

# Effects of bio-organic fertilizer on soil fertility, microbial community composition, and potato growth

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**ABSTRACT:** The excessive and irrational use of chemical fertilizers poses a series of environmental problems. A growing number of research studies have focused on the application of beneficial microorganisms to reduce the use of chemical fertilizers. Here, potato field experiments were conducted to investigate whether partial replacement of chemical fertilizers with bio-organic fertilizers containing *Bacillus velezensis* BA-26 had an effect on plant growth, soil fertility, and soil microbial community composition. Three treatment methods were used in this study: organic fertilizer (OF), bio-organic fertilizer (BOF), and chemical fertilizer (CF). The results showed that the biomass and soluble sugar content of potato were significantly increased with BOF treatment. The soil electrical conductivity, available phosphorus (AP), available potassium (AK), urease, and alkaline phosphatase activity also improved with BOF treatment. Further analysis revealed that BOF treatment increases bacterial diversity and reduces fungal diversity. Potentially, pathogenic microorganisms; such as *Fusarium*, *Verticillium*, and *Botryotrichum*; treated with BOF were significantly decreased compared with CF treatment. Redundancy analysis showed that soil conductivity and AP had significant effects on bacterial and fungal community composition. Thus, the results suggest that the application of bio-organic fertilizer could reduce the use of chemical fertilizers by promoting potato growth, improving soil fertility, and affecting microbial community composition.

**KEYWORDS:** bio-organic fertilizer, potato biomass, soil nutrients, microbial community

## INTRODUCTION

Potato is an important global food resource and one of the major economically significant crops in China. Chemical fertilizers are widely used in potato cultivation; however, their excessive use has resulted in lower yield, deteriorating quality, and weakening resistance to pathogens. Long-term large-scale application of chemical fertilizers not only results in soil consolidation [1] but also leads to increasing pollution of soil, atmospheric, and aquatic systems, which severely affects further agricultural development [2–4]. Research studies have recently focused on fertilizer reduction and the use of alternative fertilizers. Straw, animal dung, and other organic fertilizer are applied to replace a portion of the chemical fertilizer. In addition to using organic fertilizers, plant growth-promoting microorganisms (PGPM) can be applied to reduce the amount of fertilizer used [5, 6]. Studies have

found that a variety of microorganisms can promote plant growth and increase plant stress resistance, such as *Pseudomonas* [7], *Bacillus* [8], *Azospirillum* [9], and endophytic actinobacteria [10]. Without adding organic material, when PGPMs are directly added to the soil, they are not effective in their function because of lack of nutrition. They can be combined with organic fertilizers, thus benefiting from the anti-stress and pro-growth effects of both microorganisms and organic fertilizers, to achieve the sustained and stable release of fertilizer nutrients [11].

A bio-organic fertilizer (BOF) combines functional microorganisms with suitable substrates and is more effective than microorganisms directly added to the soil. It is widely regarded as a promising way for organisms to inhibit soil-borne pathogens and promote plant growth [12, 13]. The composition and diversity of the soil microbial community is very important to soil health, and soil enzyme activity is the index of soil biological activ-

ity [14, 15]. Increasing continuous cropping years results in a decrease in soil nutrients and enzyme activity [16]. Previous studies have reported that biological organic fertilizer improves soil quality and soil enzyme activity [17] and increases the activity of functional microorganisms [18], as well as effectively inhibits soil-borne diseases and promotes plant growth [19].

This experiment selected a representative potato rotation field in Chengde City, Hebei Province, China. The purpose of this study was to explore whether partial replacement of fertilizer with BOF containing *B. velezensis* BA-26 had effects on plant growth, soil fertility, and soil microbial community.

## MATERIALS AND METHODS

### Preparation of BOF

*B. velezensis* BA-26 was isolated from the rhizosphere soil of healthy potatoes. It was cultured in Nutrient Broth (NB) (Shanghai Bowei Co., Ltd., China) at 28 °C and stored at 4 °C on slants. Preserved *B. velezensis* BA-26 was inoculated in the NB and cultured in a shaker at 32 °C, 180 rpm, for 48 h. Calculations indicated that the number of spores in the prepared fermentation broth was  $4 \times 10^8$ /ml. The prepared fermentation broth was mixed with an organic fertilizer. The ratio of fermentation broth to organic fertilizer was 1:10. Organic manure was prepared from mature pig manure compost, which contained 40.5% organic matter, 29.4% H<sub>2</sub>O, 3.7% N, 2.4% P<sub>2</sub>O<sub>5</sub>, and 1.1% K<sub>2</sub>O.

### Field experiments

The experimental field is located in Zhangjiawan, Weichang County, Chengde City, Hebei Province, China (117.9205°E, 42.3476°N). The soil type in this area is sandy loam. It has deep soil, good aggregate structure, abundant soil moisture, and good permeability. The basic physical and chemical properties of the experimental field are as follows: available nitrogen, 41.45 mg/kg; available phosphorus, 26.12 mg/kg; available potassium, 115.00 mg/kg; organic matter, 7.10 g/kg; pH 6.11 (soil-water ratio: 2.5:1); and conductivity, 101.42 us/cm. The potato, variety Favorita, was planted on April 5, 2018. The field experiment used a random block design: each block area was  $6 \times 6 = 36 \text{ m}^2$ , single row planted, row spacing was 70 cm, and plant spacing was 25 cm. The field treatments were designed as follows: (1) CF: 100% chemical fertilizer (N:P:K = 12:19:16); (2) OF: 75% chemical fertilizer +

organic fertilizer; and (3) BOF: 75% chemical fertilizer + BOF. The application rate of organic fertilizer or bio-organic fertilizer was 1800 kg/ha, and the field was treated with regular watering.

### Sample collection

Sample collection was conducted on July 17, 2018. Each plot was sampled using a five-point sampling method. Three potato plants were randomly selected at each point. Plant height, stem diameter, and chlorophyll content were measured, and then the potatoes were dug out for biomass measurement. Soil samples were collected from the root area, and five soil samples were evenly mixed together into one combined sample, kept in a Ziplock<sup>®</sup> bag, and stored at -80 °C until DNA extraction.

### Determination of potato growth index and tuber quality

Potato plant height was determined using a folding ruler and measuring the distance between the highest growing point and the ridge surface. Stem diameter was determined using a Vernier caliper. Chlorophyll content was determined using an ECA-051 portable chlorophyll meter. Biomass was measured by drying potatoes and then weighing. Protein and soluble sugar contents were determined using a Pierce<sup>™</sup> rapid gold BCA protein assay kit (Thermo Fisher Scientific Co., Ltd., USA) and a Plant Soluble Sugar assay kit (Comin Biotech Co., Ltd., China), following the manufacturer's instructions, respectively. Vitamin C (VC) content was determined using the 2,6-dichloroindophenol titration method [20]; fresh potatoes were ground with 5 ml of 2% oxalic acid for dissolution in 50 ml volumetric flasks for volumetric adjustment and fully dissolved. The pure filtrate was precipitated using filter paper and, then, titrated with 2,6-dichlorophenol indophenol solution.

### Soil physical and chemical property analysis

Soil bulk density was measured using the cutting ring method after drying the soil cores at 105 °C for 48 h. Soil samples were air-dried and passed through a 2-mm aperture sieve. The method of measuring soil pH and conductivity involved weighing 10 g of dry soil and placing it in a beaker containing 30 ml of distilled water. The mixture was thoroughly mixed, and after standing for 30 min, the pH and conductivity of the soil were, respectively, measured with a pH and conductivity meter (Mp521 Lab pH/conductivity meter, Japan) [21]. The soil organic matter was determined using the

oil bath heating-potassium dichromate ( $K_2Cr_2O_7$ ) volumetric method [22]. Briefly, the temperature of the oil bath was 180 °C, boiled for 5 min, 0.4 mol/l  $K_2Cr_2O_7$ - $H_2SO_4$  solution was used to oxidize the soil organic matter, and the remaining  $K_2Cr_2O_7$  was used in  $FeSO_4$  for titration. Soil available phosphorus (AP) and available potassium (AK) were determined following Shen et al [23], and soil available nitrogen (AN) was determined using an alkaline hydrolysis diffusion method [24].

### Soil enzyme activity

Soil urease, catalase, sucrase, and phosphatase activities were, respectively, determined using a soil urease activity detection kit, soil catalase activity detection kit, soil sucrase activity detection kit, and soil acid phosphatase activity detection kit (Solarbio Technology Co., Ltd., China), following the manufacturers' instructions.

### DNA extraction

Total microbial genomic DNA was extracted using a DNeasy PowerSoil Kit (QIAGEN, Inc., Netherlands), following the manufacturer's instructions and stored at -20 °C until analysis. The quantity and quality of the extracted DNAs were measured using a NanoDrop ND-1000 spectrophotometer (Thermo Fisher Scientific, Waltham, MA, USA) and agarose gel electrophoresis, respectively.

### PCR amplification and illumina sequencing

PCR amplification of the bacterial 16S rRNA genes V3-V4 region was performed using the forward primer 338F (5'-ACTCCTACGGGAGGCAGCA-3') and the reverse primer 806R (5'-GGACTACHVGGGTWTCTAAT-3'). For amplification of fungal ITS sequences, the forward primer ITS5F (5'-GGAAGTAAAAGTCGTAACAAGG-3') and the reverse primer ITS1R (5'-GCTGCGTTCTTCATCGATGC-3') were used. Sample-specific 7-bp barcodes were incorporated into the primers for multiplex sequencing. The PCR amplification system consisted of 5 µl of a 5 × reaction buffer, 5 µl of a 5 × GC Buffer, 2 µl of 2.5 mM dNTPs, 1 µl of 10 µM forward primer, 1 µl of 10 µM reverse primer, 2 µl of 20 ng/µl the DNA template, 8.75 µl of ddH<sub>2</sub>O, and 0.25 µl of Q5 DNA polymerase (New England Biolabs, Inc., USA). The thermal cycling conditions comprised an initial denaturation at 98 °C for 2 min, followed by 25 cycles consisting of denaturation at 98 °C for 15 s, annealing at 55 °C for 30 s, and extension at 72 °C for 30 s, with a final extension of 5 min at 72 °C and hold at 10 °C. PCR amplicons were

purified with Agencourt AMPure Beads (Beckman Coulter, Indianapolis, IN, USA) and quantified using the PicoGreen dsDNA assay kit (Invitrogen, Carlsbad, CA, USA). After the individual quantification step, amplicons were pooled in equal amounts, and paired-end 2 × 250 bp sequencing was performed using the Illumina Novaseq platform with NovaSeq 6000 SP reagent kit (Shanghai Personal Biotechnology Co., Ltd., Shanghai, China) for 500 cycles.

### Statistical analysis

The majority of the result parameters were analyzed with a single factor ANOVA. The IBM SPSS 25.0 software was used to calculate and count the results using an ANOVA and Duncan multirange test. Statistical significance was considered at  $p < 0.05$ . Sequence data analyses were mainly performed using QIIME and R packages (V3.2.0). OTU-level alpha diversity indices were calculated using the OTU table in QIIME. A redundancy analysis (RDA) was conducted using CANOCO5. Excel software version 2016, GraphPad Prism version 8, and Origin Pro 2018 were used for statistical analysis and mapping.

### Accession number

The sequence data generated in this study were deposited to the NCBI database under accession numbers PRJNA646630 (bacterial sequences) and 646645 (fungal sequences).

## RESULTS AND DISCUSSION

### Potato growth indicators and tuber quality parameters

Different treatment methods strongly influenced potato growth and tuber quality (Table 1). Growth indicators showed that the plant height, stem diameter, and biomass of potato plants treated with BOF significantly ( $p < 0.05$ ) increased by 7.77%, 8.42%, and 11.07%, respectively, compared with those of plants with chemical fertilizer (CF) treatment. The height and biomass of potato plants treated with organic fertilizer (OF) were also significantly ( $p < 0.05$ ) higher than those of the CF treatment. This study showed that replacing some CFs with BOFs promotes the growth of potatoes. BOFs have been shown to have a great potential in promoting plant growth [25]. Soluble sugar content of the BOF-treated potatoes significantly ( $p < 0.05$ ) increased by 45.37% and 53.92% compared with the OF and the CF treatments, respectively. Compared with the CF treatment, vitamin C content in the BOF and OF treatments significantly increased by 6.25%

**Table 1** The growth index and tuber quality of potato.

Treatment	Plant height (cm)	Stem diameter (mm)	Chlorophyll (mg)	Biomass (g)	Sugar content (g/kg)	Protein content (g/kg)	VC content (mg/kg)
OF	68.30 ± 0.55 <sup>b</sup>	19.59 ± 0.15 <sup>a</sup>	39.60 ± 0.51 <sup>a</sup>	63.08 ± 0.87 <sup>b</sup>	1.08 ± 0.03 <sup>b</sup>	1.04 ± 0.04 <sup>a</sup>	165.33 ± 6.09 <sup>a</sup>
BOF	70.86 ± 0.64 <sup>a</sup>	19.95 ± 0.31 <sup>a</sup>	40.88 ± 0.87 <sup>a</sup>	66.44 ± 1.82 <sup>a</sup>	1.57 ± 0.02 <sup>a</sup>	1.03 ± 0.02 <sup>a</sup>	153.00 ± 3.63 <sup>b</sup>
CF	65.82 ± 0.96 <sup>c</sup>	18.40 ± 0.51 <sup>b</sup>	39.38 ± 0.70 <sup>a</sup>	59.82 ± 1.05 <sup>c</sup>	1.02 ± 0.02 <sup>c</sup>	1.05 ± 0.05 <sup>a</sup>	144.00 ± 2.46 <sup>c</sup>

Data are the mean ± standard error ( $n = 3$ ) and, within each column, different letters indicate significant differences (ANOVA,  $p < 0.05$ , Duncan's test).

and 14.81%, respectively. However, protein content in the three treatments did not significantly differ. Organic farming can improve soluble curing agent in fruits, and dissolve solidifying agents, such as sugar and other compounds (vitamin C and phenolic compounds), that contribute to the nutritional quality of fruits [26]. BOF treatment increased the content of soluble sugar and vitamin C in potatoes (Table 1). This is consistent with the results of Ye et al [9], who found that BOFs can increase soluble sugar and vitamin C content in tomatoes.

#### Physical and chemical properties of soil and enzyme activity

Table 2 shows the physical properties and nutrient content of soil. BOF treatment significantly ( $p < 0.05$ ) increased soil pH compared with CF and OF treatments, whereas OF treatment showed no significant difference compared with CF. Electrical conductivity of the BOF and OF treatments significantly ( $p < 0.05$ ) improved by 30.65% and 20.70%, respectively. Soil pH and electrical conductivity are important soil properties. They play key roles in the formation of soil and the growth of plants and animals in the soil. This study found that BOF treatment significantly improved soil pH and conductivity. Compared with CF and OF treatments, soil organic matter (OM), available phosphorus (AP), and available potassium (AK) levels significantly ( $p < 0.05$ ) increased with BOF treatment. The increase in soil fertility was related to OM and a variety of beneficial microorganisms. Soil fertility and plant health improve with increasing organic matter content [27]. Moreover, the beneficial microorganisms contained in the BOF promoted the conversion of soil nutrients, induced the accumulation of available nutrients, and increased the levels of effective nutrients in soil [13]. The application of BOF significantly increased soil nutrient levels and improved soil fertility (Table 2).

The degree of enzyme activity in the soil is an important indicator of soil health. Soil urease is

the driving force of soil metabolism and reflects soil fertility to some extent. Soil phosphatase can accelerate the dephosphorization rate of organophosphorus and affect the decomposition and transformation of organophosphorus in soil [15]. Soil sucrase is an important catalytic enzyme that affects the soil carbon cycle. Soil catalase catalyzes the decomposition of hydrogen peroxide in the soil, reducing the toxic effect of hydrogen peroxide on crops [28]. Fig. 1 shows that the urease activity in soil significantly increased with BOF treatment by 33.37% and 17.41% ( $p < 0.05$ ), respectively, compared with the activity with CF and OF treatments. The alkaline phosphatase activity also increased by 29.90% and 7.5% ( $p < 0.05$ ), respectively, compared with CF and OF treatments. Compared with CF and OF treatments, the sucrase activity was increased in BOF treatment, but there was no significant ( $p > 0.05$ ) difference between BOF and CF treatments. No significant ( $p > 0.05$ ) difference in catalase activity was observed among the three treatments. This study found that the application of BOF significantly increased the activity of rhizosphere soil alkaline phosphatase and urease activity (Fig. 1), which is consistent with the findings of Marcote et al [29].

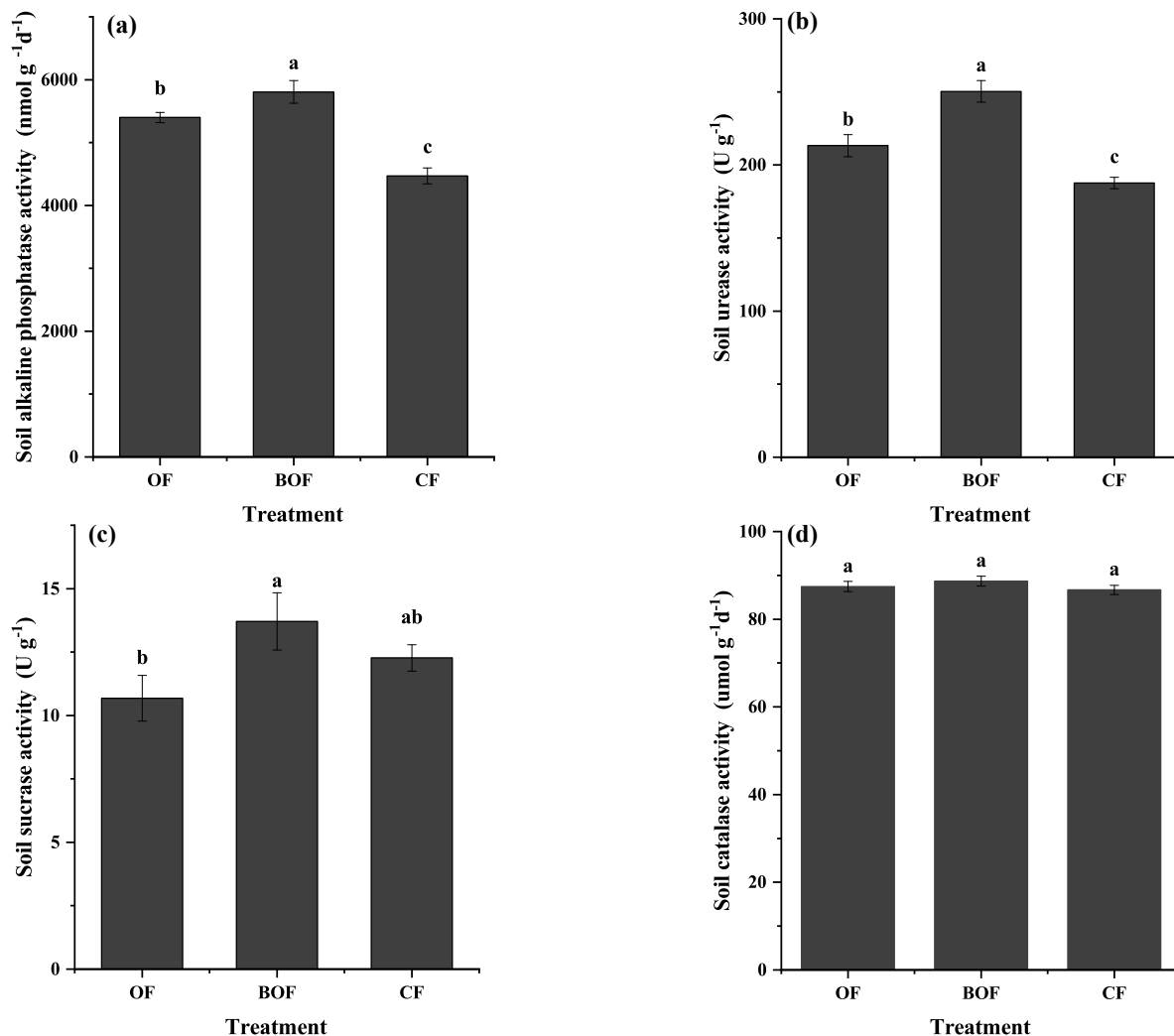
#### Alpha diversity of soil microbials

Table 3 shows the alpha diversity index of bacteria and fungi. Chao1 and Ace indices were used to represent abundance, Shannon to represent diversity, Pielou's evenness to represent evenness, and Good's coverage for coverage. For bacteria, compared with CF treatment, Chao1, Shannon, and Ace indices significantly increased with BOF treatment ( $p < 0.05$ ). Compared with OF treatment, Chao1 and Ace indices increased with BOF treatment. No obvious difference in the evenness and Good's coverage was observed among the three treatments. The alpha diversity of fungi was contrary to that of bacteria; BOF treatment significantly reduced the Chao1, Ace, and Shannon indexes. Soil microbial diversity is a key factor affecting soil health and

**Table 2** Physical and chemical properties of soil.

Treatment	pH	EC (us/cm)	Volume weight (g/cm <sup>3</sup> )	OM (g/kg)	AP (mg/kg)	AK (mg/kg)	AN (mg/kg)
OF	8.22 ± 0.05 <sup>b</sup>	181.61 ± 8.47 <sup>a</sup>	1.30 ± 0.01 <sup>a</sup>	10.40 ± 0.59 <sup>b</sup>	34.26 ± 0.57 <sup>b</sup>	191.50 ± 8.54 <sup>b</sup>	55.07 ± 3.86 <sup>a</sup>
BOF	8.34 ± 0.07 <sup>a</sup>	191.81 ± 10.55 <sup>a</sup>	1.30 ± 0.03 <sup>a</sup>	11.32 ± 0.21 <sup>a</sup>	38.36 ± 1.02 <sup>a</sup>	231.67 ± 7.57 <sup>a</sup>	54.85 ± 1.45 <sup>a</sup>
CF	8.20 ± 0.05 <sup>b</sup>	146.81 ± 3.87 <sup>b</sup>	1.33 ± 0.05 <sup>a</sup>	10.31 ± 0.50 <sup>b</sup>	35.53 ± 0.67 <sup>b</sup>	180.17 ± 6.81 <sup>b</sup>	53.14 ± 1.77 <sup>a</sup>

EC, electric conductivity; OM, organic matter; AN, available nitrogen; AP, available P; AK, available K. Data are the mean ± standard error (n = 3) and, within each column, different letters indicate significant differences (ANOVA, p < 0.05, Duncan's test).



**Fig. 1** Effects of different treatments on soil enzyme activities: (a) soil alkaline phosphatase activity; (b) soil urease activity; (c) soil sucrase activity; and (d) soil catalase activity. Different letters indicate significant differences (ANOVA, p < 0.05, Duncan's test).

quality. Agricultural treatments can affect soil microbial diversity [30]. Soil microflora plays a central role in promoting the decomposition of loaded OM and nutrient cycling, particularly the most abundant

bacteria group, which is indispensable for soil ecological services [30, 31]. This study found that BOF treatment significantly increased bacterial diversity and decreased fungal diversity (Table 3).

**Table 3** Alpha diversity of soil bacteria and fungi.

Microbe	Treatment	Chao1	Shannon	Pielou_e	Ace	Goods_coverage (%)
Bacteria	OF	7963.76 ± 350.17 <sup>b</sup>	11.42 ± 0.05 <sup>ab</sup>	0.89 ± 0.003 <sup>a</sup>	7458.50 ± 259.59 <sup>b</sup>	98.84 ± 0.16 <sup>a</sup>
	BOF	8888.59 ± 396.86 <sup>a</sup>	11.34 ± 0.06 <sup>a</sup>	0.89 ± 0.004 <sup>a</sup>	8202.57 ± 280.83 <sup>a</sup>	98.92 ± 0.34 <sup>a</sup>
	CF	7326.04 ± 526.75 <sup>b</sup>	11.39 ± 0.04 <sup>b</sup>	0.89 ± 0.003 <sup>a</sup>	6995.60 ± 652.44 <sup>b</sup>	98.54 ± 0.16 <sup>a</sup>
Fungi	OF	326.26 ± 28.66 <sup>a</sup>	6.17 ± 0.17 <sup>a</sup>	0.74 ± 0.01 <sup>a</sup>	325.73 ± 28.11 <sup>a</sup>	99.99 ± 0.001 <sup>a</sup>
	BOF	243.47 ± 78.81 <sup>b</sup>	5.76 ± 0.23 <sup>b</sup>	0.74 ± 0.02 <sup>a</sup>	242.85 ± 78.58 <sup>b</sup>	99.99 ± 0.001 <sup>a</sup>
	CF	323.59 ± 25.26 <sup>a</sup>	6.35 ± 0.34 <sup>a</sup>	0.76 ± 0.05 <sup>a</sup>	322.77 ± 25.00 <sup>a</sup>	100.0 ± 0.001 <sup>a</sup>

Data are the mean ± standard error ( $n = 3$ ) and, within each column, different letters indicate significant differences (ANOVA,  $p < 0.05$ , Duncan's test).

### Bacterial and fungal community composition

Microbial community can be used as an important factor for evaluating soil fertility, and beneficial microorganisms in the soil can prevent soil-borne diseases [32]. Understanding the species and distribution of microorganisms is essential to the control of plant diseases [33]. Fig. 2 shows the relative abundance of bacteria and fungi at the phylum level. Proteobacteria, Acidobacteria, Actinobacteria, Chloroflexi, Gemmatimonadetes, Bacteroidetes, Rokubacteria, and Nitrospirae (relative abundance > 1%) were the predominant bacteria in all treatments (Fig. 2a). No significant ( $p > 0.05$ ) difference in the relative abundance of the predominant phyla was observed among the three treatments. For fungi, Ascomycota, Basidiomycota, Mortierellomycota, and Olpidiomyota (relative abundance > 1%) were the predominant fungi in all treatments (Fig. 2b). The results showed that the main components of soil fungi were Ascomycota and Basidiomycota, which are similar to those observed in the soil of peas [34] and peanuts [35]. Ascomycota contains many plant pathogens. Ascomycetes are often inhibited in soils where diseases are controlled [36]. The relative abundance of Ascomycota in the BOF treatment was significantly ( $p < 0.05$ ) decreased compared with the CF treatment. The abundance of Ascomycota was also decreased in the OF treatment, which may be because the application of OF increased beneficial bacteria in the soil, thereby inhibiting some fungi [37].

The relative abundance of bacteria and fungi at the genus level is shown in Fig. 3. The top 10 bacterial genera were *Sphingomonas*, *RB41*, *MND1*, *Nitrospira*, *Gaiella*, *Lysobacter*, *Haliangium*, *Ochrobactrum*, *Ellin6067*, and *Subgroup 10* (Fig. 3a). The relative abundance of *MND1* in the BOF treatment was higher than in the OF and CF treatments and was significantly ( $p < 0.01$ ) different from the CF

**Table 4** Relative abundance of *Bacillus* under different treatments.

Treatment	Relative abundance of <i>Bacillus</i>
OF	0.0025 ± 0.0001 <sup>b</sup>
BOF	0.0030 ± 0.0002 <sup>a</sup>
CF	0.0023 ± 0.0001 <sup>b</sup>

Data are the mean ± standard error ( $n = 3$ ) and, within each column, different letters indicate significant differences (ANOVA,  $p < 0.05$ , Duncan's test).

treatment. The relative abundance of *Sphingomonas* and *Lysobacter* treated with BOF was also higher than ( $p > 0.05$ ) in the other two treatments. A known beneficial bacteria *Sphingomonas* can inhibit tobacco black rot [38]. The relative abundance of *Bacillus* in BOF treatment was significantly increased (Table 4). Compared with OF and CF treatments, the relative abundance of *Bacillus* in BOF treatment was significantly ( $p < 0.05$ ) increased by 20% and 30.43%, respectively. For fungi, *Tausonia*, *Humicola*, *Mortierella*, *Fusarium*, *Lecanicillium*, *Sollicocozyma*, *Verticillium*, *Botryotrichum*, *Pseudogymnoascus*, and *Aspergillus* were the top 10 predominant genera (Fig. 3b). The relative abundance of *Fusarium*, *Verticillium*, and *Botryotrichum* in the BOF treatment significantly ( $p < 0.01$ ) decreased by 46.72%, 46.18%, and 58.46%, respectively, compared with the CF treatment. Compared with OF treatment, the relative abundance of *Fusarium* in BOF treatment significantly ( $p < 0.05$ ) decreased by 36%. In contrast, the relative abundance of *Mortierella* significantly ( $p < 0.05$ ) increased compared with the CF and OF treatments. *Mortierella* is enriched in disease-free soil [39]. *Mortierella* has not yet been used as a biological control agent, but some strains have been shown to produce antifungal and antibacterial metabolites [40].

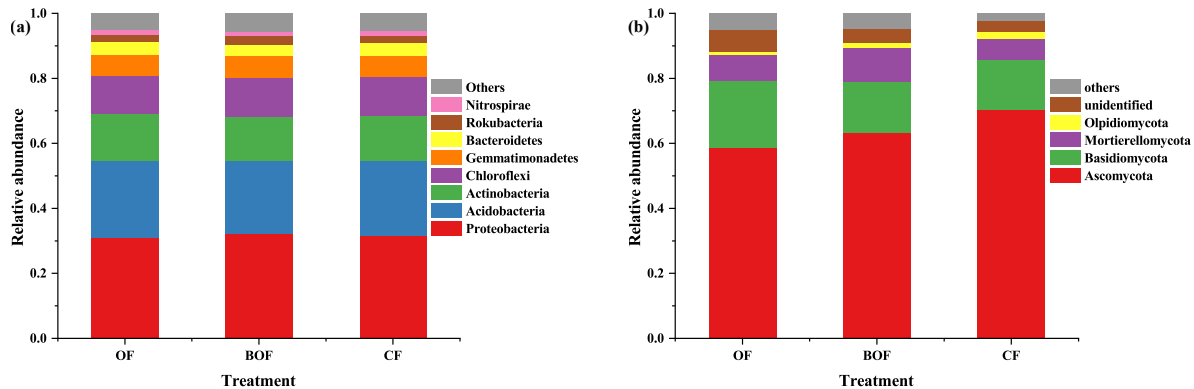


Fig. 2 Effects of different treatments on relative abundance of soil microbes at the phylum level: (a) bacteria and (b) fungi.

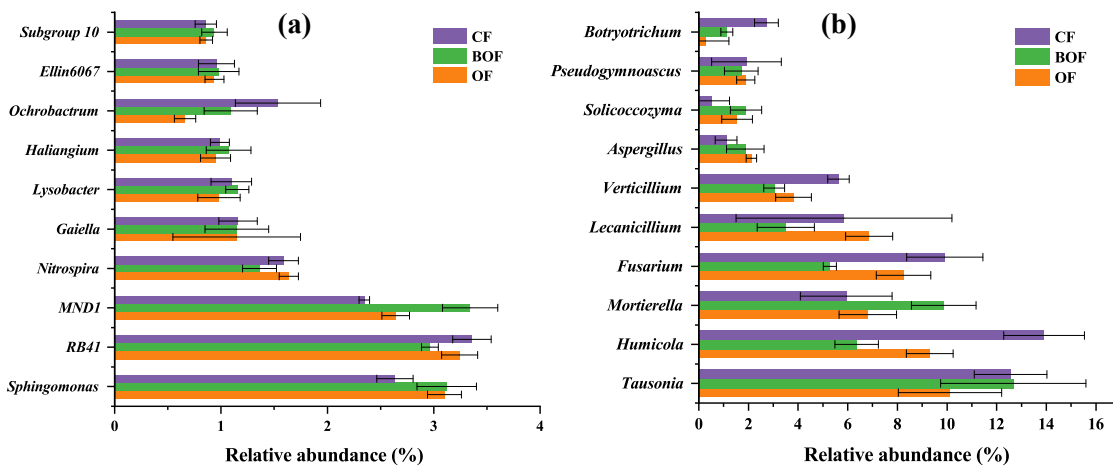


Fig. 3 Effects of different treatments on relative abundance of soil microbes at the genus level: (a) bacteria and (b) fungi.

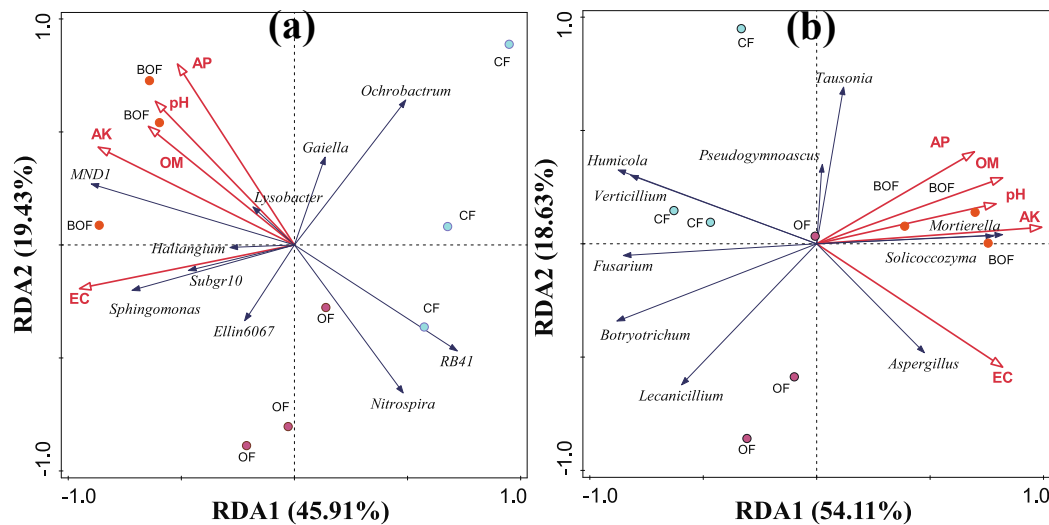
**Effects of environmental factors on bacterial and fungal communities**

To determine which environmental factors affect the composition of soil bacterial and fungal communities, RDA analysis was conducted (Fig. 4). For bacteria, the first two components of RDA accounted for 45.91% and 19.43% of the total variation (Fig. 4a). For fungi, the first two components of RDA explain 54.11% and 18.63% of the total variation (Fig. 4b). In bacteria, the electrical conductivity and AP were positively correlated to *Sphingomonas*, *MND1*, *Subgr10*, and *Lysobacter*. In fungi, the electrical conductivity and AP were negatively correlated to *Verticillium*, *Botryotrichum*, and *Fusarium* and positively correlated to *Mortierella* and *Sollicocozyma*. RDA analysis revealed that the soil electrical conductivity and AP significantly influence microbiological compositions (Table S1), which is

consistent with previous studies that AP [39] and soil electrical conductivity [41] play important roles in bacterial community formation. A previous study showed that a higher soil P content was associated with a lower incidence of wheat *Rhizoctonia* root rot [42], and AP content is negatively correlated to banana *Fusarium* wilt [39]. Based on the above results, BOF treatment may affect the soil microbial community by increasing soil electrical conductivity and AP content.

**CONCLUSION**

Field experiments using bio-organic fertilizers as replacement for chemical fertilizers had shown that potato growth and improve tuber quality could be promoted. The application of bio-organic fertilizers also improved soil fertility, increased bacterial diversity, and reduced fungal diversity. The relative abundance of harmful fungi, such as *Fusarium*,



**Fig. 4** Analysis of the correlation between microorganisms and environmental variables in soil samples at the genus level: (a) bacteria and (b) fungi.

*Verticillium*, and *Botryotrichum*, was reduced by bio-organic fertilizers. Soil bacterial and fungal composition was primarily driven by electrical conductivity and AP. This work provided a preliminary theoretical basis for reducing the use of chemical fertilizers.

#### Appendix A. Supplementary data

Supplementary data associated with this article can be found at <http://dx.doi.org/10.2306/scienceasia1513-1874.2021.039>.

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### Appendix A. Supplementary data

**Table S1** Significance of the soil physicochemical properties in explaining the microbial community structure obtained from the RDA results.

Soil property	Bacteria		Fungi	
	<i>F</i> -value	<i>p</i> -value	<i>F</i> -value	<i>p</i> -value
EC	5.2	0.006	3.6	0.016
AP	3.0	0.020	8.0	0.002
pH	0.8	0.576	0.6	0.682
OM	0.7	0.652	1.5	0.216
AK	0.8	0.612	1.2	0.386

EC, electric conductivity; OM, organic matter; AP, available P; AK, available K.