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# Effects of sweet potato intercropping in banana orchard on soil microbial population diversity

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## Abstract

**Purpose:** This study was purposely designed to understand the effects of intercropping banana and sweet potato on soil microbial community. The research question addressed was what were the differences in population number, population diversity and dominant population of soil microorganisms between interplant bananas with sweet potatoes and banana monoculture.

**Methods:** The Illumina MiSeq high-throughput sequencing technology was used to detect and analyse the population composition and structure of soil microorganisms in banana field.

**Results:** The results showed that from May to September, the number of soil bacterial population in intercropping sweet potato was 5.54–28.67% higher than that in monoculture, and the richness and diversity of the population were significantly or extremely significantly higher than that in monoculture. The number of dominant bacterial population was less than that in monoculture, and the relative abundance of non dominant population was 10.58–58.81% higher than that in monoculture. The number, abundance and diversity of soil fungal populations in intercropping were higher than those in monoculture.

**Conclusions:** The intercropping of banana and sweet potato has a significant effect on regulating the composition structure of soil microbial population and improving the abundance and diversity of microbial population. There has a great significance to improve the micro ecological environment of banana root soil and promote the stable and sustainable development of banana industry.

**Keywords:** Banana, Planting model, Microbial diversity, Population composition and structure

## Introduction

Banana (*Musa nana* Lour.) is second only to citrus in terms of global output and sales. It is mainly distributed in Asia, Africa, and South America. It is one of the most important fruit crops in tropical and subtropical areas (Arvanitoyannis and Mavromatis 2009; Dita et al. 2018). Because of its rich nutrition and easy absorption and digestion, banana is a fresh fruit widely enjoyed by consumers. In some countries in Africa and Central

and South America, banana is one of the important staple foods (Varma and Bebbber 2019; Tripathi et al. 2017). However, in recent years, due to the harm of *Fusarium* wilt, the production and development of the banana growing industry has been seriously threatened, resulting in a downward trend in planting area (Dong et al. 2020). The number of plants infected by *Fusarium* wilt accounted for 10%–40% of damaged plants in the banana plot, and in some plantations more than 90% of plants were infected (Huang et al. 2012). The damaged banana plants showed yellowing and withering of leaves, failure to bud and fructify normally, and serious decline in yield and quality (Ploetz 2015). Some studies have shown

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that the reasons for the occurrence and prevalence of banana Fusarium wilt are as follows: first, planting varieties singly and poor disease resistance of main varieties (Heslop-Harrison and Schwarzscher 2007); second, soil acidification and reduction of soil microbial diversity (Dita et al. 2018; Peng et al. 2014); third, poor cultivation measures (Pegg et al. 2019; Liu et al. 2019). Among them, soil acidification and the reduction of microbial diversity are the main reasons for the serious epidemic of banana Fusarium wilt (Shen et al. 2015; Li et al. 2019). In order to solve the problem of the cultivation of single varieties and the poor disease resistance of main varieties, breeders in major producing countries around the world have screened and bred varieties with strong resistance to Fusarium wilt, such as "Zhongjiao 9" (Zhang et al. 2021), Taiwan "Xinbei banana," "Nantianhuang" (Xu et al. 2017), Baodao banana (Hwang and Ko 2004) in China and so on. Although these varieties have strong disease resistance, due to their poor quality, long growth period, or poor cold resistance (Li et al. 2019), they have not been accepted by most growers and consumers and cannot be planted in a large area (Zhang et al. 2013). The main reason for soil acidification and the decrease in microbial diversity is the excessive application of chemical fertilizer and pesticides and fungicides during banana planting, resulting in the deterioration of soil structure and texture and the reduction of microbial population and quantity (Zhou et al. 2014; Huang et al. 2013). In addition, there are also some problems in the cultivation and planting system of banana. For example, most banana plantations have been subject to continuous cropping and monoculture for many years, aggravating plant diseases and insect pests year by year, resulting in soil and water loss, soil nutrient imbalance, structural deterioration, etc. (Tan et al. 2021; Xu et al. 2012). Banana Fusarium wilt is a soil borne vascular disease (Maryani et al. 2019). At present, the pathogen that infects bananas is *Fusarium oxysporum* Cuba specialized physiological race 4 (foc4) (Wang et al. 2020a) and it can grow in the range of 22–34 °C, but grows most vigorously under weak acidic conditions of 26–30 °C and pH 5. The banana plants are easily infected by it at 25–28 °C and soil water holding capacity > 25% (Pegg et al. 2019; Lin et al. 2010; Lin et al. 2000). The contents of soil organic matter and nutrients are closely related with the occurrence of Fusarium wilt. In banana orchards with Fusarium wilt, the contents of organic matter, CEC, total N, total P (ion), available P, available B, and exchangeable Ca in soil are lower than those in non-diseased orchard soil (Furtado et al. 2009). The genetic diversity of bacteria in the rhizosphere and non-rhizosphere soil of a diseased sample plot was lower than that of a healthy sample plot. The number and species of culturable bacteria, fungi, and actinomycetes in the

rhizosphere and non-rhizosphere soil of diseased plants in a diseased sample plot were also lower than those of healthy plants, and the number of pathogenic bacteria increased with the increase in plant susceptibility. The content of *Bacillus* in diseased plots was 17% higher than that in healthy plots (Bubici et al. 2019; Lian et al. 2008).

At present, the main technical measures to control banana Fusarium wilt are to apply alkaline fertilizer and lime, spray biocontrol solution on the roots of plants (Fan and Li 2014), or rotate and interplant with sugarcane (Zeng et al. 2019), peanut (Pattison et al. 2014), corn (Wang et al. 2015), leek (Huang et al. 2012; Zhang et al. 2013), and other crops. However, these technical measures have not been accepted by most banana growers and have not been popularized and applied in a large area due to the high input cost and complex cultivation and management. Therefore, we need to find a more suitable intercrop mode so as to change the cultivation pattern of banana continuous monoculture. Sweet potato stems and leaves grow vigorously, long growth period, creeping on the ground growth, sweet potato adaptability and regeneration, do not choose the soil, easy to survive, in winter could be survival, the next year continue to grow, is an excellent intercropping crop (Bovell-Benjamin 2007). At present, there is no report on the impact of planting sweet potato in banana garden on soil microbial diversity. In this paper, the effect of intercropping sweet potato on fungal and bacterial diversity in banana orchard were studied, so as to provide a theoretical basis for changing the planting mode of banana.

## Materials and Methods

### Test material

The tested banana variety was "Guijiao 1" and the sweet potato was "Pushu 32."

### Testing methods

The experiment was conducted in the banana planting base of Fusui agricultural science new town of Guangxi University from March 2018 to October 2020. The experimental site is located in the south subtropical monsoon climate region, with an annual precipitation of 1050–1300mm and an annual average temperature of 21.3–22.8°C. The soil fertility of the test site was as follows: available nitrogen 69.98 mg kg<sup>-1</sup>, available phosphorus 118.13 mg kg<sup>-1</sup>, available potassium 71.45 mg kg<sup>-1</sup>, organic matter 19.09 g kg<sup>-1</sup>, pH 4.50. Two treatments were set up in the experiment: the intercropping of banana and sweet potato and banana monoculture, marked as a and b, respectively. The planting density of banana is 124 plants/666.67m<sup>2</sup>, the area of each experimental plot was 81 m<sup>2</sup>, and the row and plant spacing of banana was 2.7×2m. The experiment was repeated three

times. Banana seedlings were planted on March 15, 2019, and two lines of sweet potato seedlings were planted between the rows of bananas on April 12. The row and plant spacing of sweet potato seedlings was 1×0.5m. The management measures followed for the banana, such as field fertilization, irrigation, and pest control, are the same as those used in production. The growth status of the banana orchard during the experiment is shown in Fig. 1.

#### Collection of soil samples in the test site

In May 2019, soil temperature and humidity measuring probes were installed in 5cm, 10cm, and 20cm soil layers of the banana plot to monitor and record the temperature and moisture content. In May, July, and September 2020, respectively, the litter and other mulch on the soil surface 30–50cm away from the banana plant were removed, and then samples 0–20cm from the soil surface were collected with the soil sampler from the field for the banana monoculture and the banana interplanted with sweet potato. The samples were collected and samples from 3–5 points from each experimental plot were mixed, debris such as animal and plant residues in the soil samples were removed, and the samples then bagged, placed in an ice box, and transported back to the laboratory for storage at - 20°C.

#### Determination of microbial diversity

The soil samples were sent to Beijing BioMarker Biotechnology Co., Ltd. to construct a small fragment library for high-throughput sequencing by using the second-generation sequencing technology Illumina and paired end sequencing. The v3–v4 region of 16S in bacteria was amplified and the ITS1 region in fungi was amplified. The soil samples from the intercropping with sweet potato in May, July, and September were labeled May / A, July

/ A, and Sep. /A, respectively, and that of the monoculture banana were labeled May / B, July / B, and Sep. / B, respectively. Raw reads obtained from sequencing were filtered using Trimmomatic v0.33 software, and then primer sequences were identified and removed using Cutadapt 1.9.1 software to obtain high quality reads. High quality reads stitched together using FLASH v1.2.7 software to obtain clean reads. The chimeric sequences were identified and removed using UCHIME v4.2 software to obtain the final effective reads. Subsequent bioinformatic analysis based on effective reads: OTU clustering based on a specific threshold (97% selected by default). The taxonomic annotation of the feature sequences was performed using a plain Bayesian classifier with SILVA as the reference database, and the taxonomic information corresponding to each feature could be obtained, and the sample community composition was counted at each level. Species abundance tables at different taxonomic levels were generated using QIIME software to compare differences in soil bacterial and fungal community composition between treatments.

#### Statistical analysis

Microsoft Excel 2010 software was used to process and draw the data, and IBM SPSS 26.0 was used for analysis of variance. All data and measurement results were expressed as average values.

## Results

### Effects of intercropping sweet potato in a banana orchard on the population and diversity of the soil bacteria and fungi community

It can be seen from Table 1 that during May to September, the number of soil bacterial communities of intercropping sweet potato was 476.00–511.67 and that of banana monoculture was 397.67–451.00. The number of



**Fig. 1** Field picture of banana plantation treated in the experiment. a=Sweet potato intercropped on a banana plantation. b= Banana monoculture

**Table 1** Quantity and diversity index of the bacterial community in the soil in sweet potato intercropping and monoculture in a banana orchard

Treatment	Number of colonies (pieces)	Ace index	Chao1 index	Shannon index
May/A	511.67±14.22Aa	1870.39±25.71Aa	1861.28±50.34Aa	9.29±0.03Aa
May/B	397.67±17.62Bb	1458.26±54.62Bb	1478.19±55.27Bb	7.99±0.13Bb
July/A	476.00±2.65Aa	1859.18±12.28Aa	1911.12±43.57Aa	9.51±0.11Aa
July/B	451.00±34.18Aa	1748.65±41.78Ab	1719.86±95.24Ab	9.16±0.15Ab
Sep/A	484.67±18.15Aa	1874.71±16.35Aa	1907.80±27.12Aa	9.45±0.04Aa
Sep/B	435.00±15.59Ab	1570.61±95.21Bb	1624.03±66.76Bb	8.61±0.04Bb

Samples were taken in May, July, and September. May/A = Intercropping treatment in May. May/B = Monoculture treatment in May. July/A = Intercropping treatment in July. July/B = Monoculture treatment in July. Sep/A = Intercropping treatment in September. Sep/B = Monoculture treatment in September. Different lowercase letters and uppercase letters indicate that there are significant differences between the two treatments in the same month at the levels of  $P < 0.05$  and  $P < 0.01$ , respectively

soil bacterial communities of intercropping increased by 28.67%, 5.54%, and 11.42% respectively in different months compared with that of monoculture, and the difference in May and September reached a significant level, but in July, there was no significant difference between intercropping and monoculture. The Ace and Chao1 indexes of community abundance of soil bacteria in intercropping were higher with 1859.18–1874.71 and 1861.28–1911.12 respectively than the 1458.26–1748.65 and 1478.19–1719.86 of the monoculture. The difference between the two treatments reached a significant or very significant level. The Shannon index of bacterial community diversity in the intercropping soil was 9.29–9.51, higher than that of 7.99–9.16 in the monoculture, and the difference reached a significant or extremely significant level in different months. The results showed that intercropping sweet potato in banana orchard could significantly improve the number, abundance, and diversity of the bacterial community in the soil.

The population of the fungal community in the soil subject to intercropping during May, July, and September was 154.33–198.33, and more than 112.00–147.00 in the monoculture (Table 2). But the difference between the two treatments did not reach a significant level. The

Ace and Chao1 indexes of soil fungi community in intercropping were 568.17–735.51 and 451.54–653.29, respectively, higher than 514.66–687.47 and 375.37–541.45 in monoculture. However, only in May, the difference in the Chao1 index between the two treatments reached a significant level, while the other differences were not significant. The Shannon index of soil fungi in intercropping was 5.92–6.72, and that of monoculture was 5.27–6.57. The Shannon index in intercropping in May and September was higher than that of the monoculture, while that of intercropping in July was lower than that of the monoculture, but the difference between the two treatments in three months was not significant. The results showed that intercropping sweet potato had a certain effect on the number, abundance, and diversity of soil fungi in the banana orchard.

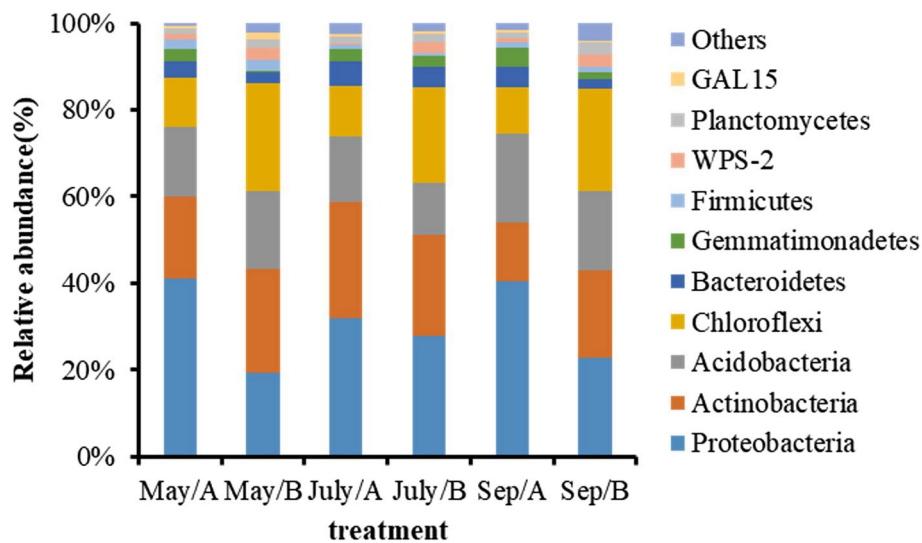
#### Effects of sweet potato intercropping in the banana orchard on the main bacterial phyla and population composition of the soil

The composition and relative abundance of soil bacterial community structure at the phylum classification level are shown in Fig. 2. *Proteobacteria*, *Actinobacteria*, *Acidobacteria*, *Chloroflex*, *Bacteroidetes*,

**Table 2** Quantity and diversity index of the fungi community in the soil in sweet potato intercropping and monoculture in a banana orchard.

Treatment	Number of colonies (pieces)	Ace index	Chao1 index	Shannon index
May/A	198.33±48.52Aa	735.51±74.49Aa	653.29±54.09Aa	5.92±0.92Aa
May/B	143.00±44.19Aa	659.87±94.06Aa	465.19±87.11Ab	5.27±0.69Aa
July/A	164.33±45.28Aa	726.27±152.18Aa	618.71±91.93Aa	6.35±0.48Aa
July/B	147.00±45.08Aa	687.47±161.94Aa	541.45±115.33Aa	6.57±0.31Aa
Sep/A	154.33±63.07Aa	568.17±42.07Aa	451.54±5.74Aa	6.72±0.68Aa
Sep/B	112.00±69.40Aa	514.66±33.32Aa	375.37±82.64Aa	6.25±0.13Aa

Samples were taken in May, July, and September. May/A = Intercropping treatment in May. May/B = Monoculture treatment in May. July/A = Intercropping treatment in July. July/B = Monoculture treatment in July. Sep/A = Intercropping treatment in September. Sep/B = Monoculture treatment in September. Different lowercase letters and uppercase letters indicate that there are significant differences between the two treatments in the same month at the levels of  $P < 0.05$  and  $P < 0.01$ , respectively

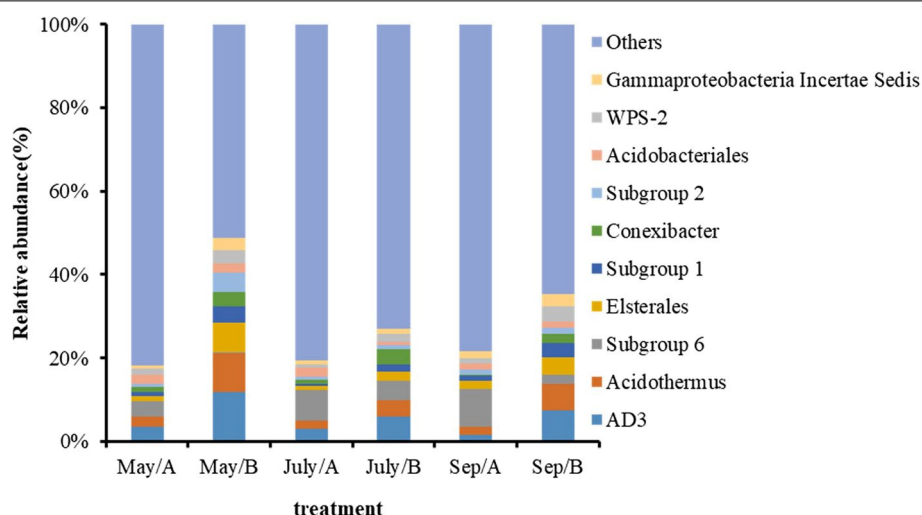


**Fig. 2** Relative abundance of main bacterial phyla communities in soil in intercropping and monoculture of a banana orchard. May/A = Intercropping treatment in May. May/B = Monoculture treatment in May. July/A = Intercropping treatment in July. July/B = Monoculture treatment in July. Sep/A = Intercropping treatment in September. Sep/B = Monoculture treatment in September

and *Gemmatimonadetes* were the dominant bacteria in the banana plot soil, which accounted for more than 88%. During May to September, the relative abundances of these six main bacterial phyla were 31.83–41.04%, 13.83–26.94%, 15.03–20.38%, 10.86–11.65%, 3.87–5.77%, and 2.71–4.43%, respectively, and that of the monoculture were 19.20–27.86%, 20.07–24.13%, 12.00–18.39%, 21.91–24.73%, 2.02–4.90%, and 0.33–2.39%, respectively. The relative abundances of *Proteus*, *Acidobacteria*, *Bacteroidetes*, and *Blastomonas* in intercropping were greater than those of the monoculture, and their monthly average abundances were increased by 67.92%, 8.64%, 64.37%, and 327.76% respectively. In May and September, the relative abundances of *Proteus* and *Blastomonas* were significantly higher than those of the monoculture, while the monthly average relative abundances of *Actinomycetes* and *Campylobacter* decreased by 12.62% and 51.65% compared with the monoculture. The results showed that the intercropping of sweet potato in the banana plot had a great effect on the community structure and composition of the main bacterial phyla in the soil, and the relative abundance of *Proteus*, *Acidobacteria*, *Bacteroides*, and *Blastomonas* increased significantly, but the relative abundance of *Actinomycetes* and *Campylobacter* reduced.

The composition, structure, and relative abundance of the main bacterial populations in soil between the intercropping of sweet potato and the monoculture were quite different. Among the detected bacterial populations, the dominant bacterial populations with relative abundance of more than 1% in the soil intercropped with sweet potato in May and September were *AD3*,

*Acidotherrmus*, *Subgroup 6*, and *Acidobacteriales*, and the relative abundances of other non-dominant populations were 81.78% and 78.29%. While dominant populations in the monoculture were *AD3*, *Acidotherrmus*, *Elsterales*, *Acidobacteriaceae Subgroup 1*, *Conexibacter*, *WPS-2*, and *Gammaproteobacteria Incertae*, and the relative abundances of other populations were 51.17% and 64.62%. But in July the dominant bacterial populations in the intercropping were *AD3*, *Acidotherrmus* and *Subgroup 6*, *Conexibacter*, and *Acidobacteriales*, the relative abundance of other populations was 80.7%, and those of the monoculture were *AD3*, *Acidotherrmus*, *Subgroup 6*, *Elsterales*, *Acidobacteriaceae Subgroup 1*, *Conexibacter*, *WPS-2*, and *Gammaproteobacteria Incertae*, the relative abundance of other populations was 72.98%. Among these dominant soil bacterial populations, the relative abundance of *AD3*, *Acidotherrmus*, *Elsterales*, *Acidobacteriaceae Subgroup 1*, *Conexibacter*, and *WPS-2* was lower than that in the monoculture, and the difference reached a significant or extremely significant level, while the relative abundance of *Subgroup 6* and other populations was significantly or extremely significantly higher than that in the monoculture (Fig. 3). The results showed that sweet potato intercropping in the banana orchard had a significant effect on regulating the composition and structure of the soil bacterial population, the relative abundance of the soil dominant bacterial population was reduced, and that of the non-dominant bacterial population increased. The relative abundance of the non-dominant population increased by 10.58–58.81%.

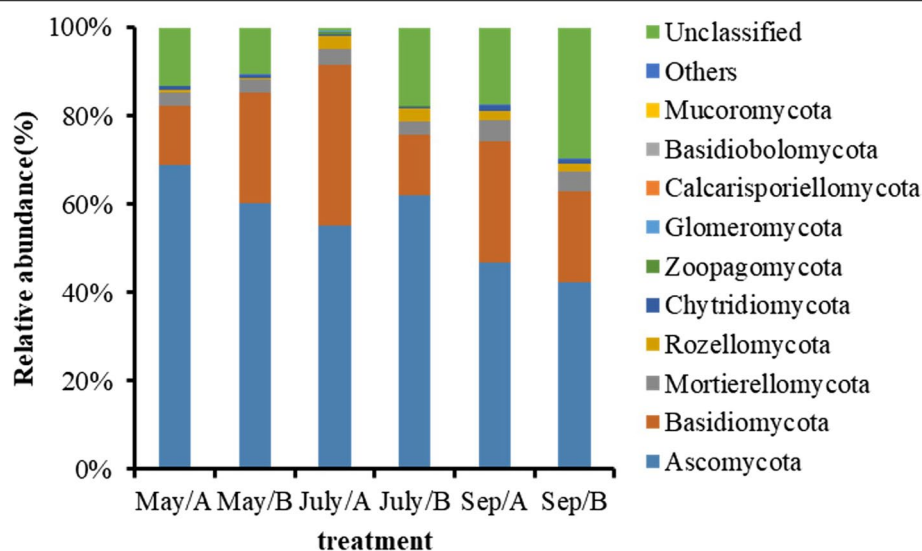


**Fig. 3** Relative abundance of main bacterial populations in soil in banana intercropping and monoculture. May/A = Intercropping treatment in May. May/B = Monoculture treatment in May. July/A = Intercropping treatment in July. July/B = Monoculture treatment in July. Sep/A = Intercropping treatment in September. Sep/B = Monoculture treatment in September

#### Effects of sweet potato intercropping in the banana orchard on the composition and structure of the main fungi phyla and population composition in the soil

At the phylum classification level, the composition and relative abundance of the soil fungal community in the banana orchard are shown in Fig. 4. During May to September, *Ascomycota*, *Basidiomycota*, *Mortierellomycota*, *Rozellomycota*, *Chytridiomycota*, and *Glomeromycota* were the dominant fungi, and the number of communities of these dominant fungi accounted for more than

86%. In which the relative abundances of *Ascomycota* were the highest with 46.79–68.88% for intercropping and 42.33–61.95% for monoculture. The relative abundances of the other five population groups in the intercropping were 13.43–36.53%, 2.81–4.63%, 0.76–2.93%, 0.45–1.27%, and 0.05–0.27% respectively, those in the monoculture were 13.9–24.88%, 2.91–4.31%, 0.35–2.85%, 0.24–0.99%, and 0.00–0.19% respectively. The monthly average relative abundance of the six dominant groups in intercropping was higher than that in monoculture, but only in July the



**Fig. 4** Relative abundance of main fungal phyla communities in soil in intercropping and monoculture of a banana orchard. May/A = Intercropping treatment in May. May/B = Monoculture treatment in May. July/A = Intercropping treatment in July. July/B = Monoculture treatment in July. Sep/A = Intercropping treatment in September. Sep/B = Monoculture treatment in September

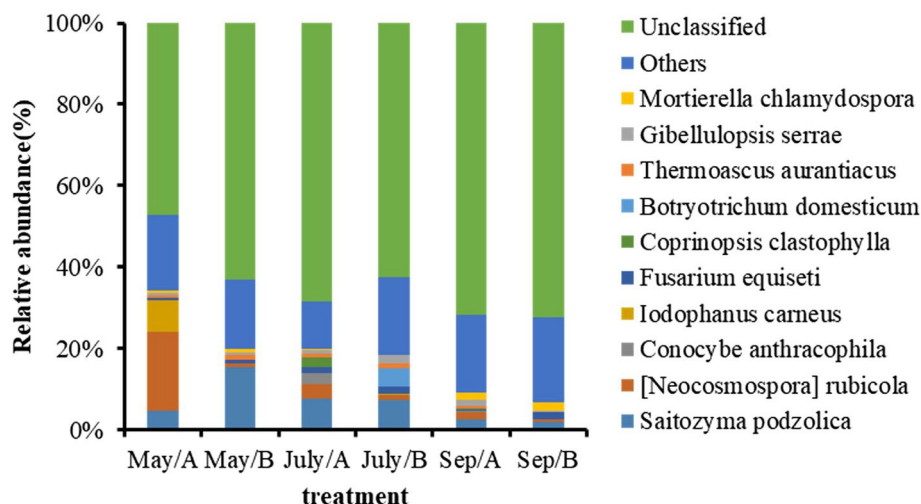
relative abundance of *Basidiomycetes* and *Coccidiomycetes* was significantly higher than that in monoculture, and that of the remaining fungi community between intercropping and monoculture did not reach a significant level in three months. The results showed that intercropping sweet potato had an important regulatory effect on the relative abundance of *Basidiomycetes* and *Coccidiomycetes* in the banana plot soil, but had little effect on other fungal communities.

In different periods of banana growth, the composition and structure of soil fungal populations in intercropping with sweet potato were very different from those in monoculture (Fig. 5). In May, the relative abundance of soil fungi in intercropping reached more than 1% including *Podzolica*, *Neocosmospora rubicola*, and *Iodophanus*, in which, the highest relative abundance was *Neocosmospora rubicola* (19.43%), followed by *Iodophanus carneus* (7.62%), and *Saitozyma podzolica* (4.81%). While there was only *Saitozyma podzolica* and *Neocosmospora* in the banana monoculture, their relative abundance was more than 1%, being 15.42% and 1.00%, respectively. The relative abundance of *Neocosmospora\_rubicola* and *Iodophanus carneus* in intercropping was significantly higher than that of monoculture, and that of *Saitozyma podzolica* was significantly lower than that of monoculture. There was no significant difference in the other fungal populations between intercropping and monoculture. In July, the dominant fungal population in the intercropping soil was made up of *Saitozyma podzolica*, *Neocosmospora rubicola*, *Conocybe anthracophila*, *Fusarium equiseti*, and *Coprinopsis*, and that in the monoculture was *Saitozyma podzolica*, *Neocosmospora\_rubicola*, and

*Fusarium equiseti*. The relative abundance of three populations including *Neocosmospora\_rubicola*, *Conocybe anthrophila*, and *Coprinopsis cladophylla* in intercropping was significantly higher than that in monoculture, and there was no significant difference between other non-dominant populations between the two treatments. In September, only *Saitozyma podzolica* and *Neocosmospora rubicola* constituted the dominant fungal population in the intercropping soil, while those in the monocultured soil were *Saitozyma podzolica* and *Fusarium equiseti*. The relative abundance of other communities was less than 0.7%. The relative abundance of *Neocosmospora rubicol* and *Coprinopsis clastophylla* population in intercropping was significantly higher than that in monoculture, while that of the *Fusarium equiseti* population was significantly lower than that in monoculture, and there was no significant difference in the other non-dominant fungal populations between intercropping and monoculture. In addition, the relative abundance of unclassified soil fungal populations was 47.27–71.80% in intercropping and 62.31–72.17% in monoculture. The results showed that the intercropping of sweet potato in the banana orchard could regulate the composition and structure of the main soil fungi population and the relative abundance of dominant populations was improved significantly and that of *Saitozyma podzolica* and *Fusarium equiseti* was reduced.

## Discussion

The indicators reflecting microbial community abundance mainly include the Chao1 and ACE index. The Shannon index indicates microbial community diversity.



**Fig. 5** Relative abundance of main fungal populations in soil in banana intercropping and monoculture. May/A = Intercropping treatment in May. May/B = Monoculture treatment in May. July/A = Intercropping treatment in July. July/B = Monoculture treatment in July. Sep/A = Intercropping treatment in September. Sep/B = Monoculture treatment in September

The greater the value of these indicators, the greater the microbial community abundance and diversity (Grice et al. 2009). The results of this study showed that intercropping sweet potato in the banana orchard had an important effect on improving the number and diversity of the soil microbial community. The main reason is that the diversity and richness of the soil microbial population are affected by environmental factors such as soil temperature, humidity, pH value, organic matter, and other soil properties. Studies have shown that the diversity and abundance of soil bacteria and fungi are negatively correlated with temperature (Fu et al. 2020) and positively correlated with soil humidity (Huang et al. 2019), pH, and organic matter content (Tang et al. 2020; Zhong et al. 2010; Du and Geng 2021). A further result of our study was that after intercropping sweet potato in the banana plot, the soil pH value, organic matter, and water content were significantly increased, and the soil temperature of the topsoil in summer was reduced (Li et al. 2022).

Sweet potato was planted in March in spring under normal conditions, and its stem and vine length reached more than 1m by May, basically covering the inter row of banana because it was a fast-growing crop. The exposed soil between the rows in the banana plot was covered with sweet potato stems and leaves, and the topsoil was protected by avoiding the strong summer sunlight. The evaporation loss of soil moisture and the temperature of the topsoil were reduced, and the scouring of topsoil in the case of heavy rainfall slowed down, thus the loss of soil water and nutrients was reduced. In addition, the stems and leaves of sweet potato grew vigorously, branches and leaves were constantly formed, and a large number of dead branches and leaves returned to the soil, increasing the organic matter of the soil through their decay. At the same time, the stems and leaves of sweet potato are rich in mineral elements such as iron, calcium, magnesium, potassium, and phosphorus, and these minerals were released into the soil (Chen et al. 2014; Ishida et al. 2000), which increased the effective mineral nutrient content of the topsoil, thus the pH value of the soil was increased and the structure and aeration performance of the soil improved (Cao et al. 2020; Qiu 2019; Ge et al. 2014). So the soil microecological conditions were more suitable for the growth and reproduction of bacteria and fungi. The stem and leaf of the sweet potato that died, returned to the soil becoming a source of carbon and nitrogen for the microorganisms (Sun et al. 2014) so that different types of microbial community have sufficient carbon and nitrogen sources, thus more microbial populations could grow and proliferate. Therefore, intercropping sweet potato has a good effect on increasing the number, abundance, and diversity of soil bacteria and fungi, which was similar to the effect of intercropping

*Senna tora*(L.)Roxburgh and leek with banana (Wang et al. 2020b).

Under the condition of intercropping sweet potato, the relative abundance of dominant bacterial and fungal communities in the soil at the phylum classification level was higher than that in monoculture, but the number of dominant bacterial populations was reduced by 3 populations, while the relative abundance of other non-dominant populations was higher than that in monoculture, increased by 10.58–58.81%. But the effects on fungal populations are different. The number of dominant fungal populations in intercropping is 1–2 more than that in monoculture, and the relative abundance of dominant populations is higher than that in monoculture, which is similar to the effect of increasing organic fertilizer and returning straw to the field in the tidal soil area of the North China Plain (Jiang et al. 2019; Wu et al. 2020). However, there are some differences with the research results of Wu and others in the effects on different dominant bacterial and fungal populations, which may be related to the differences of soil type, temperature, and humidity. The reason may be related to the increase in the abundance of the non-dominant bacterial population. Soil organic matter is an important source for microbial nutrition and energy. The microbial activity is also limited by soil nutrition availability (Tan et al. 2021). When other bacterial populations grow and compete with the dominant community for limited carbon and nitrogen sources, the growth of the dominant bacterial population is limited due to the limitation of the amount of organic nutrients in the soil, resulting in a decrease of its abundance. But the fungi can coexist with plants to form mycorrhizal (Wu et al. 2020), in the early stage of growth, they obtain nutrients from plants, are less affected by restricted soil nutrients, high temperature and drought, thus the dominant fungal population can grow and proliferate.

In addition, the effect of soil temperature on the growth of bacteria and fungi is different. The results of this study showed that in July with the highest temperature, the population number and relative abundance of bacteria are lower than in May and September with lower temperature. It is speculated that when the temperature was > 30°C, the growth of some heat-resistant bacterial communities was inhibited, and the growth of humidity loving bacterial communities was limited by the high temperature and the decline of soil humidity, thus the number of bacterial populations and their relative abundance decreased (Sayer et al. 2017; Ishaq et al. 2020; Vries et al. 2018). The number and relative abundance of dominant fungal populations in intercropping were higher than those in monoculture, but the difference between different months was not as large as that of bacterial populations. The reason may be related to

the strong heat resistance of fungi (Vries and Shade, 2013; Barnard et al. 2013). Studies have reported that most fungal populations isolated from soil and compost in many places in China were thermophilic and heat-resistant fungi (Liang et al. 2011a, b). These heat-resistant fungal populations could grow and proliferate even under high temperature conditions. The composition and structure of the soil microbial population are affected by soil micro ecological conditions, and play an important role in soil nutrient metabolism and transformation, thus affecting the growth and development of crops. The improvement of microbial diversity in the crop rhizosphere and the enhancement of the reproductive activities of beneficial microbial populations would help to promote crop growth (Dai et al. 2017; Dai et al. 2020; Berg, 2009). On the other hand, the vigorous reproductive activity of harmful microbial populations would inhibit the growth and development of crops (Pei et al. 2010; Kong 2007).

## Conclusions

The results of this paper showed that the intercropping of banana and sweet potato has an important effect on regulating the community and structure of soil bacteria and fungi, and improved the richness and diversity of soil microbes. Therefore, this planting model offers many benefits, such as improving the soil micro ecological environment and increasing the content of soil organic matter. Its popularization and application will help to promote the stable and sustainable development of the banana industry.

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Not applicable

## Authors' contributions

Y.P. and W.X. designed the study and wrote the manuscript. Y.P., J.L. and S.X. performed the experiments. Y.P. and W.X. analyzed the data. D.F. and Y.D. revised the manuscript. The authors read and approved of the final manuscript.

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## Availability of data and materials

The datasets used and/or analyzed during the current study are available from the corresponding author on reasonable request.

## Declarations

## Ethics approval and consent to participate

Not applicable.

## Consent for publication

Not applicable.

## Competing interests

The authors declare that they have no competing interests.

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