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Research Article

Differences in Rhizosphere Microbial Community Structure and Composition in Resistance and Susceptible Wheat to Fusarium Head Blight

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Fusarium head blight (FHB) is a serious disease of wheat that threatens wheat production worldwide. In this study, high-throughput sequencing technology was used to analyze the rhizosphere soil microbial metagenomes of 4 wheat cultivars with different levels of resistance to FHB. The results showed that there were differences in the diversity, structure, and composition of rhizosphere microorganisms between resistant and sensitive varieties. The rhizosphere soil bacterial diversity of the resistant wheat varieties Su Mai 3 and Yang Mai 16 was higher than that of the susceptible wheat varieties Zheng Mai 9023 and Zhou Mai 20. The diversity of rhizosphere fungi in resistant varieties was lower than that in susceptible varieties, but the abundance was higher than that in susceptible varieties. Variety was found to alter the community structure of wheat rhizosphere microorganisms. Resistant varieties SM3 and YM16 and moderately susceptible variety ZM9023 had similar microbial community structure, while highly susceptible variety ZM20 was significantly different from other varieties. The study is aimed at analyzing the effects of wheat varieties of different resistance to FHB on the composition and abundance of rhizosphere soil microbial community to screen out bacteria or fungi that can be used to control FHB, providing the theoretical basis for FHB biological control.

1. Introduction

Bread wheat (*Triticum aestivum* L.) is one of the most significant crops, and its global production ranks the third followed by corn and rice [1]. Wheat diseases are a key factor affecting the quality and yield of wheat, and the occurrence of wheat diseases results in severe losses [2]. FHB is a fungal disease caused by various *Fusarium* species, such as *Fusarium graminearum*, *F. culmorum*, and *F. moniliforme*. The different geographical distribution and climatic environment result in dominant species variation. For example, *F. graminearum*, *F. culmorum*, *F. poae*, and *F. avenaceum* are the most important dominant species in Europe [3, 4], while the main pathogenic species is only *F. graminearum* in China [5]. Infected wheat

grains were contaminated by the fungal toxin produced by *F. graminearum*, which can chronically remain in food chain. The contaminated food is dangerous to animals and humans and can even cause death [6–8].

At present, chemical control has been regarded as the significant measures to control FHB in China. The long-term use of pesticides not only enhances the resistance of the pathogenic microorganisms but also pollutes the environment [7]. Now, scientists focus on the cooperation with microbial populations in plant rhizosphere and the relative relationship applying to agricultural systems [9–11].

The soil is an essential material for plant survival. Besides, the soil microbial community has a direct impact on plant growth and development [12, 13]. There are significant differences between the community structure of different plants varieties and microorganisms. Both individual strains of bacteria and the rhizosphere soil microorganism community play important roles in plant health [14, 15]. Plant rhizosphere with a rich microbial diversity exhibits dynamic interactions [16]. The microbiome is an extended genome or secondary genome, including bacteria, fungi, viruses, protozoa, and archaea [17, 18]. Isolation of wheat rhizosphere soil can yield rhizosphere microorganisms. Beneficial rhizosphere microorganisms not only enhance host resistance but also synthesizes hormones that benefit plant growth and promote plant metabolism [19, 20]. Zhao et al. found that plant endophytes are correlated with rhizosphere microorganisms to some extent through exploring the bacterial community structure between root endophytes and rhizosphere soil on the traditional rice (*Oryza sativa*) variety "Yuelianggu" in the Yuanyang terraces [21, 22]. Li et al. have examined the impact of rhizosphere soil microorganism diversity on resistant cotton Verticillium wilt, which shows that the dominant rhizosphere fungal species of disease-resistant was significantly stronger than that of disease-susceptible in control cotton Verticillium wilt fungus. Furthermore, they found that rhizosphere beneficial microorganisms could regulate the composition of the rhizosphere soil microorganism community, which is likely to control effectively cotton Verticillium wilt [23]. The correlation between rhizosphere soil microorganism diversity differences and resistance disease could be explored through the diversity analysis on rhizosphere soil microorganism communities of different disease-resistant varieties on metabolic functions and structures [24].

With the development of molecular biology and bioinformatics, the plant microbiome has enhanced potentially agricultural production, which is expected to meet future food demand worldwide [20, 25]. In this study, the rhizosphere microbiomes of different FHB resistant in wheat varieties were analyzed to elucidate the differences in rhizosphere soil microbial diversity. This study provides the theoretical basis for green prevention and control of FHB.

2. Materials and Methods

2.1. Experimental Materials. The seeds of the test wheat are retained in our laboratory. Wheat varieties included the high-resistant variety of FHB "Su Mai 3" (SM3), the medium-resistant variety "Yang Mai 16" (YM16), the medium-susceptible variety "Zheng Mai 9023" (ZM9023), and the high-susceptible variety "Zhou Mai 20" (ZM20). In the wheat seedling stage, the fertilizer, water, pests, diseases, and weed should be managed strictly according to the technical requirements of local agricultural production. Five-point sampling method was used to sample wheat at heading stage and flowering stage. In order to reduce the test error caused by environmental factors, different wheat varieties were planted in plot. The samples in this study were collected from the experimental plots of continuous cropping.

2.2. Sample Collection. The samples in the present study were collected in Jingzhou District, Jingzhou City, Hubei Province, located in the Jianghan Plain with annual average temperature at 15.9-16.6°C, annual frost-free period of 242-263 days, and annual average precipitation at 904-1127 mm. The experiment was carried out in the experimental field of Jingzhou high and new technology industrial development zone in Jingzhou District, Jingzhou City (longitude: 112.121781, latitude: 30.355227, and altitude: 37 m).

The samples were taken by digging up an intact wheat plant and gently shaking the plant with soil to dislodge it completely. The soil sample that fell off was regarded as the nonrhizosphere soil, and the soil sample that adhered to the plant root systems was regarded as the rhizosphere soil [26]. To maintain the integrity of the root systems, first the soil of wheat roots was dug at least 15 cm, and interrhizosphere soil with about 500 g was collected from each plot. Then, the soil was sieved by a 20 mesh screens, subsequently placed in sterile bags and numbered, and finally stored at -80°C.

2.3. DNA Extraction and Amplicon Generation. Wheat rhizosphere soil DNA was extracted using DNeasy PowerMax Soil Kit (QIAGEN) according to the manufacturer's instructions. The quality and quantity of extracted DNA were checked on 1% agarose gel stained with ethidium bromide. The diluted soil genomic DNA was used as template for PCR amplification using the following primers. For fungi, ITS1 region primers were used: F (ITS1): 5′-CTTGGTCAT TTAGAGGAAGTAA-3′ [27] and R (ITS4): 5′-GCTGCG TTCTTCATCGATGC-3′ [28]. Bacteria were amplified using universal primers 27F: 5′-ACTCCTACGGGAGGCAGCA-3′ and 1492R: 5′-GGACTACHVGGGTWTCTAAT-3′ [29] to amplify the V3-V4 region of 16S rRNA. The PCR amplifications for each sample were conducted in a 50 μl reaction system that contains 5.0 μl 10× PCR buffer, 1.0 μl dNTPs, 0.5 μl (10 μM) of each forward and reverse primer, 0.5 μl DNA polymerase, 1 μl template DNA, and 42.5 μl ddH_2O. The PCR program consists of the following: 94°C, 5 min, followed by 35 cycles (94°C, 30 s; 55°C, 30 s; and 72°C. 1 min) and by a final extension step at 72°C, 5 min. The PCR products were verified by agarose gel electrophoresis, and the target bands were purified using EasyPure® Quick Gel Extraction Kit (TransGen Biotech, China). The PCR-amplified products from each sample were quantified and homogenized, and a paired-end

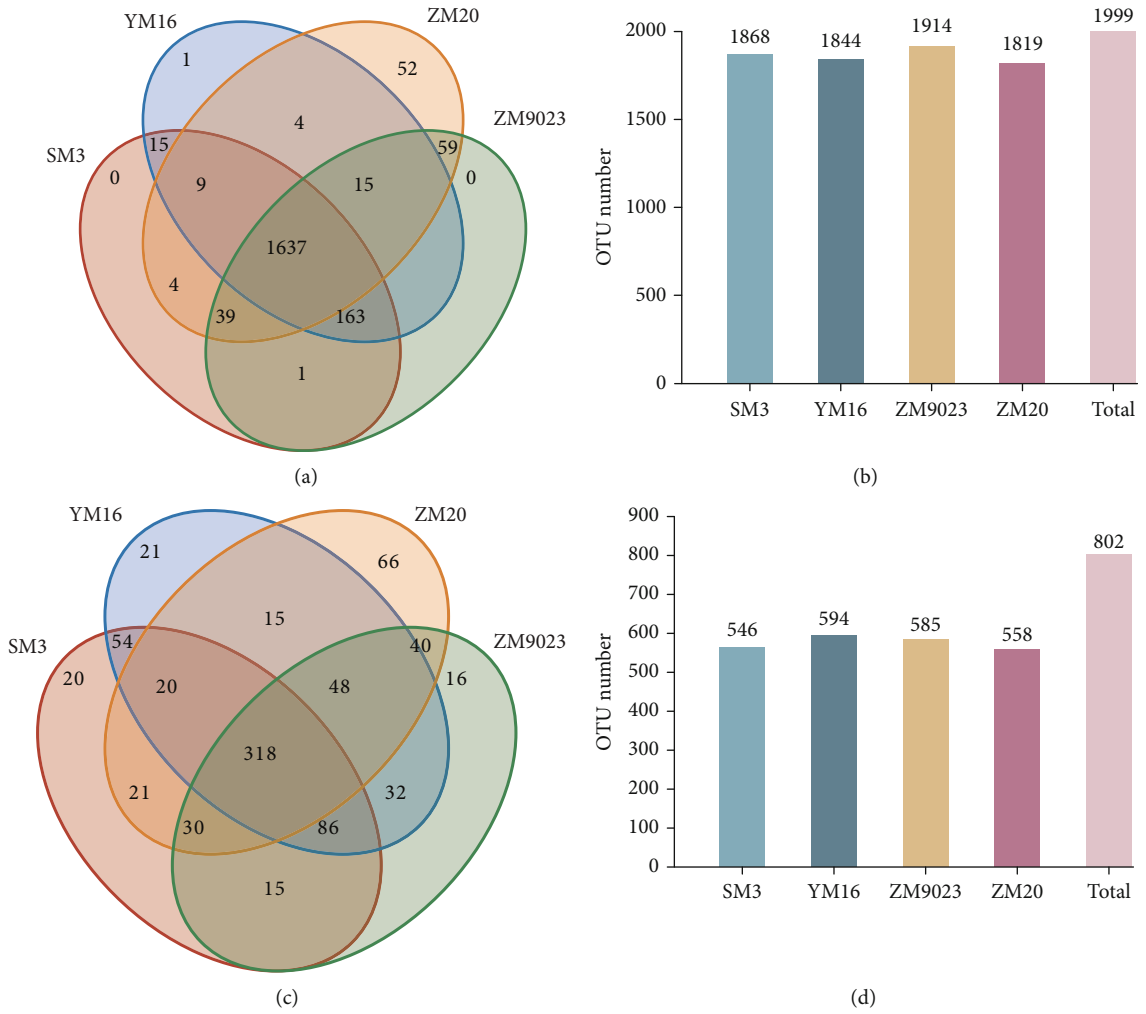


Figure 1: Veen and OTU analysis of different resistant wheat varieties: (a, b) bacteria; (c, d) fungi.

sequencing library was constructed and sequenced using the Illumina HiSeq platform of Biomarker (Beijing, China).

2.4. Statistical Analysis. Sequences were clustered at 97% similarity level using QIIME (version 1.8.0) software. The obtained OTUs were taxonomically annotated based on Silva (bacteria) and UNITE (fungi) taxonomic databases (https://ngdc.cncb.ac.cn/databasecommons/database/id/4075). All data was analyzed using a one-way ANOVA at the $P < 0.05$ level for significance of differences. According to the distribution of OTU in different samples, mothur software (version v.1.30) was used to calculate the α-diversity index values of each sample at 97% similarity level. It includes the Chao1 index, Shannon index, Simpson index, and ACE index. For β-diversity, QIIME 1.9.1 software was used to calculate the diversity distance matrix, and the sample community distance matrix was used to analyze the similarity and difference of microbial community structure of different samples.

3. Results and Discussion

The effects of different FHB-resistant varieties on rhizosphere soil microorganisms were elucidated through sampling analysis of experimental fields. In this study, we explored the effects of different wheat varieties with resistance and susceptibility to FHB on the diversity, structure, and function of rhizosphere soil microbial population by high-throughput sequencing.

3.1. Sequencing Quality Evaluation. A total of 1,099,541 pairs of reads were obtained from 12 bacterial samples, and a total of 1,020,929 clean tags were generated by splicing and filtering of double-ended reads. Each sample included at least 62,894 clean tags, with an average of 85,077 clean tags. Tags were clustered at a 97% similarity level, and 1999 and 802 OTUs were obtained from bacteria and fungi, respectively (Figures 1(b) and 1(d)). There were 1637 OTUs shared by the bacteria of four varieties wheat, 1824 OTUs shared by SM3 and YM16, and 1750 OTUs shared by ZM9023 and ZM20. There are only 1 unique OTU in YM3, 52 unique OTU in ZM20, and no unique OTU in SM3 and ZM9023 (Figure 1(a)).

A total of 543,495 pairs of reads were obtained from 12 bacterial and fungi samples of four wheat varieties, each with three biological replicates. A total of 469,498 clean tags were generated by quality control and double-end splicing. Each

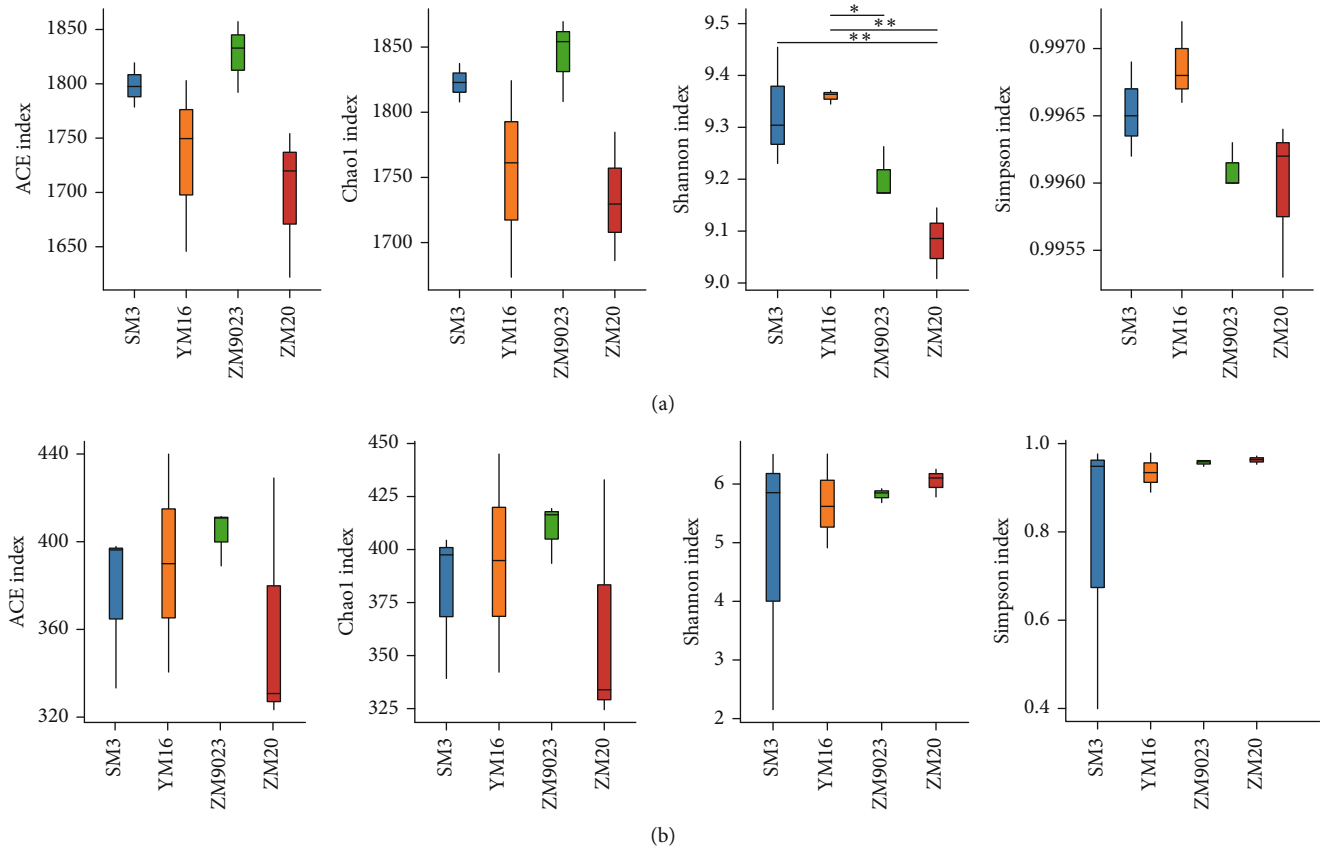
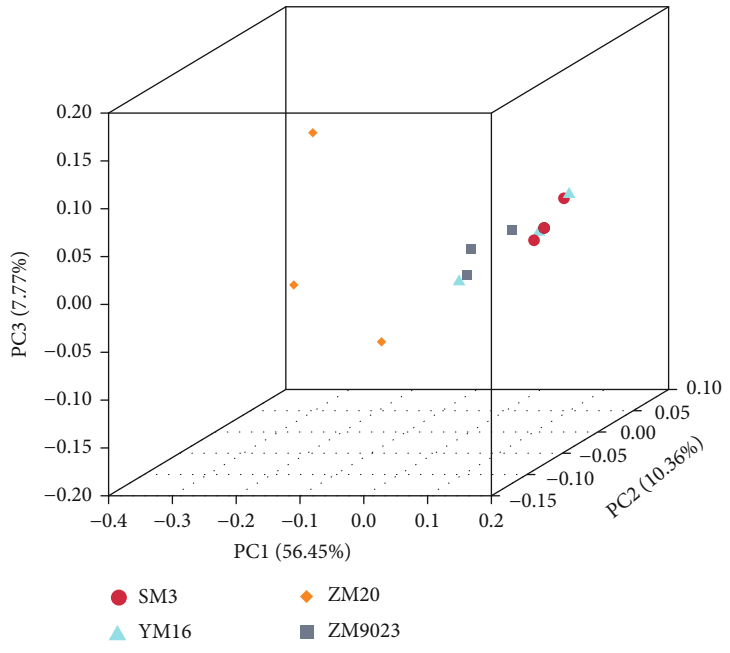


Figure 2: The α-diversity analysis on bacterial (a) and fungal (b) in four wheat varieties. $^{*}P < 0.05$; $^{**}P < 0.01$.

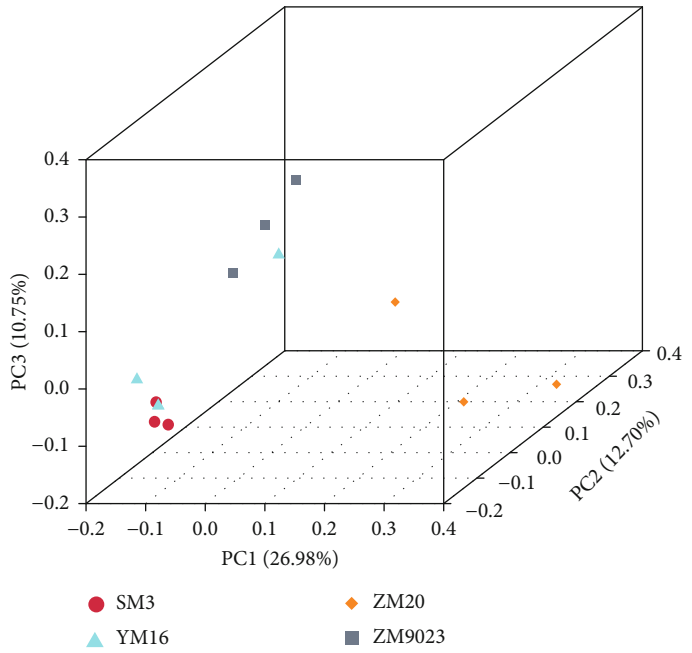
sample included at least 29,408 clean tags, with an average of 39,125 clean tags. The fungus has a total of 802 OTUs. We found that the four varieties share 318 OTUs, 1824 common OTUs in the two FHB-resistant varieties SM3 and YM16 and 436 common OTUs in the susceptible varieties ZM9023 and ZM20. SM3, YM16, ZM9023, and ZM20 have 20, 21, 16, and 66 unique OTUs, respectively (Figure 1(c)). The quality assessment of sequencing data is shown in Supplement Table 1 and 2.

3.2. The Bacterial Diversity of Resistant Varieties Was Higher than That of Susceptible Varieties, and the Fungal Diversity Was Lower than That of Susceptible Varieties. The species diversity and abundance of different wheat varieties with rhizosphere microorganisms were assessed using the ACE index, Chao1 index, Shannon index, and Simpson index. Bacterial ACE index and Chao1 index presented ZM9023 > SM3 > YM16 > ZM20, but there was no significant difference ($P_{ACE} = 0.077$, $P_{Chao1} = 0.064$) (Figure 2). The Shannon index presented SM3 > YM16 > ZM9023 > ZM20. Besides, the Shannon index of resistant varieties was significantly higher than that of susceptible varieties ($P_{Shannon} = 0.005$), which was consistent with the results of Li et al. [30]. Wu et al.'s study also showed that the bacterial α-diversity of Chinese wheat yellow mosaic virus- (CWMV-) resistant varieties (FRW) was higher than that of susceptible varieties (FSW) [31]. The Simpson index was YM16 > SM3 > ZM20 > ZM9023, in which there was also no significant difference ($P_{Simpson} = 0.072$). The bacterial diversity of the resistant varieties SM3 and YM16 was higher than that of the susceptible varieties ZM9023 and ZM20. However, the highest bacterial abundance among the four varieties was ZM9023, followed by SM3, YM16, and ZM20 (Figure 2(a)). The fungal α-diversity indices in four varieties are shown in Figure 2(b), with the greatest species diversity in ZM20 and the highest fungal abundance in YM16 ($P_{ACE} = 0.67$, $P_{Chao1} = 0.64$, $P_{Shannon} = 0.67$, and $P_{Simpson} = 0.49$, Figure 2(b)).

3.3. The Microbial Community Structure of the Highly Susceptible Cultivar ZM20 Was Significantly Different from That of the Other Three Cultivars. We conducted PCoA analysis on the bacterial and fungal community structure in the rhizosphere soil of resistant wheat cultivars, and the result showed that both bacterial and fungal communities were primarily clustered by resistant varieties. The resistance varieties SM3 and YM16 and moderately susceptible variety ZM9023 had similar microbial community structure, while the highly susceptible variety ZM20 differed significantly to others (Figures 3(a) and 3(b)). We analyzed different wheat rhizosphere for bacterial and fungal PCoA based on binary-Jaccard algorithm. The samples were closer, and the similarity was greater. As shown in Figure 3, the cumulative contribution of the variance on the first three principal components for soil bacteria and fungi was 74.53% and 50.43%, respectively, while the remaining principal components



(a)



(b)

Figure 3: Continued.

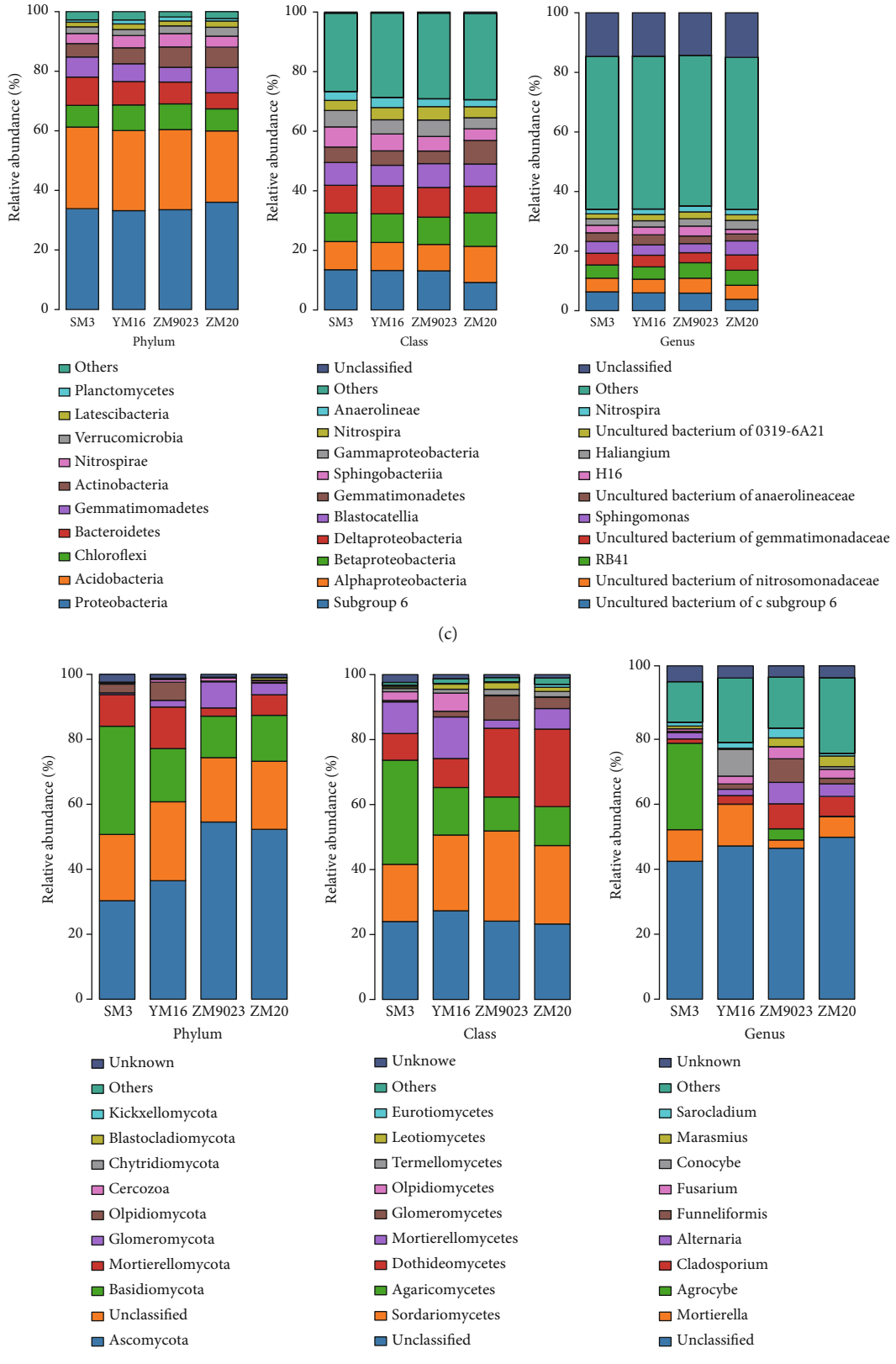


Figure 3: The β-diversity analysis (a, b) on different wheat varieties and species distribution (c, d). PCoA analysis on rhizosphere bacteria (a) and fungi (b) in wheat. Species distributions of four wheat rhizosphere bacteria (c) and fungi (d) are plotted from left to right with the top ten relative abundances at the phylum, class, and genus taxonomic levels.

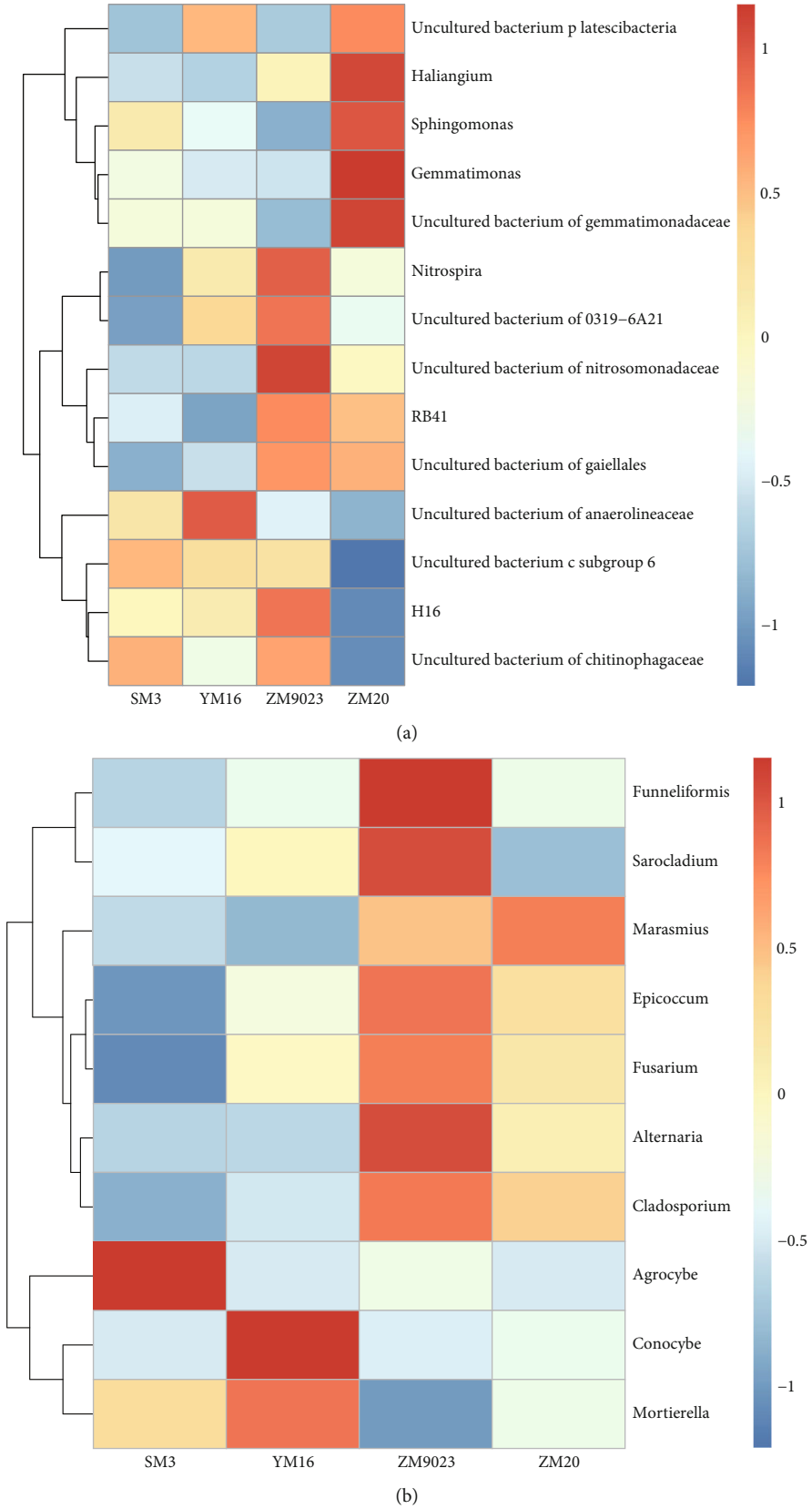


Figure 4: Heat map of species abundance (abundance > 0.05) at the taxonomic level of rhizosphere bacterial (a) and fungal (b) genera in different wheat varieties.

contributed less and were ignored. Therefore, the first three principal components (PC1, PC2, and PC3) were regarded as the main factors exploring the mycota differences. SM3, YM16, and ZM9023 were clustered together; ZM20 were also clustered together. The results showed that SM3, YM16, and ZM9023 had similar community structure, and there were significant differences between them and ZM20 (Figure 3(a)). The PCoA analysis on soil fungal showed that the composition and structure of SM3 and YM16 soil fungi overlapped and their microbial community structure was similar to some degree. Furthermore, PC3 and PC2 were considered the significant factors leading to the difference in fungal communities between ZM9023 and resistant varieties. PC1 and PC3 were considered the key factors causing the difference in fungal communities between ZM20 and resistant varieties (Figure 3(b)). Kopecky et al. found that both resistant and sensitive species had the differences on the diversity, structure, and composition of soil bacterial communities [32–34]. Differences in rhizosphere soil microorganisms of different wheat cultivars may be caused by different plant genotypes, which may affect the composition and abundance of annual plant microbial communities. The study of El Arab et al. showed that under controlled conditions, the population structure of two different genotypes of wheat root soil microorganisms was different [35]. Genotypic effects were also found in soil rhizosphere microbial community composition of different soybean varieties [36]. The composition, diversity, and abundance of bacteria and fungi in the rhizosphere of chickpea with different genotypes were also significantly different [37]. At different stages of potato development, different varieties also affect the abundance of rhizosphere microflora [38].

3.4. Differences in Rhizosphere Soil Microbial Composition of Different Wheat Varieties. Different resistant wheat varieties with top 10 community composition of rhizosphere microorganisms at the phylum, class, and genus taxonomic levels are shown in Figures 3(c) and 3(d). Other species were regarded as others. Unclassified indicated species that did not have taxonomic annotation. The major interrhizosphere bacteria in different wheat varieties were Acidobacteria (27.4%) and Proteobacteria (33.9%), followed by Chloroflexi, Bacteroidetes, Gemmatimonadetes, Actinobacteria, Nitrospirae, Verrucomicrobia, Latescibacteria, and Planctomycetes at the phylum taxonomic level. Proteobacteria play a vital role in plant growth and development, such as in hormone synthesis, ferritin production, dissolved phosphate, and nitrogen fixation [39–41]. Acidobacteria are mainly involved in carbon [42], nitrogen [43], and sulfur [44] circulation in plant metabolism, promoting plant growth and development [45], establishment of biofilms [46, 47], production of extracellular polysaccharides [48], synthesis of secondary metabolites [49–51], and improving plant stress resistance [52–56].

The bacteria top 1 in SM3, YM16, and ZM9023 was subgroup 6, and in high-resistance species, SM3 was Alphaproteobacteria at the phylum taxonomic level. *Proteobacteria* are involved in the biosynthesis of plant hormones and polyamines, phosphate dissolution, and nitrogen fixation [9, 20, 22].

Species in the genus taxonomic level top 10 followed *Nitrosomonadaceae*, *Gemmatimonadaceae*, *Anaerolineaceae*, *Sphingomonas*, *Haliangium*, and *Nitrospira*, but most of them were nonculturable bacteria (Figure 3(c)). The enrichment of *Nitrosomonadaceae*, the restoration of the rhizosphere environment [57], and the nitrification and use of soil micronutrient by plants [58, 59] are discussed of Lovley et al.

High-resistant varieties with microbial abundance were less than that of other varieties, while high-susceptible varieties ZM20 uncultured bacterium *Latescibacteria* and uncultured bacterium of *Gemmatimonadaceae*, *Haliangium*, *Sphingomonas*, and *Gemmatimonas* were higher than other varieties (Figure 4(a)).

The top 10 of the phylum fungi were Basidiomycota, Ascomycota, Mortierellomycota, Glomeromycota, Olpidiomycota, Cercozoa, *Chytridiomycota*, Kickxellomycota, and Blastocladiomycota. Sordariomycetes dominated in the phylum taxonomic level. Ascomycota shows positive effects on facilitating plants nitrogen assimilation and participating in the decomposition of plant residues [60]. Basidiomycota also rapidly metabolizes organic substrates in the rhizosphere soil, and its abundance is affected by the degradation of plant residues [61].

Agaricomycetes and *Sordariomycetes* dominated in the class interrhizosphere fungi. The biodegradability of *Agaricomycetes* has a profound effect on alleviating soil organic compound pollution [62].

The dominant genus in the high-resistant species SM3 was *Agrocybe* (26.6%) (Figure 3(d)). In addition, the microbial abundance of SM3 and ZM20 was relatively low (Figure 4(b)).

4. Conclusions

The α-diversity analysis showed that the bacterial diversity of resistant varieties was higher than that of susceptible varieties. The highest abundance of moderately susceptible varieties was ZM9023, followed by SM3 and YM16. The lowest abundance of highly susceptible varieties was ZM20. The Shannon index of rhizosphere bacteria in resistant varieties was significantly higher than that in susceptible varieties. The rhizosphere fungal diversity in resistant varieties was lower than that in susceptible varieties, but their abundance was higher than that in susceptible varieties (Figure 2(b)). We analyzed the differences of rhizosphere microorganisms in different wheat varieties via OTU and binary algorithm. The results showed that moderately susceptible varieties SM3, YM16, and ZM9023 had similar microbial community structure, while the highly susceptible variety ZM20 was significantly different to that of moderately susceptible varieties (Figures 4(a) and 4(b)). The principal component analysis (PCoA) on microbial community showed that resistant varieties changed the quantity and composition of wheat rhizosphere with bacterial and fungal communities.

In this study, the differences of rhizosphere microbial communities of different resistant varieties of wheat were analyzed. In the next step, we will isolate and identify the microorganisms in these soils to determine which kind of microorganisms regulate the resistance to FHB in wheat.

Data Availability

Data are available upon request.

Conflicts of Interest

The authors declare no competing interests.

Authors' Contributions

Han Li and Mingshuang Tang contributed equally to this work.

Acknowledgments

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Supplementary Materials

Supplementary 1. Supplement Table 1: quality assessment of fungal diversity sequencing.

Supplementary 2. Supplement Table 2: quality assessment of bacterial diversity sequencing.

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