Response of soil bacterial community to different fertilization patterns in young oasis farmland

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Abstract

Fertilization in farming systems should not only optimize crop yields and soil fertilizer but also maintain soil biodiversity and functions. In young oasis farmland, knowledge regarding soil bacteria respond to fertilization strategies is very limited. We performed a 12-year field experiment to evaluated the effects of organic manure, mineral fertilizer, and their combination on a typical young oasis farmland in Northwest China, and quantified soil bacterial diversity and composition by using high-throughput DNA sequencing on the Illumina MiSeq platform. Our results showed that maize yield was highest in the pure organic manure treatment and significantly higher than that of the low mineral fertilizer treatment. Organic manure application significantly increased soil nutrient content, while the organic manure level also positively influenced soil nutrient content. Soil bacterial diversity was more sensitive to the application of organic manure than mineral fertilizer. The PERMANOVA results confirmed that bacterial community composition changed along an organic manure level gradient, which was not observed for mineral fertilizer. Organic manure application promoted the abundance of the copiotrophic group, while the environment resistant group were abundant in the only mineral fertilizer treatments. The present study indicated the critical role of organic manure application for increasing crop yield, soil fertility, and soil bacterial diversity while optimizing the community composition of soil bacteria, emphasizing the contribution and importance of organic manure application to overall soil health.

Key words: Bacterial diversity, Crop yield, Mineral fertilizer, Organic manure, Sandy texture

1. Introduction

Fertilization is an important agricultural management strategy to increase crop productivity and has been applied globally for decades (Hu et al., 2017). About 40% of the worldwide supply of dietary protein in the mid-1990s originated from mineral nitrogen (N) fertilization (Alley, 2004). Optimized fertilization in agriculture has been found to greatly increase crop yield and soil fertility, but fertilization strategies in practice often lead to low nutrient use efficiency and environmental problems, such as soil degradation, eutrophication, nutrient leaching into groundwater, and greenhouse gas emission (Zhang et al., 2011). Numerous studies have revealed the fertilization influences on crop productivity and environment issues (Xia et al., 2017), but only a few have attempted to synthesize this information on a global scale because of the large variation present among environmental factors, such as distinctive climate, soil, and crop conditions, which has often led to contradictory results regarding various farming systems (Seufert et al., 2012).

Soil microorganisms in agroecosystems play important roles in organic matter decomposition, nutrient cycling, and bioremediation (Bei et al., 2018). However, the intensive agronomic activities of modern agricultural practices heavily impact microbial communities (Babin et al., 2019). Many studies have focused on how fertilization practices in agriculture influence soil microbial diversity and community structure (Xun et al., 2016; Hu et al., 2017). For example, Hartmann et al., (2015) reported that the application of organic fertilizer shifted the structure of the soil microbiota community by increasing richness, decreasing evenness, and reducing dispersion when compared to that of mineral fertilizer application. Bei et al., (2018) also suggested that organic fertilizer can have a greater influence on the general structure of the soil microbial community compared to that of mineral fertilizers in the short term. The effects of agricultural management on the soil microbiome are complex and diverse, and retrieving universally valid conclusions of fertilization practices is difficult (Hartmann et al., 2015). This information is ultimately necessary for evaluating the response of soil microbes to fertilization practices in various farmland systems, yet it is still lacking for specific farmland ecosystems, such as young farmlands in desert oases.

Oases, which coexist with deserts, are the main locations for human settlements and agricultural production in arid and semi-arid regions (Wang et al., 2020). Over the past several decades, rapid agricultural development has resulted in frequent desert to farmland transitions in the desert oasis regions of Northwest China (Zhang et al., 2018). Recently transitioned farmlands, or young oasis farmland, have been distributed along the edges of oases and have relatively short cultivation times. Given that young oasis farmlands typically have soil with a sandy texture and poor nutrients content, high mineral fertilizer input have usually been employed to secure crop yields with serious associated environmental risks, such as groundwater nitrogen
contamination (Su et al., 2010). Effective fertilization strategies are essential for improving the management of nutrients in these soils while reducing the associated environmental risks.

A long-term field experiment with different fertilization treatments was conducted to evaluate the effectiveness of fertilization strategies in a typical young oasis farmland. Our previous studies revealed that fertilization strategies significantly influenced soil nutrient content and crop yields in this region (Yang et al., 2015). However, whether changes in soil fertility affected the soil microbial community remained unknown. Thus, the main objective of this study was to elucidate the effects of fertilization strategies on the soil microbial community of young oasis farmland and thereby advance our understanding of how agricultural management strategies affect soil biological processes in this region.

A young oasis farmland ecosystem within the desert-oasis ecotone of Northwest China was selected for this study, and a 12-year field experiment with different fertilization treatments was performed. Bacterial diversity and community composition were analyzed by high throughput sequencing technologies. The experiment allowed us to determine whether different fertilization treatments affected the soil nutrient contents, crop yield, or bacterial community structure. We also aimed to identify the relationship between soil nutrients and the soil bacterial community. Specifically, we addressed the following hypotheses: 1) the soil bacterial community would respond differently to different fertilization strategies; 2) soil nutrients would constitute the main factor affecting the response of the soil bacterial community to different fertilization strategies.

2. Materials and Methods

2.1 Site descriptions and experimental design

The field experiment was conducted beginning in 2005 at the Linze Inland River Basin Research Station (39°21' N, 100°11’ E, elevation 1367 m) in Linze county, Gansu province, Northwest China. The region of the study site has a typical desert climate with cold winters and dry hot summers. The long-term mean annual precipitation is approximately 117 mm, and the mean annual temperature is 7.6°C (Yang et al., 2019). The soil in the region is classified as Aridic Ustipsamments and had the following properties in the top 0–20 cm layer prior to the start of the experiment: pH 8.9, 0.66 g kg⁻¹ total N (TN), 13.38 g kg⁻¹ soil organic matter (SOM), 65.8% sand, 20.1% silt, and 14.1% clay.

The experimental design was a randomized block design with nine fertilization treatments and three replicates (9 × 3 = 27 plots; plot size: 3.7 m × 3.7 m). The treatments included various combinations of different organic manure and mineral fertilization rates applied to crops. The organic manure was collected from composted domestic animal waste, and the fertilizer application details and nutrient analysis of the organic manure have been given in a previous paper (Yang et al., 2015). Considering that there was likely to be little impact on the soil bacterial community, two no-mineral K fertilizer treatments and two medium fertilizer treatments were excluded in the present study, and thus five treatments (15 plots) were selected to analyze soil bacterial diversity: (1) M, (2) C1, (3) C2, (4) CM1, (5) CM2. The M treatment represent pure manure treatment (30 t organic manure ha⁻¹), C1 and C2 represent 150-90-90 kg N-K₂O-P₂O₅ ha⁻¹ and 300-225-225 kg N-K₂O-P₂O₅ ha⁻¹ mineral fertilizer application rate for maize, respectively. The CM1 and CM2 represent 150-90-90 kg N-K₂O-P₂O₅ ha⁻¹ mineral fertilizer and 30 t organic manure ha⁻¹ and 300-225-225 kg N-K₂O-P₂O₅ ha⁻¹ and 15 t organic manure ha⁻¹ for maize, respectively. Detailed information regarding the fertilization, irrigation, and other agronomic practices employed in this study can be found in previous papers (Yang et al., 2015).

2.2 Soil sampling

Soil samples for soil nutrient and microbial analyses were taken from the 15 plots after the crop harvest in September 2018. In each sampling plot, three quadrats (1 m²) were randomly selected, and four soil cores from the 0–20 cm soil layer were collected from each quadrat and then thoroughly mixed. Thus, there were three soil samples from each plot and a total of 45 soil samples from the 15 plots. Each soil sample was separated into two subsamples in the laboratory. The first set of sub samples was stored at ~80°C for subsequent DNA analysis, while the second set of sub samples was further mixed (i.e., three samples from the same plot were mixed into one composite sample), air-dried, and passed through a 2-mm sieve for soil physical and chemical property analysis. In addition, two undisturbed core samples in each plot were collected by using a steel cylinder (volume 100 cm³) to determine the soil bulk density (BD, g cm⁻³).

2.3 Soil physical and chemical property analysis

For details regarding the methodology of soil physical and chemical property analysis, refer to the methods of Bao, (2010). The soil particle-size analysis followed the pipette method in a sedimentation cylinder using sodium hexametaphosphate as the dispersing agent. Soil organic matter (SOM, g kg⁻¹) was measured by Walkley-Black dichromate oxidation, and total nitrogen (TN, g kg⁻¹) was measured by the micro-Kjeldahl procedure. Available N (AN, g kg⁻¹) was determined by using the alkalizable diffusion method, while total phosphorus (TP) was determined with a spectrophotometer (UV-2450, Shimadzu Company, Kyoto, Japan) after H₂SO₄-HClO₄ digestion. Available P (AP) was determined by the Olsen method, and available potassium (AK) was determined with the colorimetric method with NH₄OAc extraction. Soil pH and electrical conductivity (EC, µS cm⁻¹) were measured in a soil-water suspension (1:1 and 1:5 soil-water ratio, respectively) using EC and pH meters (PC-5200, Alalis Company, Suzhou, China).

2.4 DNA extraction, PCR amplification and DNA sequencing

Total soil microbial DNA from each sample was extracted with the EZNA soil DNA Kit (Omega Bio-tek, Norcross, USA) by following the manufacturer’s protocols. The DNA extraction efficiency was checked by electrophoresis with raw DNA samples on 1% agarose gel. The concentration and purity of the raw DNA were then checked using a NanoDrop DN-2000 spectrophotometer (Thermo Scientific, Wilmington, USA).

An amplicon survey of the v3-v4 hypervariable regions of the bacterial 16S rRNA gene was implemented with primers 338F (5’-ACTCCTACGGGAGGCAGCAG-3’) and 806R...
Treatments were evaluated by a one-way analysis of variance of richness, Shannon diversity, and Simpson diversity indices.

2.5 Statistical analysis

Four alpha-diversity indices, i.e., the Sobs, Chao1 estimator of richness, Shannon diversity, and Simpson diversity indices were calculated. Significant differences among treatments were evaluated by a one-way analysis of variance (ANOVA) followed by a Tukey post-hoc HSD test. Bacterial community composition was visualized by non-metric multidimensional scaling (NMDS) based on a Bray-Curtis dissimilarity matrix. A permutational multivariate analysis of variance (PERMANOVA) was conducted to test the significance of Bray-Curtis dissimilarity. PERMANOVA was also used to examine the effects of fertilization on the composition of the soil bacterial community. A distance-based redundancy analysis (RDA) was used to examine the effects of soil parameters on the bacterial community. In order to eliminate the collinear relationship between the environmental factors, Variance Inflation Factor (VIF) analysis was used for variable selection. Variables with VIF values <10 were retained in the RDA analysis, while all other variables were eliminated. All statistical analyses were performed in the I-Sanger cloud platform (Sanger Information Technology Co., Ltd., Shanghai, China).

3. Results

3.1 Crop yield and soil properties

On average, the maize yield per treatment followed the order of M > CM2 > C2 > CM1 > C1, with a rate of increase of 23.1%, 12.7%, 11.7%, and 9.9%, respectively, compared to that of the lowest crop yield C1 treatment. The maize yield was significantly higher in the M treatment than in the C1 treatment (P < 0.05), but there were no significant differences in yield among the other four treatments (P > 0.05).

The soil chemical and physical properties in the 0–20 cm soil layer are listed in Table 1 and were strongly influenced by the fertilizer treatments (Table 1). The average SOM values in the M, C1, C2, CM1, and CM2 treatments were 23.6, 8.3, 9.1, 21.9, and 14.3 g kg⁻¹, respectively. The organic manure level had a significant effect on SOM, and SOM in the two high organic manure treatments (M and CM1) was significantly higher than that of the CM2 treatment, which contained no organic manure treatments (C1 and C2) (P < 0.01). TN ranged from 1.13 to 2.00 g kg⁻¹, with the maximum and minimum values observed in the M and C1 treatments, respectively. The maximum and minimum AN values were found in the M and C1 treatments–99.3 mg kg⁻¹ and 41.3 mg kg⁻¹, respectively. On average, TN and AN in the high

Table 1. Soil properties in top 20 cm layer in different fertilization treatments.

| Parameters | Treatments |
|------------|------------|
|            | M          | C1         | C2          | CM1         | CM2         |
| SOM (g kg⁻¹) | 23.6 ± 1.0 a | 8.3 ± 0.7 c  | 9.1 ± 0.3 c  | 21.9 ± 1.2 a | 14.3 ± 0.7 b |
| TN (g kg⁻¹)  | 2.00 ± 0.08 a | 1.13 ± 0.03 c | 1.15 ± 0.03 c | 1.93 ± 0.10 a | 1.54 ± 0.04 b |
| TP (g P₂O₅ kg⁻¹) | 1.40 ± 0.04 bc | 1.29 ± 0.06 c | 2.17 ± 0.15 a | 1.68 ± 0.03 b | 2.04 ± 0.11 a |
| AN (mg kg⁻¹) | 99.3 ± 2.7 a  | 41.3 ± 2.8 c  | 42.8 ± 0.7 c  | 93.6 ± 6.0 a  | 65.3 ± 2.9 b  |
| AP (mg P₂O₅ kg⁻¹) | 64 ± 6 b  | 66 ± 6 b  | 182 ± 17 a  | 192 ± 2 a  | 203 ± 12 a  |
| AK (mg K₂O kg⁻¹) | 177 ± 9 a  | 120 ± 0 b  | 137 ± 9 b  | 187 ± 9 a  | 130 ± 15 b  |
| pH          | 8.58 ± 0.02 b | 8.84 ± 0.01 a | 8.61 ± 0.08 b | 8.53 ± 0.03 b | 8.52 ± 0.03 b |
| BD (g cm⁻³) | 1.25 ± 0.05 c  | 1.47 ± 0.01 a  | 1.43 ± 0.01 ab | 1.27 ± 0.03 c  | 1.38 ± 0.02 b  |

Note: Differing lower letters indicate significant differences (P < 0.05) between fertilization treatments within a variable. M: organic manure application only; C1: low mineral fertilizer application; C2: high mineral fertilizer application; CM1: low mineral fertilizer combined with high organic manure application; CM2, high chemical fertilizer combined with low organic manure application. SOM: soil organic matter; TN: total nitrogen; TP: total phosphorous; AN: available nitrogen; AP: available potassium; AK: available potassium; BD: bulk density.
organic manure treatments were 27.6% and 72.4% higher than that of the low organic manure treatments and 47.7% and 129.4% higher than that of the no organic manure treatments, respectively.

Mineral fertilizer levels had significant influence on TP and AP, as treatments with higher P applications (C2 and CM2) had higher TP and AP. Overall, TP ranged from 1.40 to 2.17 g P\(_{2}O_{5}\) kg\(^{-1}\), with the highest value observed in the C2 treatment. In addition, the average AP was 141 mg P\(_{2}O_{5}\) kg\(^{-1}\) in the CM2 treatment and a minimum of 64 mg P\(_{2}O_{5}\) kg\(^{-1}\) in the M treatment. On average, TP and AP in high mineral fertilizer treatments (C2 and CM2) were 41.8% and 50.4% higher than that of the low mineral fertilizer treatments (C1 and CM1), and 49.2% and 200.7% higher than that of the no fertilizer treatment (M), respectively.

Overall, AK ranged from 120 to 187 mg K\(_{2}O\) kg\(^{-1}\), and the maximum value of AK was found in the CM1 treatment, followed by the M treatment. In two high organic manure treatments (M and CM1), AK was significantly higher than that of the other treatments \(P < 0.01\). Furthermore, pH ranged from 8.58 to 8.84, with an average value of 8.61. In the C1 treatment, pH was significantly higher than that of the other treatments \(P < 0.01\), but there were no significant differences in pH among the other fertilizer treatments. BD ranged from 1.25 to 1.47 g cm\(^{-1}\) with the maximum and minimum value observed in the C1 and M treatments, respectively. Contrary to what was observed for SOM, TN, and AN, organic manure application significantly decreased BD. On average, BD in the no organic manure treatments were 5.1% and 15.1% higher than that of the low and high organic manure treatments, respectively.

### 3.2 Bacterial diversity and composition

After trimming, a total of 3078055 sequences were obtained, with sequence numbers ranging from 46795 to 87438 among samples. Sequences were assigned to 7284 OTUs in total. The bacterial OTUs were further clustered into 40 phyla, 111 classes, 217 orders, 428 families, 802 genera, and 1734 species.

Fertilizer treatments significantly affected bacterial alpha diversity (Figure 1). The bacterial Sobs index ranged from 3721 to 4311, and the maximum value was found in the CM2 treatment, which significantly higher than that of the C1 and C2 treatments \(P < 0.01\). The Shannon index ranged from 6.90 to 7.13, and the values of this index were significantly higher in the M, CM1 and CM2 treatments than that of the C1 and C2 treatments \(P < 0.01\). The Chao index per treatment followed the order of CM2 > M > CM1 > C2 > C1, and the Chao index value of the treatment CM2 was 3.8%, 7.8%, 12.4%, and 15.7% higher than that of the M, CM1, C2, and C1 treatments, respectively. The Simpson index showed the opposite trend with regard to the Sobs, Shannon, and Chao indices and was significantly higher in the C2 and C1 treatments than in the M, CM1, and CM2 treatments.

Across all the treatments, the dominant bacterial phyla were Proteobacteria (26.8% average relative abundance), Acidobacteria (19.4%), Chloroflexi (17.0%), and Actinobacteria (13.3%; Figure 2). Other phyla that comprised a substantial \(>1.5\%\) amount of the bacterial community were Gemmatimonadetes (8.3%), Firmicutes (3.6%), Bacteroidetes (3.1%), and Nitrospirae (1.8%). The functional groups that presented low total abundance \(<1.5\%\) included, Planctomycetes (1.4%), and Saccharibacteria (1.1%). Only a small proportion of the bacterial OTUs (1.04%) were not identified.

The NMDS ordination plots of the Bray-Curtis dissimilarities of the soil bacteria were used to compare the composition of bacterial community among soil samples (Figure 3). The NMDS plot revealed a clear separation between the samples collected from the different treatments. The PERMANOVA also revealed that the fertilizer treatments had a significant effect on bacterial community
composition \( F_{2,44} = 6.75, R^2 = 0.40, P < 0.01 \). The samples taken from the treatments with different organic manure application rates (0, 15, and 30 t ha\(^{-1}\)) were clearly clustered into three groups \( (C1+C2, CM2, \text{and } M+CM1) \). The results of the PERMANOVA confirmed that the composition of the bacterial community changed according to the availability of organic manure in soil \( F_{2,44} = 10.28, R^2 = 0.33, P < 0.01 \). The overlaps between the C1 and C2 groups suggests that community composition did not significantly change along a mineral fertilizer gradient.

### 3.3 Response of crop yield and soil bacterial community to soil nutrients

There were significant relationships between crop yield and soil nutrients (Table 2). In particular, SOM, TN, AN, and AK were positively correlated with crop yield, while pH and BD were negatively correlated with crop yield.

The RDA analysis was performed to identify the major environmental variables controlling the community structure. Of all soil variables tested, SOM, TN, AN, AK, pH, and BD were significantly correlated with the bacterial community (the \( R^2 \) values were 0.84, 0.84, 0.87, 0.57, 0.36, 0.78, respectively). After the VIF analysis to eliminate the collinear relationships between variables, six variables (i.e., TN, TP, AP, AK, pH, and BD) were used in the RDA analysis. The TN, AK, BD, and pH variables were represented with long arrows and significantly correlated with the bacterial community, while TP and AP were represented with short arrows and weakly correlated with the bacterial community (Figure 4). The TN, AK, pH, and BD variables were close to the first axis, while the TP and AP variables were close to the second axis. Considering the variation explained by the RDA

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**Fig. 2.** Nonmetric multidimensional scaling (NMDS) pattern of bacterial communities (OTU level) in response to different fertilization treatments. Communities are compared using Bray-Curtis distance similarities based on the abundance of OTUs.

**Fig. 3.** Relative abundances of soil bacteria at phylum level.
axes, the first and second axes were able to explain 29.18 and 9.56% of the variation present in the soil bacterial community, respectively. Together, these six soil property indices explained 38.74% of the variation of the soil bacterial community.

4. Discussion

In our previous experiment from 2006–2012, the lowest maize yields were found in the pure manure treatment (M) (Yang et al., 2015). In contrast, after the 12-year experiment, the M treatment showed the highest maize yield, which was 11% and 16% higher than that of the mineral fertilizer combined with organic manure treatments and the pure mineral fertilizer treatments, respectively. This result provides important evidence for the development of organic agricultural practices. However, this crop yield response was not observed in another experiment in a nearby study area, in which a pure manure treatment resulted in continuously low crop yields throughout the whole experimental period (Sun and Suo, 2011). Soil in young oasis farmland typically has a sandy texture and low nutrient content; therefore, organic manure application in the present study was especially efficient in increasing soil fertility in this study area. For example, compared with that of the initial year of the experiment (2006) (Yang et al., 2015), SOM in the M, CM1, and CM2 treatments increased 100.3%, 156.5%, and 44.7%, respectively, after 12 years. The pure organic manure treatment (M) had the highest SOM among all treatments in 2018, which could be the main reason for observed yield increase in this treatment. However, the different yield responses in a study by Sun and Suo, (2011) were likely due to the small changes in soil nutrients. Given that the initial soil nutrient levels were high, organic manure application was not able to efficiently increase soil fertility in their study. Thus, these results and those of our study indicate that the magnitude of the impact of organic fertilizer application on crop yield and soil nutrient content is often related to the initial soil fertility level.

Organic manure application significantly decreased BD, indicating that the soil structure was improved by organic manure application. However, TP and AP did not significantly respond to organic manure application, but increased significantly with mineral P fertilizer application. It can be concluded that P was not the limiting element in this young oasis farmland, and additional P fertilizer application would only result in more soil P loss. The lower observed pH values in the M treatment in this study are contrary to the results of studies that have reported that organic fertilizer application can raise soil pH (Xun et al., 2016; Bei et al., 2018). Considering that the soil in our research region was more alkaline compared to that of other studies, we can conclude that organic manure application can alleviate soil pH and not only reduce or raise it.

In agreement with our first hypothesis, the results of our study revealed that soil bacterial diversity and community composition differed significantly among the different fertilization treatments. Positive effects of organic fertilizer application on soil bacterial diversity were observed, which agree with the results of Xun et al., (2016) and Cambisoli Bei et al., (2018). When analyzing the effects of mineral fertilizer on soil bacterial diversity, some contradictory conclusions emerged. For example, Nguyen et al., (2018) reported that mineral N fertilizer increased the abundance and diversity of soil bacteria. However, Martin et al., (2017) reported that soil microbial communities, both bacterial and fungal, responded weakly to long-term mineral N fertilization. In the present study, there were

| SOM | TN | TP | AN | AP | AK | pH | BD |
|-----|----|----|----|----|----|----|----|
| CY  | 0.51** | 0.49** | 0.07NS | 0.48** | 0.28NS | 0.53** | -0.54** | -0.51** |

SOM: soil organic matter; TN: soil total nitrogen; TP: total phosphorus; AN: available nitrogen; AP, available potassium; AK, available BD: soil bulk density. ** are significant at $P < 0.01$, NS are no significant.

Fig. 4. Redundancy analysis (RDA) of soil bacterial (symbols) and environmental factor (arrows) under different fertilization treatments. Only significant soil chemical properties are fitted as vectors onto each ordination plot. TN, total nitrogen; TP, total P; AK, available K; AP, available P; BD, soil bulk density.
no significant difference in soil bacteria diversity between the two mineral application treatments (C1 and C2). The result could be attributed to that mineral application did not significantly affect soil SOM and TN, and thus did not influence resource availability for different bacterial groups (Martin et al., 2017). In addition, the study did not include a no-fertilizer treatment, and differences in bacterial diversity between the fertilization and the no-fertilizer treatments may have been significant.

In the present study, Proteobacteria, Acidobacteria, Chloroflexi, and Actinobacteria were the most abundant bacterial phyla (Xun et al., 2016; Bei et al., 2018). The composition of the soil bacterial community was strongly affected by the different treatments. When compared to that of the application of mineral fertilizer alone, it can be readily seen that the relative abundance of Proteobacteria was highest in the organic manure application treatments (M, CM1, and CM2), which is consistent with what has been observed in previous studies (Bei et al., 2018). It has been suggested that most Proteobacteria members exhibit copiotrophic attributes, and their relative abundances is highest in soils with high organic carbon content (Noah et al., 2007), which was supported by the results of our experiment. However, the relative abundance of Acidobacteria and Gemmatimonadetes was only high in the mineral fertilizer treatments (C1 and C2). According to Noah et al., (2007), bacteria belonging to the Acidobacteria phylum were the most abundant phyla in soils with very low resource availability, and their relative abundance was reduced in an individual soil amended with high concentrations of organic carbon. Debruyne et al., (2011) revealed that the relative abundance of Gemmatimonadetes bacteria was inversely correlated to soil moisture and that these bacteria are adapted to environments with drier soils. It appears that the Acidobacteria and Gemmatimonadetes bacterial groups are usually resistant to harsh environmental conditions, and a reduction in the abundance of these groups indicated an improvement in the dress environment. Thus, it can be concluded that the decrease in the relative abundances of Acidobacteria and Gemmatimonadetes in the M, CM1, and CM2 treatments was mainly due to improved soil nutrient content in these treatments consequently relieved both resource and water limitation stress. The population dynamics of Chloroflexi members were closely related to the accumulation of dissolved matter, and Chloroflexi may possibly contribute to the nitrification process (Sorokin et al., 2012). Consistent with this, we found a higher relative abundance of Chloroflexi bacteria in the CM1 and CM2 treatments, indicating that the combined application of organic and inorganic fertilizer can promote the decomposition and transformation of SOM. Actinobacteria presented high abundance in the high SOM treatments (M, CM1, and CM2), and these observations are consistent with those of a field experiment (Zhang et al., 2019). Similarly, we found that the phylum Firmicutes was also abundant in the M, CM1, CM2 treatments, and these results are supported by those of Horn et al., (2014) who reported an increase in Firmicutes with water and organic matter addition in a polar desert.

There are many studies that support the our second hypothesis that soil nutrients would constitute the main factor affecting the change of the soil bacterial community in different fertilization strategies (Bei et al., 2018; Nguyen et al., 2018; Zhang et al., 2019). For example, Bei et al., (2018) reported that soil C and N availability are the major factors that determines the structure of the soil microbial community. Therefore, it is expected that observed differences in soil bacterial communities among the different fertilization treatments may be largely related to the soil nutrient differences caused by different fertilization strategies. Our results confirmed this expectation and both soil bacterial diversity (Table 3) and the structure of the bacterial community (Figure 4) were significantly correlated with soil nutrient variables. Soil bacterial diversity indices were significantly and positively correlated with SOM, TN, and AN (Table 3), and these findings agree with prior results (Li et al., 2017). Previous studies have also reported that among physicochemical factors, pH is the dominant factor in that shapes the community composition and species diversity of soil bacteria (Wan et al., 2020). These results were supported by those of our study, and a negative correlation was found between pH and soil bacterial diversity (Table 3), indicating that a decrease in pH improved soil bacterial diversity. In addition, Figure 4 also shows that pH had a significant effect on the composition of the soil bacterial community. In the present study, soil BD was also closely related with the soil microbial communities, which is supported by the results of the study by Sun et al., (2020), who reported that soil BD was the main environmental factor that explained the observed variability in microbial diversity in their study. Given to the relationships between soil properties and the soil bacterial community, we can conclude that the improvement of the soil environment is beneficial for the development of the soil bacterial community and thus soil health.

### 5. Conclusions

In young oasis farmland with sandy soil texture, our study showed that the short-term application of organic fertilizer alone can lead to a reduction in crop yield, but the long-term application of organic fertilizer can gradually increase crop yield and has the particularly positive effect of increasing soil fertility. Integrated

### Table 3. Pearson correlation coefficients between soil bacterial diversity indices and soil properties.

| Index | SOM | TN | TP | AN | AP | AK | pH | BD |
|-------|-----|----|----|----|----|----|-----|-----|
| Sob   | 0.41** | 0.45** | 0.25** | 0.43** | 0.15** | 0.04NS | −0.39NS | −0.42NS |
| Chao  | 0.55* | 0.59* | 0.26** | 0.57* | 0.25** | 0.21NS | −0.57* | −0.54* |
| Shannon | 0.63* | 0.64* | 0.14NS | 0.63* | 0.26NS | 0.45NS | −0.68** | −0.54* |
| Simpson | −0.34NS | −0.32NS | −0.06NS | −0.32NS | −0.08NS | −0.30NS | 0.43NS | 0.24NS |

*are significant at $P < 0.05$, **are significant at $P < 0.01$, NS are no significant. SOM: soil organic matter; TN: soil total nitrogen; TP: total phosphorus; AN: available nitrogen; AP: available potassium; AK: available BD: soil bulk density. **are significant at $P < 0.01$, NS are no significant.
strategies to combine organic manure and mineral fertilizer application can ensure stable the crop yields and while increasing soil nutrient content. While mineral fertilizer application had little impact on soil nutrients, it posed a greater environmental risk than that of organic fertilizer. Organic fertilizer application significantly increased soil bacterial diversity. In addition, the composition of the bacterial community compositions was significantly different among treatments with different organic manure application rates. With regard to the improvement of soil nutrient content, organic manure application promoted an increase in the abundance of the copiotrophic group. Due to poor soil fertility and sandy soil texture, the environmentally resistant bacterial group were abundant in pure mineral fertilizer application treatments. Overall, organic manure application, whether applied alone or in combination with mineral fertilizer, may have a profound influence improving soil productivity and promoting soil health in young oasis farmland.

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