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HAIBO WU

LIANCHUN WANG

LINAN KANG

CHAO LIU

MINGWEI LI

TÜBİTAK

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Study on the effect of planting pattern adjustment on the growth of kiwifruit inter-root microorganisms and fruit quality

Haibo WU*, Lianchun WANG, Linan KANG, Chao LIU, Mingwei LI
Faculty of Forestry, Southwest Forestry University, Kunming, China

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Abstract: As the area planted with kiwifruit continues to expand, monoculture continuous cropping is gradually becoming the main mode of its production. However, current kiwifruit soils suffer from nutrient deficiencies and increased toxicity of their own, which are harmful to their yield and quality. The study proposes a kiwifruit-maize intercrop as a starting point for adjusting the cropping pattern. It was then analysed in terms of basic soil physicochemical properties, sucrose enzyme activity, microbial species, and quantity, respectively, and compared with the kiwifruit intercropping method to verify its effect on inter-root microorganisms and fruit quality. The experimental outcomes demonstrated that the adjusted cropping pattern increased the organic matter content year by 3 years, reaching a maximum of 749.36 g·kg^{-1}, with some improvement in all basic physicochemical property indicators such as total phosphorus and fast-acting potassium compared to the preadjustment period. In terms of inter-root soil microbial growth, the kiwifruit-maize intercropping pattern increased microbial species and numbers, with significant differences compared to preadjustment ($p < 0.05$). In the comparison of fruit quality, the adjusted cropping pattern was of higher quality, with a significant difference ($p < 0.05$), indicating that this pattern can effectively improve the inter-root microbial ecology of kiwifruit, providing a reference direction for further improvement of its yield and quality.

Key words: Planting pattern, kiwifruit, inter-root microorganisms, fruit quality

1. Introduction

Kiwifruit is a perennial deciduous vine, dioecious, belonging to the kiwifruit genus of the kiwifruit family (Purohit et al., 2021; Aryafar et al., 2021; Tu et al., 2021). Kiwi fruit is mainly distributed in the northern hemisphere, with a wide range from Nepal and southeast India to Japan and Taiwan Island of China from west to east. Kiwi resources are mainly distributed in the area south of Qinling Mountains and east of Hengduan Mountains. Kiwi was successfully domesticated into a cultivated fruit tree in the 20th century. At the beginning of the 20th century, kiwifruit was discovered and introduced by New Zealanders in Yichang, Hubei Province, China (Varkonyi et al., 2021; Akagi et al., 2019; Wuet al., 2020). After nearly 25 years of domestication and decades of cultivation and promotion efforts, large-scale cultivation began to appear in the 1970s. It was not until 1978 that the kiwi industry in China began to receive the attention of the government. With the support of the government, the kiwi germplasm survey and variety selection have developed rapidly. Kiwi is a berry, which is rich in sugar, protein, amino acid, and other nutrients, and provides a large amount of minerals and vitamins for the human body (Li et al., 2022; Noori et al., 2022; Goffi et al., 2020). Because it contains more vitamin C than other fruits, it is named "the king of VC" and "the king of fruit". Kiwi fruit is soft and juicy and has a wide range of uses. In addition to being used as fresh fruit, kiwi fruit juice, canned kiwi fruit, fruit wine, preserved fruit, and other products are mainly developed and utilized through processing. The medicinal value of kiwi fruit has been discovered very early. According to records, kiwi can effectively treat osteoarthrosis, eliminate haemorrhoids, and delay hair whitening. With the study of its medicinal function, it is found that its dietary fibre can effectively promote gastrointestinal peristalsis (Chaghakaboodi et al., 2022; Ganjali et al., 2022; Ghamarnia et al., 2022). Rich antioxidant substances and kiwifruit seeds are rich in a large number of unsaturated free fatty acids, which promote blood flow, effectively prevent thrombosis, and have the function of reducing blood fat, blood pressure, and improving immunity.

Soil microorganisms assume an important role in the process of material cycling and ecosystem composition,

* Correspondence: whb5383@swfu.edu.cn

as they not only regulate the soil environment but also enhance the resistance of plants to external natural stresses and further facilitate the uptake of mineral nutrients (Lai et al., 2019). It is with these characteristics that soil microbial growth has become one of the main indicators of the health of the soil environment (Ram et al., 2019). In the context of the proliferation of commercial cultivation, monoculture kiwifruit cultivation has resulted in reduced yields, nutrient disorders, and the normal growth of inter-root microbial communities, leading to a significant increase in the incidence of soil-borne diseases such as root rot and bacterial ulcers (Meena et al., 2019). In recent years, the subject of kiwifruit fruit quality and soil microbial growth has received the attention of many professionals at home and abroad, and a series of research outcomes have been obtained. Wu Y's team measured domestic Hayward kiwifruit inoculated with this AYRSpV virus infection against a novel kiwifruit virus. The final outcomes demonstrated that symptoms such as greenish ringspot on kiwifruit leaves appeared in spring and disappeared in summer, with significant reductions in chlorophyll content, fruit yield, sugar content, sugar-to-acid ratio, and dry matter content, all of which indicated that virus infection significantly affected kiwifruit yield and that countermeasures were urgently needed (Wuet al., 2022). Neemisha's team suggested that the growth of inter-rooted plants could promote the positive ecological effects of inter-rooted bacteria (PGPR) on the environment positive effect. In this process, inter-rooted microorganisms can also release essential nutrients to improve soil quality and promote healthy plant growth. Studies have focused on the control of nutrients and diseases in the soil by inter-rhizosphere bacteria to synthesize bacterial colonies eventually confirming and promoting the use of efficient microbial inoculants developed by inter-rhizosphere microorganisms, sufficient to enhance fruit quality (Neemisha et al., 2022). The interaction between inter-rhizosphere microbial inoculants and mineral fertilizers in the soil was investigated by Sarpong et al. (2020). It was found that the plant inter-root microbiome was not only related to the health of the plant itself, but also closely related to growth and productivity. The plant microbial assemblages involved were able to interact with mineral resources in the soil to enhance fruit quality and yield (Sarpong et al., 2020). Cui et al. (2020) explored the microbial population structure of mulberry orchard soils of different use ages by using high-throughput sequencing techniques. The data demonstrated that the most abundant microbial population in the soil was 35Y and the second most abundant was 200Y soil. This indicates that the age of the forest garden has a very important influence on the structure of the bacterial community in the soil. The richness and diversity of microorganisms in the soil decrease with the age of the plantation (Cui et al., 2020).

In summary, in studies of kiwifruit soil microbial growth and fruit quality, the main focus has been on assay methods and mechanisms of influence, with less research on planting pattern adjustments. Meanwhile, few studies have been conducted on the growth of kiwifruit inter-root microorganisms under the influence of different cropping patterns and there is a lack of relevant cropping adjustment measures. The study therefore compares kiwifruit-maize intercropping patterns with kiwifruit continuous cropping patterns in terms of inter-root microorganisms and fruit quality, with a view to exploring better cropping patterns to promote further quality improvement.

2. Materials and methods

2.1. Test materials and methods

The trial area was chosen in a modern demonstration park for kiwifruit in Xi'an, Shaanxi Province, which contains 10,000 mu of organic kiwifruit cultivation. It is bordered by the Wei River in the north and the Qinling Mountains in the south, spanning three natural landform units: the Wei River Plain, the Qinling Mountains, and the Loess Plateau (Varkonyi-Gasic et al., 2019). This area has a temperate continental monsoon climate, with annual precipitation of roughly 680–800 mm, mainly concentrated between July and September, an average annual temperature of between 10 °C and 13.2 °C, a frost-free period of 225 days, and an average annual sunshine of around 1993 h. The territory is rich in water and irrigation is convenient (Liet al., 2019). The soil types are mainly loess, tidal, loam, and rice soils, which are relatively loose and well-cultivated. Thanks to its geographical location and unique natural conditions, the area is known as a major agricultural county and an important producer of fruit and grain, including mainly summer maize and winter wheat, and kiwifruit (Mondal et al 2019). The kiwifruit variety selected for the trial is the highly acclaimed 'Qinmei', which is 11 years old, with a density of 1965 plants/hm^2 and a spacing of 1.8 m × 2.8 m. The soil used for the trial was developed from a loess parent material and was soil. The soil contained 16.01 g/kg of organic matter (SOM), 141.68 mg/kg of fast-acting phosphorus (AP), 377.12 mg/kg of fast-acting potassium (AK), and 1.5 g/kg of total phosphorus (TP) in the 0–20 cm layer. The study selected two cropping patterns, kiwifruit-maize intercropping and kiwifruit continuous cropping, at two kiwifruit farms in the region. Both kiwifruit-maize intercropping and kiwifruit continuous cropping were selected at two kiwifruit sites in the region, and root microorganisms and fruit quality

were compared at 1, 2, and 3 years of planting. Basic information on the two selected sites is demonstrated in Table 1.

For the extraction of soil microbial DNA, approximately 0.36 g weight of kiwifruit inter-root soil was weighed from each of the two planting pattern areas and then run through the Power Soil DNA Isolation kit. The extracted DNA was then tested using a 1.5% agarose gel and the DNA concentration was measured by NanoDrop 2000 (Thermo). A total of 18 DNA samples were extracted from the two cropping patterns in three years, with three replicate samples wrapped for each region in each year. The V4–V5 region of the 16S rRNA of inter-rhizosphere soil bacteria was processed for amplification with the aid of primers 515F/907R, where the PCR amplification procedure was 72 °C for 10 min, 94 °C for 5 min, 94 °C for 30 s, 72 °C for 90 s, 60 °C for 60 s for 34 cycles. PCR products were quantified by QuantiFluorTM -ST Blue fluorescence quantification system and finally high-throughput sequencing was performed by the MiSeq platform (Illumina) PE250. For the determination of soil physicochemical properties, soil pH was determined by the glass electrode method with a water-to-soil ratio of 2.5:1 (Srivastava et al., 2021). Soil fast-acting potassium and fast-acting phosphorus were each preextracted with ammonium acetate and sodium bicarbonate, and their content was then determined with the aid of a flow analyser. Total phosphorus and nitrogen were determined by perchloric acid-sulphate solution-molybdenum antimony colorimetry, while nitrate nitrogen (NN) and ammonia nitrogen (AN) were determined by leaching with potassium chloride and using a flow analyser. In the determination of kiwifruit inter-root soil enzymatic activity, sucrase activity was determined by 3,5-dinitrosalicylic acid colourimetry, urease activity by indophenol blue colourimetry and potassium permanganate titration was used to determine peroxidase activity. Hydrolase activity was obtained by the fluorescein diacetate colourimetric method and acid phosphatase activity was obtained using the sodium phenyl phosphate colourimetric method. Thirty-two fruits were collected randomly at maturity from two areas of kiwifruit planting patterns: kiwifruit continuous and kiwifruit-maize intercropping, respectively. For the assessment of their fruit quality, soluble solids content was determined by a hand-held brix meter and soluble protein content by the Kaumas Brilliant Blue G-250 method. Total sugar content and total acid content were determined using the anthrone and acid-base titration methods respectively, chlorophyll content was obtained by colourimetric acetone leaching and Vc content was determined by KIO3 titration. The route of the test method is demonstrated in Figure 1.

2.2. Data processing and analysis

The PE reads obtained from sequencing were first removed from low-quality splices and sequences, and then optimized using the Usearch software platform, i.e. single sequences that were not repetitive were removed and nonrepetitive sequences were extracted. OTU (Operational Taxonomic Units) clustering was then applied to the nonrepeated sequences (excluding single sequences) based on the 97% similarity (Wu et al., 2020). Also, chimeras must be removed during the OUT clustering process to obtain accurate representative sequences for the OTUs. The entire optimised sequence is then MAP to the OTU representative sequences obtained in the previous step and those sequences that are more than 97% similar to the OTU representative sequences are selected to generate the required OTU tables. The alpha diversity of the bacteria was calculated by Mothur software, which was achieved based on the OTUs contained in the individual samples. The calculated alpha diversity includes the diversity index (Shannon, Simpson), the richness index (ACE, Chao1), and the sequencing depth index (Coverage). In contrast, to obtain species classification information for all OTUs, taxonomic analysis was implemented using the Qiime platform and the RDP classifier Bayesian algorithm for representative sequences of OTUs with 97% similarity level, and community composition was counted for each sample on Phylum, Family, Genus for 16S bacteria and the archaeal ribosome database Silva (Thorpet al., 2021). In addition,

Table 1. Basic information about the two selected planting bases.

Test area	Kiwifruit continuous cropping	Kiwi-corn intercropping
SOM (g/kg)	16.01	15.92
AP (mg/kg)	141.68	142.37
AK (mg/kg)	377.12	368.05
TN (g/kg)	0.57	0.43
TP (g/kg)	1.64	1.61

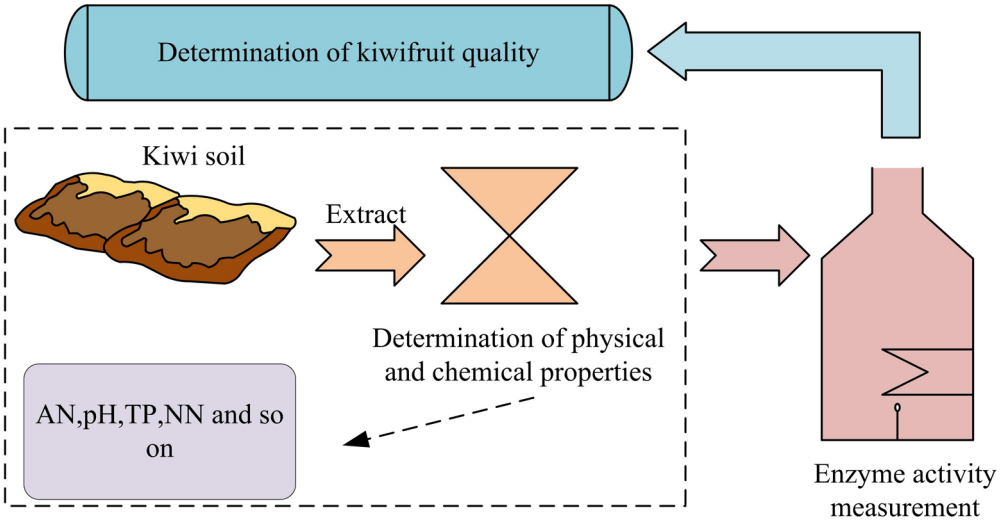

Figure 1. Experimental design route for the influence of rhizosphere microorganism growth and fruit quality of kiwifruit.

the taxa that were characteristically significant in all years of cultivation were screened by Line Discriminant Analysis Effect Size LEfSe on the Galaxy platform, with the LDA value set to 4.0. The statistical analysis was carried out using SPSS 19.0. Finally, the diversity index, richness index, OTU number, and soil physicochemical properties were compared between years by one-way ANOVA, while parameters that did not meet the chi-squared requirement were analysed by nonparity test, i.e. chi-squared test, and the trends in diversity indices were fitted by quadratic regression for year variation. The relationship between bacterial dominance and diversity indices and soil physicochemical properties was tested by Pearson correlation. The significance of differences between years in the abundance of dominant genera and the occurrence of the same clade was tested by one-way ANOVA. The functional diversity indices included the community McIntosh index (U), the community Shannon index (H), and the community Simpson index (D) were calculated as demonstrated in equation (1).

$$\begin{cases} H = -\sum Pi \cdot lnPi \\ D = 1 - \sum (Pi)^2 \\ U = \sqrt{\sum Ni^2} \end{cases} \quad (1)$$

In equation (1), Pi represents the ratio of the total relative absorbance value of the entire microplate to the relative absorbance value of i well, and Ni is the relative absorbance value of the i well. For the average colour change of the microplate wells, which represents the extent to which soil microorganisms are able to utilise a single carbon source, the calculation is in equation (2).

$$AWCD = \sum (C_i - R)/31 \quad (2)$$

In equation (2), R represents the absorbance of the control wells, C_i represents the absorbance of the i reaction well at 590 nm and $AWCD$ is the average colour change of the microplate wells.

3. Result

3.1. Effect of cropping pattern adjustment on soil physiochemical properties in the rhizosphere

The outcomes are in Table 2, which compares the physical and chemical properties of kiwifruit-maize intercropping and kiwifruit continuous cropping, including total nitrogen, organic matter, ammoniacal nitrogen, nitrate nitrogen, total phosphorus, fast-acting phosphorus, and fast-acting potassium, as well as pH, at 1, 2, and 3 years of cropping. From Table 2, soil pH tended to decrease with increasing years in the general kiwifruit cropping pattern, i.e. the kiwifruit continuous cropping pattern. In contrast, soil pH in the kiwifruit-maize intercropping pattern demonstrated less overall variation and a slight increase, with a significant difference between the two compared to each other. Soil fast-acting phosphorus (AP), total phosphorus (TP), and fast-acting potassium (AK) contents were significantly higher in the kiwifruit-maize cropping pattern than in the kiwifruit continuous cropping pattern. In terms of soil organic matter content, both cropping patterns demonstrated a greater increase with each year, but the adjusted cropping pattern was still significantly higher than the general cropping pattern. In terms of total nitrogen (TN) and nitrate nitrogen (NN) content, both cropping patterns fluctuated with

Table 2. Comparison of physical and chemical properties of kiwifruit rhizosphere soil under different planting modes.

Planting mode	Kiwifruit continuous cropping			Kiwi-corn intercropping		
Year	1	2	3	1	2	3
pH	5.18 ± 0.34a	5.12 ± 0.04ac	4.42 ± 0.16b	6.35 ± 0.07abc	6.85 ± 0.25abc	6.76 ± 0.02bc
AP (mg/kg)	9.56 ± 7.92a	9.03 ± 1.45a	9.32 ± 12.30a	9.88 ± 6.83a	10.54 ± 2.36a	28.61 ± 9.47a
AN (mg/kg)	0.12 ± 0.03a	0.03 ± 0.01b	0.07 ± 0.03ab	0.33 ± 0.02b	0.23 ± 0.15ab	0.06 ± 0.01ab
NN (mg/kg)	0.07 ± 0.04a	0.14 ± 0.08a	0.02 ± 0.01a	0.09 ± 0.02a	0.17 ± 0.03a	0.04 ± 0.01a
TN (g/kg)	0.56 ± 0.11b	1.24 ± 0.15a	1.23 ± 0.06a	0.75 ± 0.14ab	1.59 ± 0.13ab	1.47 ± 0.04ab
AK (mg/kg)	39.62 ± 9.78ab	22.84 ± 2.53b	19.03 ± 6.89ab	37.54 ± 6.25b	38.65 ± 43.31ab	38.26 ± 5.32a
TP (g/kg)	0.28 ± 0.05b	0.42 ± 0.07b	0.51 ± 0.01b	0.30 ± 0.02b	0.45 ± 0.05a	0.61 ± 0.03a
SOM (g/kg)	451.98 ± 85.24ab	502.01 ± 150.37ab	512.05 ± 198.73ab	498.52 ± 76.36a	564.29 ± 163.58b	586.41 ± 162.95a

Note: The small letter indicates the significance of the difference at 0.05 level. If the variance is homogeneous, it is F value, and if the variance is uneven, it is x^2.

increasing years, but the kiwifruit-maize intercropping pattern was higher than the former.

3.2. Effect of plant pattern adjustment on soil enzyme activity in macaque picking rhizosphere

Kiwifruit inter-root microbial growth will have a direct impact on soil enzyme activity, and soil nutrient transformation, effectiveness, and cycling are closely related to the enzyme activity it contains. In general, sucrase and urease activities in the inter-root soil correlated well with microbial growth. Sucrase activity is able to hydrolyse sucrose to give fructose and glucose, thus increasing the amount of labile nutrients in the soil. Urease, as a highly substrate-specific hydrolase, is an important player in soil nitrogen transformation and cycling and can characterise the direction and intensity of soil nitrogen biology in the transformation process. These two enzyme activities were therefore selected for analysis in the study. The changes in inter-root soil sucrase activity under the two cropping patterns are in Figure 2. Figure 2 demonstrates the variation of inter-root soil sucrase activity with the year for both kiwifruit continuous cropping and kiwifruit-maize intercropping, with the horizontal coordinates indicating the various stages of kiwifruit growth, namely germination, flowering, fruit expansion and fruit ripening, and the vertical coordinates demonstrating sucrase activity. In Figure 2, the sucrase activity of the inter-root soil of both cropping patterns decreases and then gradually increases as the kiwifruit matures. From Figure 2(a), there is a general trend of decreasing sucrase activity as the years increase in the kiwifruit succession pattern. Sucrase activity was generally higher in the first year of the three years than in the second and third years, with the highest values at the germination stage. From Figure 2(b), it can be observed that under the kiwi-maize intercropping pattern, sucrase activity fluctuated less over the three years as the number of years increased, and even demonstrated an increase at the maturity stage. A comparison between Figure 2(a) and Figure 2(b) demonstrates that the kiwi-maize intercropping pattern had a higher sucrase activity overall than the kiwi continuous crop pattern, and the difference in sucrase activity between the two was significant ($p < 0.05$).

The inter-root soil urease activity was then compared between the two patterns, as demonstrated in Figure 3. Figure 3 demonstrates the variation in soil urease activity of kiwifruit in years 1, 2, and 3 under both cropping patterns. In Figure 3, the urease activity under both cropping patterns reached its highest value at the fruit expansion stage and then declined at the fruit ripening stage, with an overall trend of increasing and then decreasing. From Figure 3(a), the overall decrease in inter-root soil urease activity under the kiwifruit continuous cropping pattern was observed as the year progressed. From Figure 3(b), there was an overall increase in soil inter-root urease activity with increasing years under the kiwifruit-maize intercrop cropping pattern. A comparison of Figure 3(a) and Figure 3(b) demonstrates that there was a significant difference ($p < 0.05$) in inter-root soil urease activity between the two cropping patterns.

3.3. OTU and diversity distribution under planting mode adjustment

The OTU and diversity distributions of the two cropping patterns were then compared and the outcoming fungal OTU and bacterial OTU numbers are in Figure 4. Figure 4(a) demonstrates the bacterial OTU counts for both cropping patterns and Figure 4(b) demonstrates

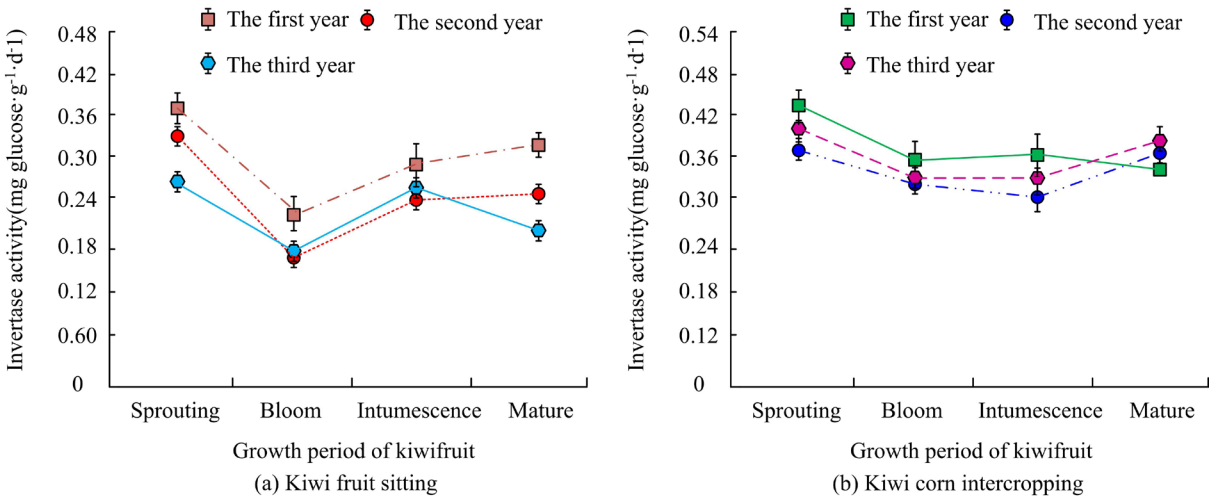

Figure 2. Changes of invertase activity in rhizosphere soil with years under two planting patterns.

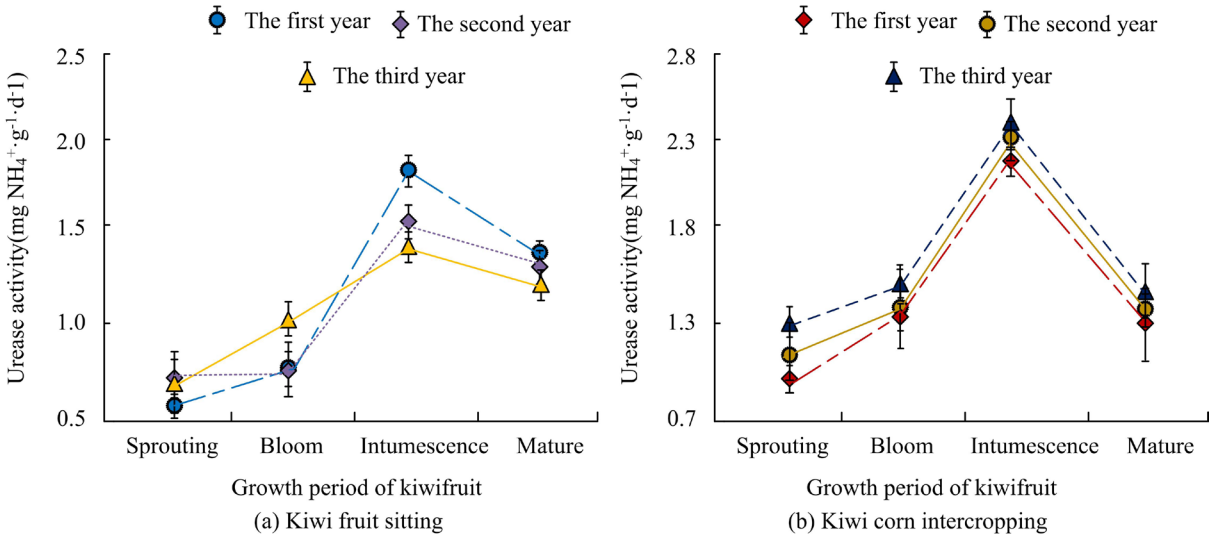

Figure 3. Comparison of urease activity in rhizosphere soil of kiwifruit under two planting modes.

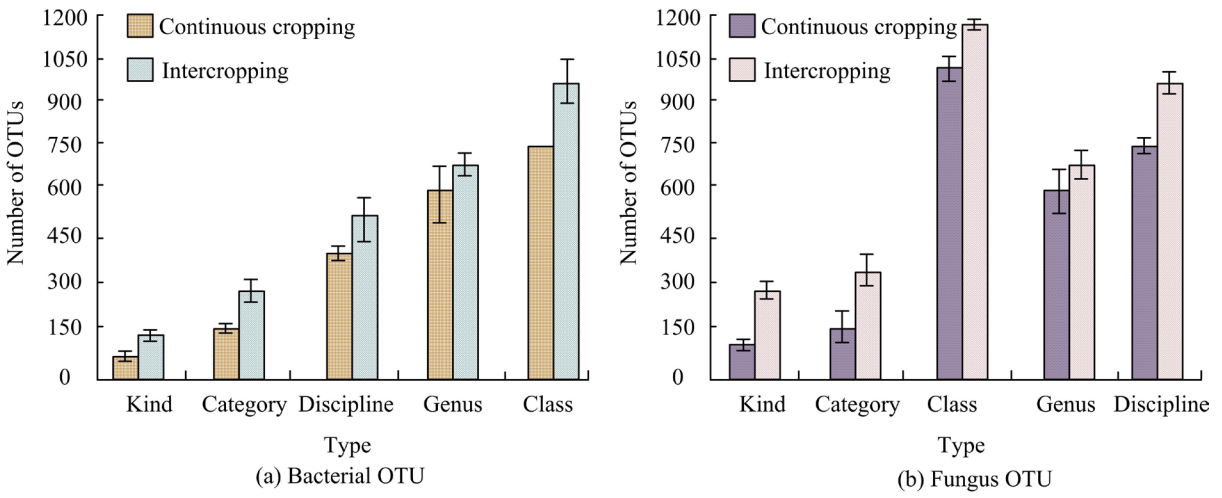

Figure 4. Number of fungal OTUs and bacterial OTUs in two planting modes.

the comparison of fungal OTU counts. In Figure 4(a), the bacterial OTU numbers under kiwifruit continuous cropping were lower than those of the kiwifruit-maize intercropping model in terms of bacterial phyla, orders, families and genera, and the largest difference in terms of species from the adjusted cropping model was around 300. The number of fungal OTUs was still lower in the kiwifruit-pick intercrop than in the kiwifruit-maize intercrop, and the latter had a maximum of 1200 OTUs in terms of fungal species in Figure 4(b).

Simpson's diversity index, Shannon's index and the number of species were analysed and the outcomes obtained are in Figure 5. In Figure 5, A represents the kiwifruit continuous cropping pattern and B represents the kiwifruit-maize intercropping pattern. In Figure 5, the kiwifruit-maize intercropping pattern was not significantly different from the kiwifruit continuous cropping pattern in terms of five indices: Chao1 index, ACE index, Simpson diversity index, Shannon index and the number of species, but only in terms of evolutionary diversity index ($p < 0.05$).

The fungal Alpha diversity index was then analysed and the outcomes are in Figure 6. Figure 6 demonstrates the outcomes of the Alpha diversity index of soil inter-rhizosphere fungi for the adjusted kiwifruit cropping pattern compared to the kiwifruit continuous cropping method. In Figure 6, the Simpson diversity index, Shannon index, and evolutionary diversity index were not significantly different between the two cropping patterns compared to each other ($p > 0.05$), and there were significant differences ($p < 0.05$) in the three indices of Chao1 index, ACE index, and the number of species.

NMDS analysis was then applied to the inter-rooted soil bacterial community in different years under both models and the outcomes are in Figure 7. The arrows in Figure 7 represent the factors that had a significant effect on the bacterial community, the dashed ellipse represents the confidence interval based on the standard deviation of the community in the kiwifruit-maize intercropping model, and the solid ellipse is the confidence interval in the kiwifruit continuous crop model. From Figure 7, the confidence intervals for the kiwifruit intercropping pattern are closer together for the bacterial communities in years 1, 2, and 3 of planting, indicating a high degree of similarity between the bacterial communities in the three years of planting in this pattern. Confidence intervals for years 1 and 2 of planting under the adjusted cropping pattern had a greater partial overlap with the confidence intervals for year 3. This indicates that AK and AN content and year had a highly significant effect on bacterial community structure, and also verifies that other inter-root soil physicochemical properties did not have a significant effect on bacterial community structure.

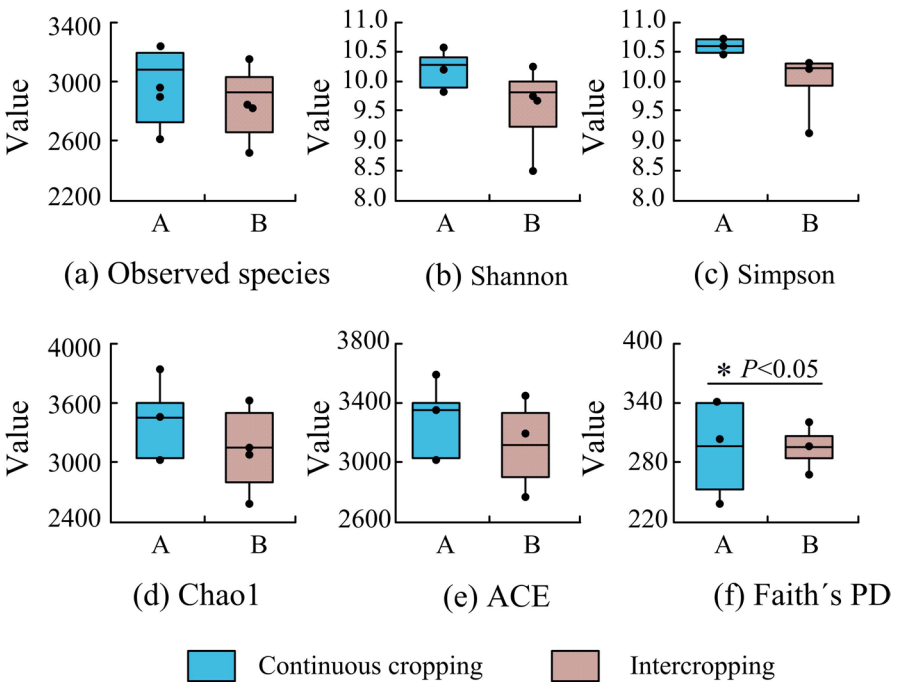

Figure 5. Alpha Diversity Index Analysis outcomes of Rhesus Monkey Rhizosphere Soil Samples.

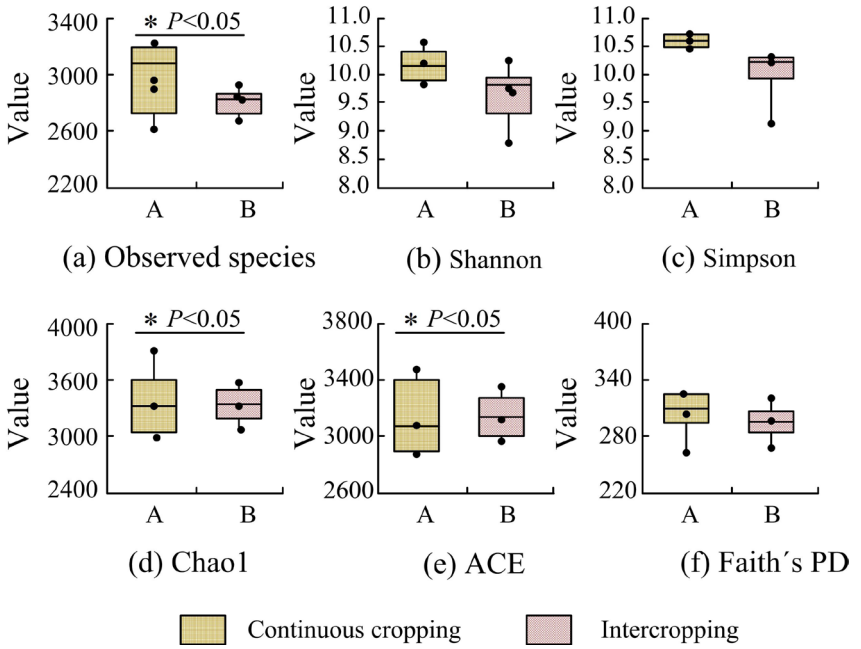

Figure 6. Alpha diversity index outcomes of fungi in rhizosphere soil of macaque under different planting patterns.

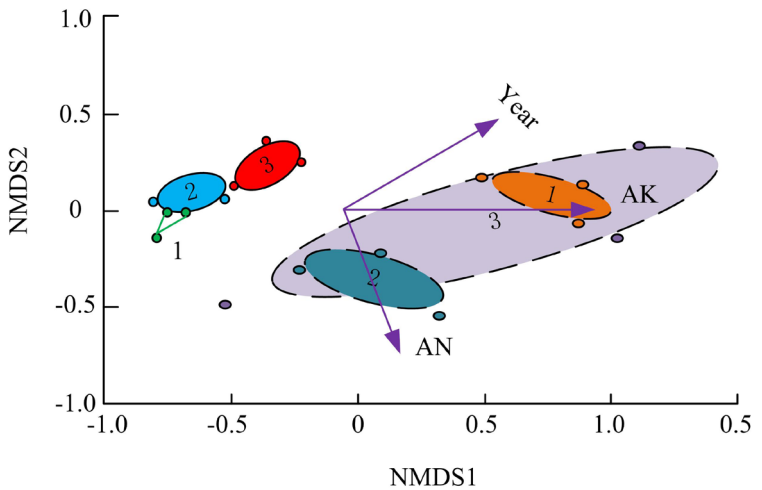

Figure 7. NMDS analysis outcomes of the bacterial community in rhizosphere soil in different years under the two models.

3.4. Comparison results of kiwi fruit quality under planting pattern adjustment

Fruit quality was compared between the two cropping patterns and the outcomes obtained are in Table 3. Table 3 compares total sugars, total acids, vitamin C, soluble protein, chlorophyll, and soluble solids in fruit quality. It can be found that there is no significant difference ($p > 0.05$) in chlorophyll and total acid in the comparison of fruit quality between the two models. The differences in the other two indicators were significant ($p < 0.05$), indicating that the kiwifruit-maize intercropping model was able to improve the fruit quality of kiwifruit in general.

4. Conclusion

In kiwifruit, the physical and chemical properties of the inter-root soil are altered under long-term continuous cropping, with a gradual decline in bacterial diversity and

Table 3. Comparison of fruit quality between two planting patterns.

Planting mode	Kiwifruit continuous cropping	Kiwifruit maize intercropping	T	p
Total sugar (%)	5.52 ± 0.07	6.77 ± 0.05	82.20	0.00
Vitamin C (mg/100g)	103.24 ± 1.39	110.68 ± 1.62	19.72	0.00
Total acid (%)	1.47 ± 0.03	1.46 ± 0.02	1.57	0.12
Chlorophyll (mg/100g)	3.92 ± 0.13	3.98 ± 0.16	1.65	0.10
Soluble solids (%)	7.06 ± 0.87	8.31 ± 0.16	7.99	0.00
Soluble protein (mg/g)	0.26 ± 0.01	0.28 ± 0.02	5.06	0.00

abundance, and an increased incidence of common soil-borne diseases, severely limiting the quality of the planting. The study investigated the effect of intercropping kiwifruit with maize on inter-rhizosphere microbial growth and fruit quality by adjusting the kiwifruit cropping pattern to compare with continuous cropping. The outcomes demonstrated that the kiwifruit-maize intercropping model was superior to the continuous crop model in terms of soil physicochemical properties such as fast-acting phosphorus (AP) and total phosphorus (TP). In the comparison of microbial species and numbers, the adjusted cropping pattern differed by up to 300 compared to preadjustment and the number of OTUs of fungal species was up to 1200. in the analysis of the bacterial Alpha diversity index, the kiwifruit-corn intercrop differed significantly ($p < 0.05$) from preadjustment only in terms of the evolutionary diversity index. In the comparison of fruit quality, the adjusted model demonstrated a significant increase in all indicators except chlorophyll and total acid, with significant differences ($p < 0.05$), indicating that the adjustment of this cropping model was effective in improving the growth of kiwifruit inter-root soil microorganisms and significantly improving their fruit quality. However, the study did not consider the disturbance of inter-rooted soil microorganisms by factors such as nitrogen fertilizer application, so the effect of different fertilizers in this regard needs to be further explored.

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