ), normal K (93 kg ha <sup>−1</sup> y <sup>−1</sup> ); N2P1K—high N (450 kg ha <sup>−1</sup> y <sup>−1</sup> ), low P, normal K; N1P2K—low N, high P (59 kg ha <sup>−1</sup> y <sup>−1</sup> ), normal K, and N2P2K—high N, high P, normal K.  | 19 years         | All fertilization regimens increased bacterial diversity and changed the structure of the bacterial community.<br>The percentage of Proteobacteria, Bacteroidetes, Gemmatimonadetes increased, while the percentage of Chloroflexi, Acidobacteria, Nitrospirae and Planctomycetes decreased.  | [18]       |
| Granada, Spain                              | Eutric Cambisol soil                            | Urea (CO(NH <sub>2</sub> ) <sub>2</sub> ), ammonium sulfate (NH <sub>4</sub> ) <sub>2</sub> SO <sub>4</sub> , potassium nitrate KNO <sub>3</sub> , final concentration—421.2 mg N kg <sup>−1</sup> dry soil  | ~4 and 16 months | All fertilizers—decrease in bacterial abundance, change in the community composition. Reduction in Actinobacteria, Chloroflexi, Gemmatimonadetes, Nitrospirae, Planctomycetes phyla, increase in Bacteroidetes, Firmicutes and Proteobacteria compared to control soil. Urea and ammonium sulfate—decrease in Proteobacteria and increase in Firmicutes compared to potassium nitrate.  | [22]       |
| Bernburg, Germany                           | Loess chernozem over limestone                  | N-fertilization: intensive—220 kg per ha as ammonium sulfate and calcium ammonium nitrate; extensive—90 kg per ha as ammonium sulfate and calcium ammonium nitrate   | 23 years         | No effect on the taxonomic composition and functional profile of the bacterial community.   | [23]       |

Table 1. Cont.

| Location                         | Soil Type   | Fertilizer  | Duration  | Microbial Community Response   | References |
|----------------------------------|---|---|-----------|--|------------|
| Central southeast Norway         | Endostagnic Cambisol with dominantly loam and silty sand textures                     | Inorganic fertilizers (N, P, K) in various quantities,<br>Organic fertilizers—green manure, digested household waste, slurry  | 25 years  | The management system affected the structure, quantity and function of soil bacteria but did not change the species richness and diversity of microbes.  | [24]       |
| Yingtian, China                  | Typic Plinthudult (Ultisol).  | Composted pig manure in quantity of 9, 18 и 27 Mg ha <sup>−1</sup>  | 18 years  | Increase in the diversity of bacteria, change in the structure of the community. Decreased relative abundance of Chloroflexi and AD3 phyla (oligotrophs); increase in the number of Proteobacteria (copiotrophs). Increase in the complexity of microbial networks.      | [25]       |
| Jiangxi, China                   | Red paddy soils   | Composted dry pig manure in quantity of 1400, 2800, 5600, 11,200, 22,400, 44,800 kg ha <sup>−1</sup>  | 5 years   | Bacterial richness and diversity did not change at low manure quantities and dropped sharply at high quantities (greater than 11,200 kg ha <sup>−1</sup> ). Decrease in the relative abundance of Acidobacteria, increase in Bacteroidetes, Ignavibacteriae, Firmicutes. | [26]       |
| Binzhou, China                   | Typical saline alluvial soil  | Composted cattle manure   | 3 years   | Manure increased the number of rhizobacteria that promote plant growth and bacterial communities associated with nutrient cycling. Bacterial communities associated with nitrogen fixation and decomposition of plant residues developed on unfertilized plots.          | [27]       |
| Pushchino, Moscow region, Russia | Greyzemic Phaeozem Albic  | Inorganic fertilizer—N180P150K150 (urea, superphosphate, potassium sulfate),<br>Organic fertilizer—fresh cattle manure 50 t ha <sup>−1</sup>  | 7 years   | Mineral fertilizers—a significant reduction in the diversity of prokaryotes. Manure—increase in the number and diversity of prokaryotes.   | [28]       |
| Yunnan province, China           | Typical paddy soils (Anthrosols)  | Well-rotted cow manure in quantity of 3.45 × 10 <sup>4</sup> , 6.90 × 10 <sup>4</sup> , 13.8 × 10 <sup>4</sup> kg hm <sup>−2</sup>  | 8 years   | There was no significant effect on the richness and diversity of soil microbial communities (bacteria, archaea or fungi), as well as the overall composition of the archaea or fungi community.  | [8]        |
| JiangSu Province, China          | Loamy soil  | Inorganic nitrogen applied as urea 180 and 300 kg ha <sup>−1</sup> ,<br>Manure-based compost  | 2 years   | Inorganic nitrogen—no effect on soil bacteria diversity. Compost—reducing the diversity of soil bacteria.  | [6]        |
| MN (state Minnesota), USA        | Loamy soils (mesic Typic Hapludolls, mesic Typic Endoaquolls, mesic Aquic Hapludolls) | Organic fertilizers—beef manure, pelleted poultry manure, Sustane® 8-2-4  | 1 year    | Granular bird droppings and Sustane®—reduction in bacterial diversity. Beef manure—no effect on variety.   | [29]       |
| Shanxi Province, China           | Newly cultivated land on the Loess Plateau (pot experiment)                           | Organic fertilizers—pig manure compost, biochar;<br>Chemical fertilizers—urea (46% N), calcium superphosphate (16% P <sub>2</sub> O <sub>5</sub> ) and potassium sulfate (52% K <sub>2</sub> O) | ~6 months | Fertilizer combination—increase in relative abundance of Betaproteobacteria, Alphaproteobacteria, Gammaproteobacteria and Gemmatimonadetes, as well as in functional abundance of genes for amino acid metabolism, membrane transport, biodegradation of xenobiotics.    | [30]       |

**Table 1.** *Cont.*

| Location  | Soil Type                                   | Fertilizer  | Duration | Microbial Community Response   | References |
|---|---|---|----------|--|------------|
| Henan Province, China                                 | Sandy loam soil<br>(Ochri-Aquic Cambosol)   | Inorganic fertilizers—urea (46% N),<br>superphosphate (16% P <sub>2</sub> O <sub>5</sub> ) and potash<br>(60% K <sub>2</sub> O);<br>Organic fertilizers—organic compost | 28 years | Organic fertilizer—a significant increase in the abundance of<br>Sphingomonas and Acidobacteria, as well as in the genes for C and N<br>metabolism and decomposition of aromatic organic compounds.  | [31]       |
| Jilin Province, China                                 | Light chernozem soil                        | Inorganic fertilizers—N, NP, NK, PK, NPK,<br>Mixed fertilizers—NPK + straw (NPKS) and<br>NPK+ manure in three combinations  | 40 years | All fertilizers—increase in bacterial $\alpha$ -diversity, change in $\beta$ -diversity.<br>Stimulation of Proteobacteria, Acidobacteria, Gemmatimonadetes,<br>Chloroflexi and Planctomycetes. Decreased Actinobacteria, Bacteroidetes,<br>Firmicutes and Cyanobacteria. | [32]       |
| Miryang, South Korea                                  | Fine silty mixed mesic Typic<br>Haplaquepts | Inorganic fertilizers—NP, NK, PK, NPK;<br>Organic fertilizers—compost<br>Mixed fertilizers—NPK + compost  | 45 years | No significant effect on the structure and diversity of soil microbial<br>community.   | [33]       |
| Abbreviations: N—nitrogen, P—phosphorus, K—potassium. |   |   |          |  |            |

Thus, fertilizers, not plants, formed the composition of the rhizosphere microbiome in agroecosystems. Long-term (47 years) use of nitrogen (N) alone for fertilizing rice soils also led to changes in soil biodiversity and rice productivity and suppressed certain beneficial bacterial phyla. However, the highest proportion of bacterial OTUs was recorded with balanced fertilization (NPK), even without manure addition. This suggests that continuous NPK application stimulates beneficial bacterial community without compromising grain yield and straw biomass [20]. This fact is confirmed by the experience of long-term unbalanced use of fertilizers (NPK, PK, NP and NK) [21]. It has been shown that the bacterial community composition changes due to fertilizers that lack one of the three components. N and P had a significant effect on certain groups of bacteria; on the contrary, K had a minimal effect. The authors hypothesized that the imbalanced NPK ratio caused by repeated fertilization may be the driving force that changes the composition of the bacterial community, rather than its diversity. Thus, it was demonstrated that unbalanced application of inorganic fertilizers influenced the composition of the bacterial community (the percentage of certain taxa changed) but had little effect on bacterial diversity.

In a number of cases, an increase in diversity was noted with the introduction of inorganic fertilizers. This way, when applying nitrogen fertilizers in the crop rotation of three crops (flax, oats, winter wheat), a linear increase in the Shannon and Simpson diversity indices with an increase in the N norm was found [34]. In reddish rice soil in southern China, 19 years of high inorganic fertilization increased bacterial biodiversity, while various fertilization methods (different ratios of N, P and K) did not make any significant difference. Bacterial biodiversity and community composition were largely influenced by the soil N:P ratio and available phosphorus. It has been noted that bacterial communities in reddish rice soil are phylogenetically and functionally altered by long-term inorganic fertilization [18].

The microbiome impact of inorganic fertilizers may also depend on the type of fertilizer itself. Thus, when urea, ammonium sulfate and potassium nitrate were added for sowing tomatoes and beans, a decrease in the richness and a change in the composition of both the main and rhizospheric bacteriome of the soil of both plants was found. In general, urea caused the greatest loss of bacterial diversity among nitrogen fertilizers. The application of nitrogen fertilizers based on ammonium and nitrates promoted the growth of copiotrophic bacteria groups, while the number of oligotrophs decreased due to nitrogen fertilizers [22]. Winter cover crops may have a protective effect against the harmful effects of chemical nitrogen fertilizers on soil biodiversity [35]. It was found that under conditions of pure steam, nitrogen fertilization did not affect the bacterial richness of the soil, but it significantly reduced microbiome diversity and uniformity.

In some cases, no significant effect of inorganic fertilization on the soil microbiome was found. In a long-term field experiment in Bernburg-Strenzfeld (Saxony-Anhalt, Germany), different nitrogen fertilization and tillage regimes were simulated. At the same time, neither taxonomic nor functional profiling of the microbiome revealed clear differences in the applied agricultural methods [23]. The same was shown by Chen et al. [24]. Neither soil disturbance, nor chemical fertilizers use, nor chemical plant protection measures had an impact on the species abundance and diversity of soil microbial communities. Thus, no differences were found between conventional and organic farming as such.

## 2.2. Impact of Organic Fertilizers/Manure

Applying a dissimilar organic fertilizer to the soil, such as compost or manure, is a more sustainable alternative to inorganic fertilization because the microbial release of nutrients lasts for longer periods of time. As a result, there is a higher microbial diversity and biomass compared to mineral fertilizers, which, in turn, can positively affect soil health [36]. However, the soil microbiome has a complex and varied structure and consists of a very large number of taxa, often with different life strategies. Therefore, the soil microbiome's reaction to organic fertilization can manifest itself in different ways depending on the time of exposure to fertilizers, their concentration, the properties of the soil itself, etc. For example, the 18-year application of pig manure to the soil (acid ultisol) significantly increased the



diversity of soil bacteria. Both manure application and its aggregation had a significant effect on the structure of the bacterial and fungal community [25]. It turned out that heavy metals in the soil, primarily Cu and Zn, were the main factors influencing the bacterial communities of this soil. The diversity of bacteria decreased sharply when the Cu content in the soil was  $>30.70 \text{ mg kg}^{-1}$  [26]. In addition, the manure impact on microbiome may vary with vegetation [27]. So, for example, during spontaneous vegetation, its application under fallow rapidly increased the number of bacteria that promote plant growth, and when growing alfalfa and dauria, suppressed it. Long-term use of manure in crops of corn, potatoes and mustard significantly increased the number and diversity of soil and rhizosphere prokaryotes [28]. It is believed that the increase in microbial biomass and diversity after application of manure may be caused by the activation of soil microbial communities, which were minor taxa in unfertilized soil. In addition, the majority of exogenous microbes from manure do not survive in soil conditions and are not detected after several months [37]. Schlatter et al. [38], in contrast, found that the solid biological material, biosolid, significantly affected bacterial communities even 4 years after its application. Bacteria of the Clostridiaceae, Norcardiaceae, Anaerolinaceae, Dietziaceae and Planococcaceae families were more abundant in soils treated with biological compounds than in synthetically fertilized soils. Thus, biosolid additives had a profound effect on soil bacterial communities, both through the introduction of bacteria originating from intestines or a bioreactor and through enrichment of potentially beneficial local soil populations.

The influence of manure on soil bacteria diversity is not always found. This way, after 8 years of applying cow manure, no changes were found in the  $\alpha$ -diversity of soil microbiocenosis when comparing fertilized and unfertilized plots [8]. Intensive application of manure-based compost for wheat and rice crops significantly increased soil microbial activity and the number of gene copies of bacteria, archaea and bacteria that oxidize ammonia. However, the variety was significantly reduced. This way, it was shown that the introduction of a large amount of compost is not always beneficial and can lead to soil quality deterioration and microbial diversity decrease. This may be due to the fact that a large amount of organic matter from manure can greatly contribute to intensive reproduction of certain groups of microbes, which leads to a decrease in bacterial diversity. In addition, manure introduction can lead to heavy metals accumulation in soils, and thus suppress the growth of microorganisms and reduce microbial diversity in soil [6].

Other organic fertilizers (pelleted poultry manure, compost, fish hydrolyzate, food hydrolyzate) and their combinations also had an impact on bacterial communities. Pelleted poultry manure caused a rapid increase in the number of bacterial taxa associated with the nitrogen cycle, such as *Nitrosospora*, *Pseudomonas*, *Pseudoxanthomonas* and *Flavobacterium*, as well as an increase in the number of opportunistic bacteria that feed on nematodes, such as *Panagrolaimus* [39]. However, Fernandez et al. [29] showed that in an organic farming system, pelleted poultry manure reduced bacterial diversity, while cow manure did not.

### 2.3. Combination of Inorganic and Organic Fertilizers

In a number of cases, a positive effect of the combined use of organic and inorganic fertilizers on the soil microbiome, soil parameters and crop yields was noted. Through the example of the Chinese Loess Plateau newly cultivated lands, it was shown that the combination of chemical and organic fertilizers can improve the species abundance and the bacterial community diversity [30]. Fertilization in this case was the most effective measure to rapidly improve soil fertility and microbial community structure. Additionally, a positive effect of long-term (28 years) application of organic and inorganic fertilizers was noted for sandy loamy soil [31].

In general, organic fertilizers had a stronger effect on soil carbon and nitrogen stocks, size and activity of microbial biomass than inorganic fertilizers. Inorganic fertilizers increased primary productivity by increasing the input of C and N through crop residues and rhizodeposition. The application of only inorganic fertilizers and a mixture of inorganic and organic fertilizers over 40 years of corn cultivation significantly increased bacterial

$\alpha$ -diversity due to increased nutrient availability. Bacterial  $\beta$ -diversity has also changed significantly with fertilization, especially manure application [32]. Yao et al. [40] found that combined fertilization for 7 years had a moderate effect on many taxa of microbes (model “MM”), and chemical fertilization had a substantial effect on a small number of taxa (model SS). The “MM” model may have been associated with the effect of the applied organic matter on the entire microbial community, and the “SS” model—with the selective stimulation of certain microbes by chemical fertilization. The “MM” model can lead to a more stable, harmonious and efficient ecosystem by maintaining microbial diversity, stimulating beneficial species and a more efficient microbial network.

A positive effect of partial replacement of inorganic fertilizers with organic fertilizers on soil properties and the structure of the bacterial community has been noted [41]. However, it is important to strike a balance, as excessive replacement of inorganic fertilizers with organic fertilizers in some cases was accompanied, along with the improvement of soil parameters, by a decrease in the yield of cultivated crops [42]. It is not always possible to find a connection between the increase in soil fertility and changes in the bacterial community. Thus, as a result of 45 years of applying organic and inorganic fertilizers to the soil of a rice field, it was found that fertilizing with compost was the best way to increase soil fertility. However, it unexpectedly turned out that long-term fertilization did not significantly affect the structure and diversity of the soil microbiome [33]. In addition, a significant factor that has a stronger effect on bacterial communities than different fertilizer regimes can be the sampling location and soil pH [43,44], and sampling time [45].

Summarizing the above, we can draw the following conclusions. For inorganic fertilizers, negative impact on soil bacterial diversity or no significant impact are more often reported. However, a number of studies have shown an increase in the diversity of soil microorganisms, especially with a balanced application of N, P and K. The effect of inorganic fertilizers can be modulated by other factors—the type of soil, cover vegetation, as well as the type of fertilizers themselves. The introduction of organic fertilizers, in particular, manure, has a more favorable effect on the diversity of soil microorganisms. This may be due to the activation of taxa, which are few in number in unfertilized soils, or to the introduction of exogenous microorganisms. However, it is important to maintain a balance, as over-application of organic matter contributes to a decrease in soil bacterial diversity and plant productivity. In a number of cases, the absence of a significant effect of organic fertilizers on soil diversity was noted, apparently due to the presence of other factors that have a stronger effect. Combining organic and inorganic fertilizers seems to be the most reasonable fertilization practice to maintain the diversity of the soil microbiome and yields. Interestingly, in earlier works, the absence of the fertilizers’ effect on the bacterial community of soils was more often reported. This may be due to the lower resolution of the methods used and the ability to consider the response of only large taxa. The development of molecular techniques, especially high-throughput sequencing, allows us to study changes in composition and diversity at the lowest taxonomic levels in more detail and to look at the influence of various factors, including cultural practices, on soil bacteria in a new way.

### 3. Tillage/No-Tillage Influence on the Bacteriocenosis of Agricultural Soils

#### 3.1. Influence of the Plowing Method on the Bacterial Community of Soils

Tillage has been an important agricultural practice for many years. However, soil damage during tillage is also a major factor in soil loss, because tillage destroys soil aggregates, buries residues and accelerates microbial activity and decomposition of plant residues [46]. In addition, tillage can significantly change the composition and diversity of soil microbial communities [47]. To avoid a compromise between soil loss due to plowing and moisture retention due to the destruction of soil capillaries, methods that are alternative to traditional disking are proposed [38]. No-till, minimal tillage, chisel plowing are examples of alternative soil preparation methods that contribute to less soil damage compared to traditional tillage [48]. Table 2 summarizes the study’s results of the impact of tillage on the bacterial community of soils.



**Table 2.** Influence of tillage/no tillage on the bacterial community of agricultural soils.

| Location                   | Soil Type   | Tillage System   | Duration | Bacterial Community Response   | References |
|----------------------------|---|--|----------|--|------------|
| Brittany, France           | Luvic Cambisol, Cambisol                                | Conventional tillage (plowing),<br>Minimum tillage (scraping the surface)  | 3 years  | Conventional tillage—increase in $\beta$ -diversity.<br>Predominance of Acidobacteria, Actinobacteria, Chloroflexi and Nitrospirae.<br>Minimum tillage—increase in $\alpha$ -diversity, functional diversity. Predominance of Proteobacteria, Bacteroidetes and Verrucomicrobia.   | [49]       |
| Sergipe State, Brazil      | Fine loamy kaolinitic isohyperthermic Typic Kandiudalfs | Conventional tillage,<br>Chisel plowing, no till   | 9 years  | Conventional tillage—the composition of microbiocenosis is closest to the fallow.<br>No till—the composition of microbiocenosis is closer to fallow than chisel plowing.   | [50]       |
| China                      | Brown loamy soil  | Deep tillage and straw returning,<br>Deep tillage and no straw returning,<br>Rotary tillage and straw returning,<br>Rotary tillage and no straw returning,<br>No tillage and straw returning,<br>No tillage and no straw returning | 1 year   | All tillage methods had no effect on the soil community structure at the phylum level.<br>Straw return increases bacterial $\alpha$ -diversity.  | [51]       |
| Bernburg, Germany          | Loess chernozem over limestone                          | Conventional mouldboard plow tillage,<br>Conservation cultivator tillage   | 23 years | Mouldboard plow tillage—increase in acidobacterial order Gp4 and alphaproteobacterial genus <i>Sphingomonas</i> .<br>At the phyla level—no difference between treatments.<br>Cultivator tillage—increase in the number of genera belonging to Alphaproteobacteria ( <i>Amaricoccus</i> , <i>Chelatococcus</i> , <i>Microvirga</i> ) and Actinobacteria ( <i>Gaiella</i> , <i>Ilumatobacter</i> , <i>Janibacter</i> , <i>Rubrobacter</i> ). | [16]       |
| Shaanxi, China             | Eum-Orthrosols (Chinese soil taxonomy)                  | Conservation tillage (chisel plow and zero tillage), Conventional tillage (plow tillage)   | 7 years  | All methods had no significant effect on the $\alpha$ -diversity of the soil community. In the rhizosphere soil, the relative abundance of Actinobacteria, Alphaproteobacteria, Bacteroidetes and Betaproteobacteria increased. Significant phylogenetic differences between the bacteria of the rhizosphere and the mound are shown.  | [52]       |
| Shaanxi, China             | Eum-Orthrosols (Chinese soil taxonomy)                  | Conservation tillage (chisel plow and zero tillage),<br>Conventional tillage (plow tillage)  | 5 years  | Conservation tillage—a more diverse community. Increase in the abundance of beneficial species of functional bacteria. High relative abundance of Firmicutes (especially <i>Bacillus</i> ).<br>Conventional tillage—abundance of Actinobacteria, Acidobacteria, Alphaproteobacteria, Betaproteobacteria and Chloroflexi.   | [53]       |
| Southern Pampas, Argentina | Typic Argiudolls and Petrocalcic Paleudols              | No tillage (NT),<br>Conventional tillage (CT)  | 34 years | The tillage system influenced the taxonomic composition. CT increased the number of Acidobacteria, Gemmatimonadetes, candidate division TM7 and class Gammaproteobacteria.<br>NT—increased the number of Nitrospirae, candidate division WS3 and Deltaproteobacteria.  | [4]        |
| Warwick, QLD Australia     | Self-mulching, black Vertisol                           | No tillage (NT),<br>Conventional tillage (CT),<br>Single strategic tillage event   | 44 years | The tillage system (NT or CT) affected the taxonomic composition of the bacterial community and did not affect $\alpha$ -diversity.<br>A single treatment did not have a significant effect on the bacterial community.  | [54]       |

Table 2. Cont.

| Location                               | Soil Type  | Tillage System   | Duration | Bacterial Community Response  | References |
|--|--|--|----------|---|------------|
| Heilongjiang Province, Chi             | Typical Mollisol   | No tillage (NT),<br>Conventional tillage (CT)  | 15 years | NT—increase in $\alpha$ -diversity at 0–5 cm of soil depth compared to the depth of 20 cm; change in the composition of the bacterial community (increase in Proteobacteria, decrease in Actinobacteria and Acidobacteria).<br>CT—no difference in diversity between 0–5 cm and 20 cm depth.<br>No noticeable difference in topsoil diversity (0–5 cm) between NT and CT. | [3]        |
| Loess Plateau (Shanxi Province, China) | Silt loam (Chromic Cambisol)                                 | No tillage (NT),<br>Conventional tillage (CT)  | 22 years | NT—increase in $\alpha$ -diversity and species richness, abundance increase in the genera <i>Sphingomonas</i> and <i>Pseudomonas</i> , decrease in the abundance of Acidobacteria.  | [55]       |
| Jilin Province, China                  | Mollisol (USDA) with a clay loam texture.                    | Integrated agricultural practice (IP),<br>Conventional practice (CP)   | 12 years | IP—increase in the richness and diversity of the bacterial community, increase in the relative abundance of Actinobacteria, Gemmatimonadetes, Verrucomicrobia, decrease in the number of Bacteroidetes, Firmicutes.   | [56]       |
| Planaltina, Federal District, Brazil   | Clayey Typic Haplustox                                       | No tillage (NT),<br>Conventional tillage (CT)  | 23 years | CT—more taxonomic sequences and reduced functional profiles.<br>NT and CT—predominance of Proteobacteria, Actinobacteria, Bacteroidetes, Firmicutes phyla.  | [57]       |
| Gembloux, Belgium                      | Silt loam inherited from the loess deposit (Cutanic Luvisol) | Conventional tillage with residue removal (CT/R−),<br>Conventional tillage with residue retention (CT/R+),<br>Reduced tillage with residue retention (RT/R+),<br>Reduced tillage with residue removal (RT/R−). | 6 years  | Conventional tillage—higher bacterial richness and diversity compared to reduced tillage.<br>Crop residue treatment methods did not affect microbial communities.   | [58]       |

Legrand et al. [49] showed that species richness and uniformity were significantly higher in the fields with minimal tillage compared to conventional farming, despite the fact that the basic microbiota were the same in the fields with the two methods used. The functional diversity of bacterial communities was also significantly higher in the fields with minimal tillage, especially in those involved in the nitrogen cycle (denitrification, respiration). However,  $\beta$ -diversity was higher in conventional farming systems compared to fields with minimal tillage. The positive effect of conservation tillage (zero plow and chisel plow) on the soil microbiome compared with the traditional one was also noted by Wang et al. [53] for drylands of China. Lopes et al. [50] showed that the composition of microbial communities in traditional tillage (lower soil quality) was closest to fallow (higher soil quality) among all tillage systems, despite the fact that all farming methods were closer to each other than fallow. However, among conservation tillage methods, zero till was closer to fallow than chisel plowing. Presumably, tillage systems affected the structure of the microbial community as a result of the topsoil inversion. The positive effect of the integrated management system (rotary tillage + straw return) on the microbiome was found. The soil in this case had the highest bacterial diversity and the lowest ratio of G+/G− bacteria. However, despite differences in tillage methods or return of corn stover, the structure of the soil community at the phylum level was similar. Significant differences were found in species diversity indices between groups with or without straw return [51]. When comparing processing with a dump plow and a cultivator, an effect on the relative number of dominant genera was observed. Cultivation (i.e., reduced) treatment resulted in an increase in the number of genera belonging mainly to Alphaproteobacteria and Actinobacteria regardless of the previous culture. Perhaps this was due to the fact that actinobacteria are more sensitive to physical disturbances due to their mycelial growth. Regardless of the previous crop, conventional plowing resulted in an enrichment of the acidobacterial order GP4 and the alphaproteobacterial genus *Sphingomonas* [16]. It is noted that in the absence of a difference in  $\alpha$ -diversity between soils under different management methods (chisel plow, zero till, plowing), significant differences can be observed between the rhizosphere and the soil bulk with each tillage technique [52].

### 3.2. Effect of No Tillage on Soil Bacterial Community

Another conservation agriculture method is no-till technology. It has the advantage of reducing soil erosion, conserving water in the soil and lowering fuel costs [59]. In no-till systems, seeds are sown directly into the soil with relatively little intervention, and crop residues are left to decompose on the surface. This leads to an improvement in the physical, chemical and biological properties of the soil and an increase in the productivity of agricultural crops [60,61]. However, the use of this technology is often accompanied by negative effects—soil compaction, strong stratification of a number of characteristics (C, N content) in depth and the formation of an acidified surface layer upon application of nitrogen fertilizers [59]. In addition, in the absence of plowing, there is a need to apply large amounts of pesticides and herbicides to control weeds. This raises the question of how no-till technology can affect the soil microbial community.

It has been shown that there are significant differences in the structure and taxonomic composition of the microbiome between soils under conventional and no-till systems [4,54]. The lack of soil cultivation in northeastern China for 15 years significantly increased  $\alpha$ -diversity (Chao 1 and Shannon indices) by 0–5 cm and changed the composition of the bacterial community, which was due to changes in the physicochemical properties (bulk density (BD) of the soil, pH and soil organic carbon). Proteobacteria, Actinobacteria, Acidobacteria, Chloroflexi and Gemmatimonadetes were the most abundant phyla in all the samples [3]. A 22-year no-till experiment in the Loess Plateau, China also showed a significant increase in bacterial  $\alpha$ -diversity. Bacterial communities varied significantly with different soil treatments, and no-till soil contained a relatively higher number of dominant *Sphingomonas* and *Pseudomonas* genera and a lower number of Acidobacteria than conventional cultivation soil [55]. Combining no-till with stubble conservation increases the

amount of bacterial OTUs [9]. The transition to zero tillage as part of integrated agricultural practice (changing row spacing during sowing, returning all plant residues) in the mollisol zone (China) has led to an increase in bacterial richness and diversity. Integrated agricultural practices have changed the physicochemical properties of the soil and, as a result, altered the structure and diversity of the microbial community [56]. However, it should be borne in mind that taxonomic diversity is not necessarily associated with functional diversity, as shown by Souza et al. [57] for the Cerrado biome, Brazil. With traditional tillage, an increase in the number of taxonomic microbial sequences and a decrease in functional profiles were observed, which, according to the author, indicates the strategy of trying to maintain soil functioning at the expense of taxa is not the most effective for some functions [57]. Here, during traditional tillage, an increase in the number of taxonomic sequences and a decrease in functional profiles were observed, which, in the author's opinion, indicates the strategy of trying to maintain soil functioning at the expense of taxa is not the most effective for some functions. The no-till technology leads to an increase in the amount of anaerobic cellulolytics and nitrogen fixers, as well as aerobic diazotrophs and amylolytics, while traditional tillage increases the amount of cultivated aerobic ammonifiers, denitrifiers, aerobic cellulolytics, actinomycetes and micromycetes [62]. In a number of cases, it has been shown that sampling time, rather than soil cultivation, was the main factor influencing the structure of the bacterial community [63,64]. In the Belgian silty loam, reduced tillage did not have a beneficial effect on the microbiome (richness and diversity were higher with conventional plowing) [58]. The depth of soil sampling had the greatest influence. This indicates that, despite all the advantages of this technology, it is not suitable for all soils. In general, in the long term, the no-till system is quite stable, which is confirmed by the insignificant effect on bacterial diversity of a single tillage after 44 years of no plowing [54].

Thus, reduced tillage and no-till methods should become an important part of sustainable agricultural development. Despite a number of difficulties of no till (the need for special equipment for sowing in untreated soil, the control of weeds and fungal pathogens, a delayed manifestation of a positive effect), its use is accompanied by an improvement in soil structure (especially in arid regions), an increase in soil biodiversity, conservation of carbon and other elements.

#### **4. Effect of Organic/Conventional Farming System on Soil Bacterial Community**

Organic farming systems are becoming more widespread. The main activities of this system are organic fertilization, straw retention, crop rotation and physical and biological means to prevent crop diseases and pests [65]. Evidence is accumulating on how soil cultivation systems affect the soil microbiome's composition and structure. Table 3 summarizes the results of studies tackling the impact of organic/conventional farming systems on soil bacterial community.

**Table 3.** Influence of the organic/conventional system on the bacterial community of agricultural soils.

| Location                            | Soil Type                                  | Farming System  | Duration   | Bacterial Community Response   | References |
|-------------------------------------|--|---|------------|--|------------|
| Western Cape Province, South Africa | Information not provided                   | Conventional system,<br>Organic system  | 4 years    | Both farming systems have the same $\alpha$ -diversity but different $\beta$ -diversity.<br>Conventional system—predominance of bacterial genera involved in the nitrogen cycle.<br>Organic system—predominance of bacterial genera involved in the carbon cycle.  | [66]       |
| Zhejiang Province, China            | Ultisol                                    | Conventional system,<br>Organic system  | 0–15 years | Both farming systems had the same diversity and richness of bacterial communities but different structure.   | [67]       |
| Near Zürich, Switzerland            | Calcareous Cambisol                        | Traditional and organic management types with different tillage intensity (no tillage, reduced tillage and intensive tillage) | 4 years    | Farming systems had little effect on the $\alpha$ -diversity of the soil bacterial community but affected its structure.<br>Organic farming—higher numbers of Firmicutes.  | [12]       |
| Chongming Island, Shanghai, China   | Sandy loam                                 | Organic farming and improved conventional farming   | 11 years   | Farming systems had little effect on the $\alpha$ -diversity of soil bacterial community but affected its structure.<br>Organic farming—increase in the number of taxa involved in the cycle of nitrogen, sulfur, phosphorus and carbon ( <i>Nodosilinea</i> , <i>Nitrospira</i> , <i>LCP-6</i> , <i>HB118</i> , <i>Lyngbya</i> , <i>GOUTA19</i> , <i>Mesorhizobium</i> , <i>Sandaracinobacter</i> , <i>Syntrophobacter</i> and <i>Sphingosinicella</i> ).<br>Conventional farming—increase in the number of taxa involved in the nitrogen cycle ( <i>Ardenscatena</i> , <i>KD1-23</i> , <i>Iamia</i> , <i>Nitrosovibrio</i> and <i>Devosia</i> ). | [65]       |
| Ostrobothnia, western Finland       | Fine sand soil                             | Organic and conventional systems with four rotations  | 18 years   | Organic rotations—higher bacterial richness compared to traditional rotations (in autumn), more diverse bacterial community.   | [68]       |
| Mikkeli, Finland                    | Coarser fine sand (sandy Aquic Haplocryod) | Conventional system,<br>organic system  | 14 years   | Both systems—minor differences between bacterial communities at the phylum level. The traditional system has more bacteria of the <i>Pseudomonas</i> genus compared to the organic system. No notable differences in $\alpha$ -diversity.  | [69]       |

When comparing organic and traditional farming systems, it was found that the soil bacterial community structure is distributed depending on the cultivation system. In traditional systems, nitrogen cycling species (*Bacillus*, *Niastella*, *Kribbella* and *Beijerinckia*) predominate, while in organic systems, the carbon cycle is dominated by *Dokdonella*, *Caulobacter*, *Mathylibium*, *Pedobacter*, *Cellulomonas*, *Chthoniobacter* and *Sorangium*. Both farming systems had the same  $\alpha$ -variety but different  $\beta$ -variety [66]. On the example of tea plantation soils in eastern China with traditional and organic management, it was shown that the diversity and richness of bacterial communities was the same in both cases, but the structure of soil bacterial communities was significantly changed depending on the type of management. Surprisingly, organic management has weakened the interconnection between soil bacteria taxa in tea plantations, suggesting greater stability of microbial associations under traditional management practices [67]. Hartman et al. [12] and Zhang et al. [65] also showed that soil microbial communities with traditional and organic methods of cultivation were primarily structured by soil cultivation, and the positive effect of organic farming on soil systems was noted. In the boreal arable soils, the farming system caused a clear shift in the composition of the microbial community. Representatives of bacteria were less diverse in the traditional farming system of grain rotation in comparison with the corresponding organic system [68].

However, the organic farming system does not always have a significant impact on the soil microbiome. This way, after 14 years of exposure to traditional and organic farming systems, the soils did not differ much in the microbiome composition [69]. The cropping system had only a slight impact on microbial biodiversity, affecting the microbiomes composition mainly at the genus level. It has been shown that both traditional and organic farming systems can support equally diverse microbial communities. A similar conclusion was reached by Chen et al. [24], finding no difference between conventional and organic farming per se. Neither soil disturbance, nor the use of chemical fertilizers, nor chemical plant protection measures had an impact on the soil microbial communities. The authors showed that the choice of farming method determines the actual structure of the microbial community, but biodiversity as a whole is almost independent of the farming system over many years. This may be due to the general resistance of soil microorganisms to various stresses.

Thus, organic farming has a number of environmental benefits through reduced agrochemical input and less soil disturbance. However, from the point of view of soil microbial communities, there are conflicting results, indicating both the positive impact of organic management methods on microbial biomass and diversity, and the absence of significant differences between organic and traditional agriculture, or even greater stability of microbial communities in traditional systems. Nevertheless, more and more data are accumulating on the positive impact of organic agriculture on soil biodiversity; therefore, in the long term, these management methods are a good alternative to traditional agriculture.

## 5. The Influence of Crop Rotation and Cover Crops on Agricultural Soils Bacteriogenesis

### 5.1. The Effect of Crop Rotation on the Bacterial Community of the Soil

Crop rotation is a sequential cultivation of different types of crops. It is an alternative strategy for maintaining soil quality compared to monoculture cropping patterns. The advantages of this strategy are improving the physical characteristics of the soil, increasing yields, reducing the need for fertilizers, reducing the accumulation of pathogens [70]. To a large extent, these effects are mediated by the soil's microbial community. This way, soil microbes are often antagonists of pathogens and, due to this, are able to suppress diseases of agricultural plants [71]. Microbial communities make nutrients available to plants by decomposing plant residues, solubilizing, producing siderophores [72]. Crops, in turn, affect soil microbiota through root exudates, plant debris and symbiotic associations, or directly altering the supply of carbon (C) to the soil, nutrient availability and soil structure (e.g., texture and aggregate distribution) [73]. Legumes are considered a preferred alternative to alternation with other types of crops, due to their high nitrogen content and the ability to bring nitrogen into the ecosystem during symbiotic nitrogen fixation [74].



Microbial communities have been shown to be more sensitive to summer cover crop rotations compared to soil cultivation systems [75].

Various studies have investigated the influence of crop rotation and cover crops on agricultural soils' microbiocenosis (Table 4). A significant effect of crop rotation (maize monocultures versus maize and wheat rotations) was confirmed by Romero-Salas et al. [64].

**Table 4.** Impact of crop rotation/cover crops on the bacterial community of agricultural soils.

| Location                                 | Soil Type                                   | Crop Rotation/<br>Cover Crops   | Duration  | Microbial Community Response  | References |
|--|---|---|---|---|------------|
| Texcoco, State of Mexico, Central Mexico | Haplic Phaeozem (Calyic)                    | Corn monoculture, corn/wheat rotation   | 26 years  | Crop rotation had a very significant impact on the structure of the bacterial community.  | [64]       |
| WI, USA                                  | Silt loam soil                              | Crop rotation—(continuous corn, continuous soybean, annual soy/corn rotation),<br>Cover crops—cereal rye and oats.  | Crop rotation—16 years,<br>Cover crops—1 season | Crop rotation affected the structure of the bacterial community and did not affect the richness and diversity.<br>Continuous corn—an increased number of the phyla Actinobacteria, Bacteroidetes, Planctomycetes in autumn; Acidobacteria, Actinobacteria, Bacteroidetes, Chloroflexi, Gemmatimonadetes, Patescibacteria, Planctomycetes, Proteobacteria, Verrucomicrobia in spring.<br>Continuous soybean—increased number of the phyla Acidobacteria, Bacteroidetes, Gemmatimonadetes, Proteobacteria, Verrucomicrobia in autumn; Acidobacteria, Bacteroidetes, Chloroflexi, Cyanobacteria, Gemmatimonadetes, Nitrospirae, Patescibacteria, Planctomycetes, Proteobacteria, Verrucomicrobia in spring.<br>Cover cultures did not affect the structure of the bacterial community. | [72]       |
| Alberta, Canada                          | Dark Brown Chernozem (Haplic Kastanozem)    | Three wheat rotations—continuous wheat (W), fallow–wheat (FW) and fallow–wheat–wheat (FWW)  | 100 years                                       | W—decrease in $\alpha$ -diversity of the bacterial community, change in its structure, increase in the number of Actinobacteria and Bacteroidetes, decrease in the number of Acidobacteria.   | [76]       |
| Sichuan Province, China                  | Percogenic paddy soils (Stagnic Anthrosols) | Crop rotations—rice–wheat (RW), rice–vegetable for 10 years (RV10), rice–vegetable for 20 years (RV20)  | 0–20 years                                      | RV—increase in $\alpha$ -diversity of bacteria and decrease in $\alpha$ -diversity of archaea; decrease in $\beta$ -diversity, decrease in the abundance of <i>Geobacter</i> spp., <i>Candidatus_Nitrosotalea</i> spp. and increase in the abundance of <i>Streptomyces</i> spp. compared to RW.  | [77]       |
| Ontario, Canada                          | Silty loam (Gray Brown Luvisol)             | Crop rotations—corn–corn–soybean–soybean (CCSS); corn–corn–soybean–winter wheat + red clover (CCSWrc)   | 35 years  | The $\alpha$ -diversity, composition and uniformity of the soil bacterial community did not differ between CCSS and CCSWrc. CCSWrc—increased number of bacteria involved in the nitrogen cycle (nitrifiers, denitrifiers).  | [78]       |
| Saskatchewan, Canada                     | Black Chernozem soil                        | Cover crop ( <i>Medicago lupulina</i> L.),<br>Crop rotation—flax ( <i>Linum usitatissimum</i> L.)–oats ( <i>Avena sativa</i> L.)–winter wheat ( <i>Sativum aestivum</i> L.) | 8 years   | <i>Medicago lupulina</i> L.—increase in bacterial $\alpha$ -diversity of soils.<br>Increase in the number of Proteobacteria, decrease in the number of Actinobacteria and Firmicutes in bulk soil, Acidobacteria in the rhizosphere.<br>Influence on the bacterial community structure—Proteobacteria and Bacteroidetes were associated with <i>Medicago lupulina</i> L.<br>Crop rotation—no effect on variety.<br>The number of Gemmatimonadetes in bulk soil is higher under wheat than under oats or flax.   | [34]       |

Table 4. Cont.

| Location                   | Soil Type  | Crop Rotation/<br>Cover Crops  | Duration | Microbial Community Response   | References |
|----------------------------|--|--|----------|--|------------|
| California, USA            | Chualar loamy sand<br>(fine loamy, mixed,<br>thermic typic<br>Argixerol) | Cover crops—<br>Legume-rye,<br>Mustard, Rye  | 6 years  | All cover crops affected the composition and size of the soil microbial community. There was an increase in the number of bacteria, especially Gram+. Increasing the frequency of cover crops has changed the relative abundance of Bacteroidetes and Deinococcus-Thermus phyla, <i>Flavobacterium</i> , <i>Nocardiodetes</i> genera.  | [79]       |
| State of São Paulo, Brazil | Typic Rhodudalf  | Cover crops—pearl millet ( <i>Pennisetum glaucum</i> ), grain sorghum ( <i>Sorghum bicolor</i> ) and Sunn hemp ( <i>Crotalaria juncea</i> ). | 15 years | Minor impact on variety. Pearl millet—increased abundance of Actinobacteria, Proteobacteria and Chloroflexi compared to fallow, Actinoplanes, Nocardioidea and Micromonospora compared to sorghum and Sunn hemp, the most complex bacterial community network. Grain sorghum—increased abundance of Proteobacteria and Patescibacteria compared to fallow, least complex bacterial community network. Sunn hemp—increased abundance of Chloroflexi and Latescibacteria compared to fallow. | [5]        |

The influence of crop rotation on the bacterial community was apparently associated with the rhizosphere of plants and/or the difference in the composition of crop residues, that is, stubble and roots left in the field. Chamberlain et al. [72] found that crop rotation affects the structure of bacterial communities in the bulk of the soil, resulting in distinct communities associated with continuously cultivated crops. At the same time, the richness and diversity did not differ depending on crop rotations—the Shannon index did not differ for the systems of continuous cultivation or crop rotation of corn and soybeans. With continuous long-term cultivation of wheat, the  $\alpha$ -diversity of soil bacteria was lower than with crop rotation and decreased with fertilization [76]. The number of Actinobacteria and Bacteroidetes was higher, and of Acidobacteria—lower than at crop rotation. The  $\beta$ -diversity analysis showed that the structure of the bacterial community during continuous cultivation of wheat with fertilization differed from the structures in other treatment options. In the 10-year rice–vegetables rotation (RV), bacterial  $\alpha$ -diversity increased compared to the rice–wheat rotation (RW), while  $\alpha$ -diversity of archaea decreased, which, presumably, could be the result of fertilization [77].

The  $\beta$ -diversity of microbes, on the contrary, significantly decreased after the transition from the rice–wheat rotation to rice–vegetables rotation, which led to a decrease in the heterogeneity in the structure of the community (composition and abundance) along the soil profiles of 0–40 cm. In addition, the transition from RW to RV markedly increased the accumulation of  $\text{NO}_3^-$  in the soil. Linton et al. [78] studied the impact of 35 years of crop diversification on the formation of diversity and community size and the activity of nitrifiers and denitrifiers and  $\text{N}_2\text{O}$  emissions after nitrogen fertilization of corn. Simple (corn–corn–soybean–soybean, CCSS) and varied (corn–corn–soybean–winter wheat + red clover, CCSWrc) crop rotations were used. The overall bacterial diversity did not differ between simple and varied crop rotations; however, the number of microbial pathways leading to soil  $\text{N}_2\text{O}$  release, ammonia oxidants and denitrifiers was increased in soils with a more varied crop history.

### 5.2. Influence of Cover Crops on Soil Bacterial Community

Cover crop production involves growing crops to protect and enrich the soil, but not for harvesting. Cover crops are usually grown between harvest and sowing of the

main crop [72]. This technology has been reported to prevent soil erosion and nutrient leaching, to facilitate weed control and carbon sequestration [80]. Winter cover crops containing legumes have a protective effect against the harmful influence of chemical nitrogen fertilization on soil biodiversity and nutrient cycling, as they can maintain soil carbon and nitrogen concentrations [35]. Cover crops affect soil through accumulation of organic residues on the soil surface, as well as through root exudates and decomposition of dead microorganisms and roots. Accordingly, different cover crops, due to differences in architecture and growth of roots, quality of rhizoexudates, etc., can have different effects on the number, structure and diversity of the soil bacterial community [5]. For example, when growing alfalfa, the number of proteobacteria increased, and the number of actinobacteria and firmicutes in the bulk of the soil and acidobacteria in the rhizosphere decreased [34]. In addition, alfalfa increased the Shannon and Simpson diversity indices of soil microbial communities. Different types of cover crops (legumes–rye, rye, mustard) in the organic vegetable growing system had different effects on the relative abundance of soil bacterial phyla [79]. For example, the abundance of the phylum Gemmatimonadetes increased with rye but decreased with mustard. After 6 years, pseudomonads content tended to decline with mustard cover crops but increased in the legume–rye system and the rye-only system. The type and frequency of cover crops changed the relative abundance of some bacteria, such as *Pseudomonas* (including species that are antagonistic to pathogens), and rhizobacteria that promote plant growth. Pearl millet (*Pennisetum glaucum*) as a cover crop has contributed to an increase in Actinobacteria, Proteobacteria and Chloroflexi in tropical Brazilian cropping systems; grain sorghum (*Sorghum bicolor*)—an increase in Proteobacteria and Patescibacteria; and Sunn hemp (*Crotalaria juncea*)—an increase *Chloroflexi* and *Latescibacteria*. The complexity of the bacterial community was highest for millet, and less for fallow, hemp and sorghum. At the same time, only an insignificant effect on the bacterial diversity index was observed, although cover crops changed the bacterial community structure [5]. An important factor affecting the structure of the soil microbiome is decomposition time of cover crops' residues [81]. The greatest  $\alpha$ -diversity and bacteria richness (Shannon and Chao1 indices) were observed in the middle of cover crops' decomposition. Microbial communities' dispersion, on the contrary, decreases over time, i.e., a community becomes more homogeneous. However, it is not always possible to detect the effect of cover crops, especially in the short term. For example, cover crops' inclusion in the crop rotation system did not lead to significant changes in the main soil bacterial community after one season. This result was likely due to the limited growth of cover crops in the first year of rooting and the limited amount of time the soil communities had to respond to this change [72].

In general, the use of crop rotation and cover crops in agricultural practice is a promising agricultural method that improves soil microbial indicators and soil quality. Due to the fact that the impact of these practices is often influenced by other factors, further research is needed on the impact of cover crops and crop rotations on soil microbial communities.

## 6. Conclusions

It is well known that soil bacteria play a critical role in maintaining soil health. The number of studies devoted to research of the agrotechnical methods' influence on soil microbiocenosis has been growing exponentially in recent years. However, it is still difficult to unambiguously identify the influence of each individual factor on the structure and diversity of the soil bacterial community, as well as to directly relate these parameters to soil fertility and crop productivity. This is due to both the wide variety of soils and climatic factors, and the significant variability of the parameters presented in the results of the work. The types of studied soils, agrotechnical methods, time and depth of sampling, and the duration of field experiments differ. For example, there may be a fundamental difference between the short- and long-term effects of organic and inorganic fertilizers on soil microbial communities. Despite this, there are general trends that indicate the negative impact of unbalanced fertilization and the long-term positive impact of the absence of

plowing on soil health. There are controversial results so far regarding the impact of organic farming systems on the soil microbiome, and more research is needed.

There is a significant gap between theoretical studies of soil health and practical agriculture. Financial investment in the productivity of agricultural plants is still several times higher than that in soil fertility. However, it is encouraging that more and more farmers are ready to use environmentally friendly agricultural practices that ensure the safety and biodiversity of soils, despite the lack of immediate effect. In addition, even traditional agricultural practices are often modified to take care of the soil health, its microbiome and the environment in general. The nearest prospect in the study of the soil bacterial community should be the development of omics technologies (metatranscriptomics, metaproteomics, metabolomics, interactomics), with the help of which it will be possible to link the diversity of bacteria to their functions, to study the mechanisms of bacterial response to the impact of various factors. Ongoing research of the agricultural impact on the soil microbiome is necessary to develop optimal methods for maintaining the productivity of agroecosystems that combine economic efficiency and environmental care. This paper recaps current knowledge about the impact of agricultural practices on the soil bacterial community of agricultural soils in order to identify gaps and priority areas for further research.

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